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(54) Title: COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF PROSTATE CANCER
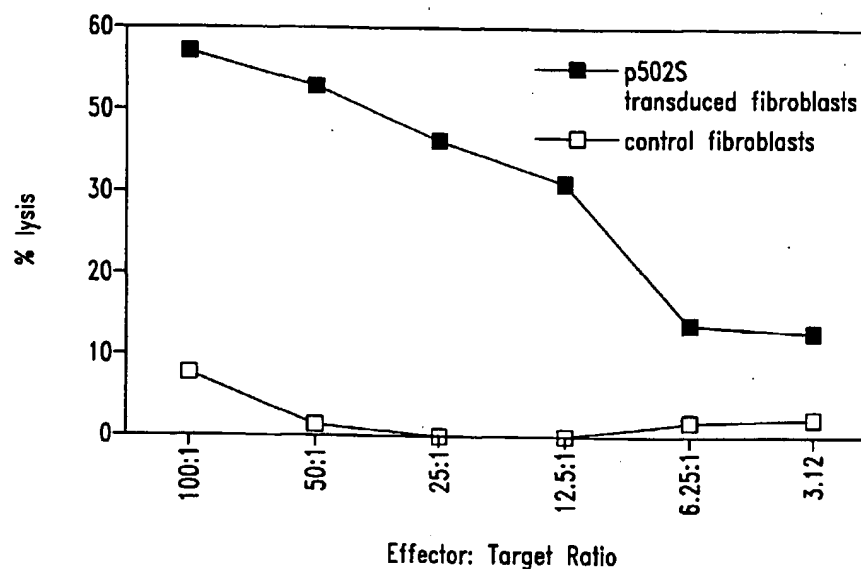
(57) Abstract: Compositions and methods for the therapy and diagnosis of cancer, particularly prostate cancer, are disclosed. Illustrative compositions comprise one or more prostate-specific polypeptides, immunogenic portions thereof, polynucleotides that encode such polypeptides, antigen presenting cell that expresses such polypeptides, and T cells that are specific for cells expressing such polypeptides. The disclosed compositions are useful, for example, in the diagnosis, prevention and/or treatment of diseases, particularly prostate cancer.

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COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF PROSTATE CANCER

TECHNICAL FIELD OF THE INVENTION

The present invention relates generally to therapy and diagnosis of cancer, such as prostate cancer. The invention is more specifically related to polypeptides, comprising at least a portion of a prostate-specific protein, and to polynucleotides encoding such polypeptides. Such polypeptides and polynucleotides are useful in pharmaceutical compositions, *e.g.*, vaccines, and other compositions for the diagnosis and treatment of prostate cancer.

BACKGROUND OF THE INVENTION

Cancer is a significant health problem throughout the world. Although Cancer is a significant health problem throughout the world. Although advances have been made in detection and therapy of cancer, no vaccine or other universally successful method for prevention or treatment is currently available. Current therapies, which are generally based on a combination of chemotherapy or surgery and radiation, continue to prove inadequate in many patients.

Prostate cancer is the most common form of cancer among males, with an estimated incidence of 30% in men over the age of 50. Overwhelming clinical evidence shows that human prostate cancer has the propensity to metastasize to bone, and the disease appears to progress inevitably from androgen dependent to androgen refractory status, leading to increased patient mortality. This prevalent disease is currently the second leading cause of cancer death among men in the U.S.

In spite of considerable research into therapies for the disease, prostate cancer remains difficult to treat. Commonly, treatment is based on surgery and/or radiation therapy, but these methods are ineffective in a significant percentage of cases. Two previously identified prostate specific proteins - prostate specific antigen (PSA) and prostatic acid phosphatase (PAP) - have limited therapeutic and diagnostic potential. For example, PSA levels do not always correlate well with the presence of

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prostate cancer, being positive in a percentage of non-prostate cancer cases, including benign prostatic hyperplasia (BPH). Furthermore, PSA measurements correlate with prostate volume, and do not indicate the level of metastasis.

In spite of considerable research into therapies for these and other cancers, prostate cancer remains difficult to diagnose and treat effectively. Accordingly, there is a need in the art for improved methods for detecting and treating such cancers. The present invention fulfills these needs and further provides other related advantages.

SUMMARY OF THE INVENTION

In one aspect, the present invention provides polynucleotide compositions comprising a sequence selected from the group consisting of:

(a)   sequences provided in SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-705, 709-774, 777, 789, 817, 823, 824, 878, 880-882, 894, 896, 907, 908, 916-919, 929-931, 938, 939 and 942;

(b)   complements of the sequences provided in SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-705, 709-774, 777, 789, 817, 823, 824, 878, 880-882, 894, 896, 907, 908, 916-919, 929-931, 938, 939 and 942;

(c)   sequences consisting of at least 20 contiguous residues of a sequence provided in SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-705, 709-774, 777, 789, 817, 823, 824, 878, 880-882, 894, 896, 907, 908, 916-919, 929-931, 938, 939 and 942;

(d)   sequences that hybridize to a sequence provided in SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-

3

606, 618-705, 709-774, 777, 789, 817, 823, 824, 878, 880-882, 894, 896, 907, 908, 916-919, 929-931, 938, 939 and 942, under moderately stringent conditions;

(e)   sequences having at least 75% identity to a sequence of SEQ ID
NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-
5   375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591,
593-606, 618-705, 709-774, 777, 789, 817, 823, 824, 878, 880-882, 894, 896, 907, 908,
916-919, 929-931, 938, 939 and 942;

(f)   sequences having at least 90% identity to a sequence of SEQ ID
NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-
10   375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591,
593-606, 618-705, 709-774, 777, 789, 817, 823, 824, 878, 880-882, 894, 896, 907, 908,
916-919, 929-931, 938, 939 and 942; and

(g)   degenerate variants of a sequence provided in SEQ ID NO: 1-
111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381,
15   382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606,
618-705, 709-774, 777, 789, 817, 823, 824, 878, 880-882, 894, 896, 907, 908, 916-919,
929-931, 938, 939 and 942.

In one preferred embodiment, the polynucleotide compositions of the
invention are expressed in at least about 20%, more preferably in at least about 30%,
20   and most preferably in at least about 50% of prostate tissue samples tested, at a level
that is at least about 2-fold, preferably at least about 5-fold, and most preferably at least
about 10-fold higher than that for other normal tissues.

The present invention, in another aspect, provides polypeptide
compositions comprising an amino acid sequence that is encoded by a polynucleotide
25   sequence described above.

The present invention further provides polypeptide compositions
comprising an amino acid sequence selected from the group consisting of sequences
recited in SEQ ID NO: 112-114, 172, 176, 178, 327, 329, 331, 336, 339, 376-380, 383,
477-483, 496, 504, 505, 519, 520, 522, 525, 527, 532, 534, 537-551, 553-568, 573-586,
30   588-590, 592, 706-708, 775, 776, 778, 780, 781, 811, 814, 818, 826, 827, 853, 855,

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858, 860-862, 866-877, 879, 883-893, 895, 897, 898, 909-915, 920-928, 932-934, 940, 941 and 943.

In certain preferred embodiments, the polypeptides and/or polynucleotides of the present invention are immunogenic, *i.e.*, they are capable of
5 eliciting an immune response, particularly a humoral and/or cellular immune response, as further described herein.

The present invention further provides fragments, variants and/or derivatives of the disclosed polypeptide and/or polynucleotide sequences, wherein the fragments, variants and/or derivatives preferably have a level of immunogenic activity
10 of at least about 50%, preferably at least about 70% and more preferably at least about 90% of the level of immunogenic activity of a polypeptide sequence set forth in SEQ ID NO: 112-114, 172, 176, 178, 327, 329, 331, 336, 339, 376-380, 383, 477-483, 496, 504, 505, 519, 520, 522, 525, 527, 532, 534, 537-551, 553-568, 573-586, 588-590, 592, 706-708, 775, 776, 778, 780, 781, 811, 814, 818, 826, 827, 853, 855, 858 or 860-862, or a
15 polypeptide sequence encoded by a polynucleotide sequence set forth in SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-705, 709-774, 777, 789, 817, 823, 824, 878, 880-882, 894, 896, 907, 908, 916-919, 929-931, 938, 939 and 942.

20 The present invention further provides polynucleotides that encode a polypeptide described above, expression vectors comprising such polynucleotides and host cells transformed or transfected with such expression vectors.

Within other aspects, the present invention provides pharmaceutical compositions comprising a polypeptide or polynucleotide as described above and a
25 physiologically acceptable carrier.

Within a related aspect of the present invention, pharmaceutical compositions, *e.g.*, vaccine compositions, are provided for prophylactic or therapeutic applications. Such compositions generally comprise an immunogenic polypeptide or polynucleotide of the invention and an immunostimulant, such as an adjuvant, together
30 with a physiologically acceptable carrier.

5

The present invention further provides pharmaceutical compositions that comprise: (a) an antibody or antigen-binding fragment thereof that specifically binds to a polypeptide of the present invention, or a fragment thereof; and (b) a physiologically acceptable carrier.

5   Within further aspects, the present invention provides pharmaceutical compositions comprising: (a) an antigen presenting cell that expresses a polypeptide as described above and (b) a pharmaceutically acceptable carrier or excipient. Illustrative antigen presenting cells include dendritic cells, macrophages, monocytes, fibroblasts and B cells.

10   Within related aspects, pharmaceutical compositions are provided that comprise: (a) an antigen presenting cell that expresses a polypeptide as described above and (b) an immunostimulant.

The present invention further provides, in other aspects, fusion proteins that comprise at least one polypeptide as described above, as well as polynucleotides

15 encoding such fusion proteins, typically in the form of pharmaceutical compositions, *e.g.*, vaccine compositions, comprising a physiologically acceptable carrier and/or an immunostimulant. The fusions proteins may comprise multiple immunogenic polypeptides or portions/variants thereof, as described herein, and may further comprise one or more polypeptide segments for facilitating and/or enhancing the expression,

20 purification and/or immunogenicity of the polypeptide(s).

Within further aspects, the present invention provides methods for stimulating an immune response in a patient, preferably a T cell response in a human patient, comprising administering a pharmaceutical composition described herein. The patient may be afflicted with prostate cancer, in which case the methods provide

25 treatment for the disease, or a patient considered to be at risk for such a disease may be treated prophylactically.

Within further aspects, the present invention provides methods for inhibiting the development of a cancer in a patient, comprising administering to a patient a pharmaceutical composition as recited above. The patient may be afflicted

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with prostate cancer, in which case the methods provide treatment for the disease, or a patient considered to be at risk for such a disease may be treated prophylactically.

The present invention further provides, within other aspects, methods for removing tumor cells from a biological sample, comprising contacting a biological sample with T cells that specifically react with a polypeptide of the present invention, wherein the step of contacting is performed under conditions and for a time sufficient to permit the removal of cells expressing the polypeptide from the sample.

Within related aspects, methods are provided for inhibiting the development of a cancer in a patient, comprising administering to a patient a biological sample treated as described above.

Methods are further provided, within other aspects, for stimulating and/or expanding T cells specific for a polypeptide of the present invention, comprising contacting T cells with one or more of: (i) a polypeptide as described above; (ii) a polynucleotide encoding such a polypeptide; and (iii) an antigen presenting cell that expresses such a polypeptide; under conditions and for a time sufficient to permit the stimulation and/or expansion of T cells. Isolated T cell populations comprising T cells prepared as described above are also provided.

Within further aspects, the present invention provides methods for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a T cell population as described above.

The present invention further provides methods for inhibiting the development of a cancer in a patient, comprising the steps of: (a) incubating CD4^{+} and/or CD8^{+} T cells isolated from a patient with one or more of: (i) a polypeptide comprising at least an immunogenic portion of polypeptide disclosed herein; (ii) a polynucleotide encoding such a polypeptide; and (iii) an antigen-presenting cell that expressed such a polypeptide; and (b) administering to the patient an effective amount of the proliferated T cells, thereby inhibiting the development of a cancer in the patient. Proliferated cells may, but need not, be cloned prior to administration to the patient.

Within further aspects, the present invention provides methods for determining the presence or absence of a cancer, preferably a prostate cancer, in a

patient comprising: (a) contacting a biological sample obtained from a patient with a binding agent that binds to a polypeptide as recited above; (b) detecting in the sample an amount of polypeptide that binds to the binding agent; and (c) comparing the amount of polypeptide with a predetermined cut-off value, and therefrom determining the presence

5   or absence of a cancer in the patient. Within preferred embodiments, the binding agent is an antibody, more preferably a monoclonal antibody.

The present invention also provides, within other aspects, methods for monitoring the progression of a cancer in a patient. Such methods comprise the steps of: (a) contacting a biological sample obtained from a patient at a first point in time

10   with a binding agent that binds to a polypeptide as recited above; (b) detecting in the sample an amount of polypeptide that binds to the binding agent; (c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and (d) comparing the amount of polypeptide detected in step (c) with the amount detected in step (b), and therefrom monitoring the progression of the cancer in the

15   patient.

The present invention further provides, within other aspects, methods for determining the presence or absence of a cancer in a patient, comprising the steps of: (a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide of the present invention; (b) detecting in the sample a

20   level of a polynucleotide, preferably mRNA, that hybridizes to the oligonucleotide; and (c) comparing the level of polynucleotide that hybridizes to the oligonucleotide with a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient. Within certain embodiments, the amount of mRNA is detected via polymerase chain reaction using, for example, at least one oligonucleotide primer

25   that hybridizes to a polynucleotide of the present invention, or a complement of such a polynucleotide. Within other embodiments, the amount of mRNA is detected using a hybridization technique, employing an oligonucleotide probe that hybridizes to an inventive polynucleotide, or a complement of such a polynucleotide.

In related aspects, methods are provided for monitoring the progression

30   of a cancer in a patient, comprising the steps of: (a) contacting a biological sample

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obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide of the present invention; (b) detecting in the sample an amount of a polynucleotide that hybridizes to the oligonucleotide; (c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and (d) comparing the

5   amount of polynucleotide detected in step (c) with the amount detected in step (b), and therefrom monitoring the progression of the cancer in the patient.

Within further aspects, the present invention provides antibodies, such as monoclonal antibodies, that bind to a polypeptide as described above, as well as diagnostic kits comprising such antibodies. Diagnostic kits comprising one or more

10   oligonucleotide probes or primers as described above are also provided.

These and other aspects of the present invention will become apparent upon reference to the following detailed description and attached drawings. All references disclosed herein are hereby incorporated by reference in their entirety as if each was incorporated individually.

15   BRIEF DESCRIPTION OF THE DRAWINGS AND SEQUENCE IDENTIFIERS

Figure 1 illustrates the ability of T cells to kill fibroblasts expressing the representative prostate-specific polypeptide P502S, as compared to control fibroblasts. The percentage lysis is shown as a series of effector:target ratios, as indicated.

Figures 2A and 2B illustrate the ability of T cells to recognize cells

20   expressing the representative prostate-specific polypeptide P502S. In each case, the number of γ-interferon spots is shown for different numbers of responders. In Figure 2A, data is presented for fibroblasts pulsed with the P2S-12 peptide, as compared to fibroblasts pulsed with a control E75 peptide. In Figure 2B, data is presented for fibroblasts expressing P502S, as compared to fibroblasts expressing HER-2/neu.

25   Figure 3 represents a peptide competition binding assay showing that the P1S#10 peptide, derived from P501S, binds HLA-A2. Peptide P1S#10 inhibits HLA-A2 restricted presentation of fluM58 peptide to CTL clone D150M58 in TNF release bioassay. D150M58 CTL is specific for the HLA-A2 binding influenza matrix peptide fluM58.

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Figure 4 illustrates the ability of T cell lines generated from P1S#10 immunized mice to specifically lyse P1S#10-pulsed Jurkat A2Kb targets and P501S-transduced Jurkat A2Kb targets, as compared to EGFP-transduced Jurkat A2Kb. The percent lysis is shown as a series of effector to target ratios, as indicated.

Figure 5 illustrates the ability of a T cell clone to recognize and specifically lyse Jurkat A2Kb cells expressing the representative prostate-specific polypeptide P501S, thereby demonstrating that the P1S#10 peptide may be a naturally processed epitope of the P501S polypeptide.

Figures 6A and 6B are graphs illustrating the specificity of a CD8$^+$ cell line (3A-1) for a representative prostate-specific antigen (P501S). Figure 6A shows the results of a ^{51}Cr release assay. The percent specific lysis is shown as a series of effector:target ratios, as indicated. Figure 6B shows the production of interferon-gamma by 3A-1 cells stimulated with autologous B-LCL transduced with P501S, at varying effector:target rations as indicated.

Figure 7 is a Western blot showing the expression of P501S in baculovirus.

Figure 8 illustrates the results of epitope mapping studies on P501S.

Figure 9 is a schematic representation of the P501S protein showing the location of transmembrane domains and predicted intracellular and extracellular domains.

Figure 10 is a genomic map showing the location of the prostate genes P775P, P704P, B305D, P712P and P774P within the Cat Eye Syndrome region of chromosome 22q11.2

Figure 11 shows the results of an ELISA assay to determine the specificity of rabbit polyclonal antisera raised against P501S.

Figures 12A(1), 12A(2), 12A(3), and B are the full-length cDNA (SEQ ID NO:777) and predicted amino acid (SEQ ID NO:778) sequences, respectively, for the clone P788P.

SEQ ID NO: 1 is the determined cDNA sequence for F1-13

SEQ ID NO: 2 is the determined 3' cDNA sequence for F1-12

SEQ ID NO: 3 is the determined 5' cDNA sequence for F1-12

SEQ ID NO: 4 is the determined 3' cDNA sequence for F1-16

SEQ ID NO: 5 is the determined 3' cDNA sequence for H1-1

SEQ ID NO: 6 is the determined 3' cDNA sequence for H1-9

5   SEQ ID NO: 7 is the determined 3' cDNA sequence for H1-4

SEQ ID NO: 8 is the determined 3' cDNA sequence for J1-17

SEQ ID NO: 9 is the determined 5' cDNA sequence for J1-17

SEQ ID NO: 10 is the determined 3' cDNA sequence for L1-12

SEQ ID NO: 11 is the determined 5' cDNA sequence for L1-12

10   SEQ ID NO: 12 is the determined 3' cDNA sequence for N1-1862

SEQ ID NO: 13 is the determined 5' cDNA sequence for N1-1862

SEQ ID NO: 14 is the determined 3' cDNA sequence for J1-13

SEQ ID NO: 15 is the determined 5' cDNA sequence for J1-13

SEQ ID NO: 16 is the determined 3' cDNA sequence for J1-19

15   SEQ ID NO: 17 is the determined 5' cDNA sequence for J1-19

SEQ ID NO: 18 is the determined 3' cDNA sequence for J1-25

SEQ ID NO: 19 is the determined 5' cDNA sequence for J1-25

SEQ ID NO: 20 is the determined 5' cDNA sequence for J1-24

SEQ ID NO: 21 is the determined 3' cDNA sequence for J1-24

20   SEQ ID NO: 22 is the determined 5' cDNA sequence for K1-58

SEQ ID NO: 23 is the determined 3' cDNA sequence for K1-58

SEQ ID NO: 24 is the determined 5' cDNA sequence for K1-63

SEQ ID NO: 25 is the determined 3' cDNA sequence for K1-63

SEQ ID NO: 26 is the determined 5' cDNA sequence for L1-4

25   SEQ ID NO: 27 is the determined 3' cDNA sequence for L1-4

SEQ ID NO: 28 is the determined 5' cDNA sequence for L1-14

SEQ ID NO: 29 is the determined 3' cDNA sequence for L1-14

SEQ ID NO: 30 is the determined 3' cDNA sequence for J1-12

SEQ ID NO: 31 is the determined 3' cDNA sequence for J1-16

30   SEQ ID NO: 32 is the determined 3' cDNA sequence for J1-21

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SEQ ID NO: 33 is the determined 3' cDNA sequence for K1-48

SEQ ID NO: 34 is the determined 3' cDNA sequence for K1-55

SEQ ID NO: 35 is the determined 3' cDNA sequence for L1-2

SEQ ID NO: 36 is the determined 3' cDNA sequence for L1-6

5   SEQ ID NO: 37 is the determined 3' cDNA sequence for N1-1858

SEQ ID NO: 38 is the determined 3' cDNA sequence for N1-1860

SEQ ID NO: 39 is the determined 3' cDNA sequence for N1-1861

SEQ ID NO: 40 is the determined 3' cDNA sequence for N1-1864

SEQ ID NO: 41 is the determined cDNA sequence for P5

10   SEQ ID NO: 42 is the determined cDNA sequence for P8

SEQ ID NO: 43 is the determined cDNA sequence for P9

SEQ ID NO: 44 is the determined cDNA sequence for P18

SEQ ID NO: 45 is the determined cDNA sequence for P20

SEQ ID NO: 46 is the determined cDNA sequence for P29

15   SEQ ID NO: 47 is the determined cDNA sequence for P30

SEQ ID NO: 48 is the determined cDNA sequence for P34

SEQ ID NO: 49 is the determined cDNA sequence for P36

SEQ ID NO: 50 is the determined cDNA sequence for P38

SEQ ID NO: 51 is the determined cDNA sequence for P39

20   SEQ ID NO: 52 is the determined cDNA sequence for P42

SEQ ID NO: 53 is the determined cDNA sequence for P47

SEQ ID NO: 54 is the determined cDNA sequence for P49

SEQ ID NO: 55 is the determined cDNA sequence for P50

SEQ ID NO: 56 is the determined cDNA sequence for P53

25   SEQ ID NO: 57 is the determined cDNA sequence for P55

SEQ ID NO: 58 is the determined cDNA sequence for P60

SEQ ID NO: 59 is the determined cDNA sequence for P64

SEQ ID NO: 60 is the determined cDNA sequence for P65

SEQ ID NO: 61 is the determined cDNA sequence for P73

30   SEQ ID NO: 62 is the determined cDNA sequence for P75

12

SEQ ID NO: 63 is the determined cDNA sequence for P76

SEQ ID NO: 64 is the determined cDNA sequence for P79

SEQ ID NO: 65 is the determined cDNA sequence for P84

SEQ ID NO: 66 is the determined cDNA sequence for P68

5   SEQ ID NO: 67 is the determined cDNA sequence for P80 (also referred

to as P704P)

SEQ ID NO: 68 is the determined cDNA sequence for P82

SEQ ID NO: 69 is the determined cDNA sequence for U1-3064

SEQ ID NO: 70 is the determined cDNA sequence for U1-3065

10   SEQ ID NO: 71 is the determined cDNA sequence for V1-3692

SEQ ID NO: 72 is the determined cDNA sequence for 1A-3905

SEQ ID NO: 73 is the determined cDNA sequence for V1-3686

SEQ ID NO: 74 is the determined cDNA sequence for R1-2330

SEQ ID NO: 75 is the determined cDNA sequence for 1B-3976

15   SEQ ID NO: 76 is the determined cDNA sequence for V1-3679

SEQ ID NO: 77 is the determined cDNA sequence for 1G-4736

SEQ ID NO: 78 is the determined cDNA sequence for 1G-4738

SEQ ID NO: 79 is the determined cDNA sequence for 1G-4741

SEQ ID NO: 80 is the determined cDNA sequence for 1G-4744

20   SEQ ID NO: 81 is the determined cDNA sequence for 1G-4734

SEQ ID NO: 82 is the determined cDNA sequence for 1H-4774

SEQ ID NO: 83 is the determined cDNA sequence for 1H-4781

SEQ ID NO: 84 is the determined cDNA sequence for 1H-4785

SEQ ID NO: 85 is the determined cDNA sequence for 1H-4787

25   SEQ ID NO: 86 is the determined cDNA sequence for 1H-4796

SEQ ID NO: 87 is the determined cDNA sequence for 1I-4807

SEQ ID NO: 88 is the determined cDNA sequence for 1I-4810

SEQ ID NO: 89 is the determined cDNA sequence for 1I-4811

SEQ ID NO: 90 is the determined cDNA sequence for 1J-4876

30   SEQ ID NO: 91 is the determined cDNA sequence for 1K-4884

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SEQ ID NO: 92 is the determined cDNA sequence for 1K-4896

SEQ ID NO: 93 is the determined cDNA sequence for 1G-4761

SEQ ID NO: 94 is the determined cDNA sequence for 1G-4762

SEQ ID NO: 95 is the determined cDNA sequence for 1H-4766

5   SEQ ID NO: 96 is the determined cDNA sequence for 1H-4770

SEQ ID NO: 97 is the determined cDNA sequence for 1H-4771

SEQ ID NO: 98 is the determined cDNA sequence for 1H-4772

SEQ ID NO: 99 is the determined cDNA sequence for 1D-4297

SEQ ID NO: 100 is the determined cDNA sequence for 1D-4309

10   SEQ ID NO: 101 is the determined cDNA sequence for 1D.1-4278

SEQ ID NO: 102 is the determined cDNA sequence for 1D-4288

SEQ ID NO: 103 is the determined cDNA sequence for 1D-4283

SEQ ID NO: 104 is the determined cDNA sequence for 1D-4304

SEQ ID NO: 105 is the determined cDNA sequence for 1D-4296

15   SEQ ID NO: 106 is the determined cDNA sequence for 1D-4280

SEQ ID NO: 107 is the determined full length cDNA sequence for F1-12
(also referred to as P504S)

SEQ ID NO: 108 is the predicted amino acid sequence for F1-12

SEQ ID NO: 109 is the determined full length cDNA sequence for J1-17

20   SEQ ID NO: 110 is the determined full length cDNA sequence for L1-12
(also referred to as P501S)

SEQ ID NO: 111 is the determined full length cDNA sequence for N1-
1862 (also referred to as P503S)

SEQ ID NO: 112 is the predicted amino acid sequence for J1-17

25   SEQ ID NO: 113 is the predicted amino acid sequence for L1-12 (also
referred to as P501S)

SEQ ID NO: 114 is the predicted amino acid sequence for N1-1862 (also
referred to as P503S)

SEQ ID NO: 115 is the determined cDNA sequence for P89

30   SEQ ID NO: 116 is the determined cDNA sequence for P90

14

SEQ ID NO: 117 is the determined cDNA sequence for P92

SEQ ID NO: 118 is the determined cDNA sequence for P95

SEQ ID NO: 119 is the determined cDNA sequence for P98

SEQ ID NO: 120 is the determined cDNA sequence for P102

5   SEQ ID NO: 121 is the determined cDNA sequence for P110

SEQ ID NO: 122 is the determined cDNA sequence for P111

SEQ ID NO: 123 is the determined cDNA sequence for P114

SEQ ID NO: 124 is the determined cDNA sequence for P115

SEQ ID NO: 125 is the determined cDNA sequence for P116

10   SEQ ID NO: 126 is the determined cDNA sequence for P124

SEQ ID NO: 127 is the determined cDNA sequence for P126

SEQ ID NO: 128 is the determined cDNA sequence for P130

SEQ ID NO: 129 is the determined cDNA sequence for P133

SEQ ID NO: 130 is the determined cDNA sequence for P138

15   SEQ ID NO: 131 is the determined cDNA sequence for P143

SEQ ID NO: 132 is the determined cDNA sequence for P151

SEQ ID NO: 133 is the determined cDNA sequence for P156

SEQ ID NO: 134 is the determined cDNA sequence for P157

SEQ ID NO: 135 is the determined cDNA sequence for P166

20   SEQ ID NO: 136 is the determined cDNA sequence for P176

SEQ ID NO: 137 is the determined cDNA sequence for P178

SEQ ID NO: 138 is the determined cDNA sequence for P179

SEQ ID NO: 139 is the determined cDNA sequence for P185

SEQ ID NO: 140 is the determined cDNA sequence for P192

25   SEQ ID NO: 141 is the determined cDNA sequence for P201

SEQ ID NO: 142 is the determined cDNA sequence for P204

SEQ ID NO: 143 is the determined cDNA sequence for P208

SEQ ID NO: 144 is the determined cDNA sequence for P211

SEQ ID NO: 145 is the determined cDNA sequence for P213

30   SEQ ID NO: 146 is the determined cDNA sequence for P219

15

SEQ ID NO: 147 is the determined cDNA sequence for P237

SEQ ID NO: 148 is the determined cDNA sequence for P239

SEQ ID NO: 149 is the determined cDNA sequence for P248

SEQ ID NO: 150 is the determined cDNA sequence for P251

5   SEQ ID NO: 151 is the determined cDNA sequence for P255

SEQ ID NO: 152 is the determined cDNA sequence for P256

SEQ ID NO: 153 is the determined cDNA sequence for P259

SEQ ID NO: 154 is the determined cDNA sequence for P260

SEQ ID NO: 155 is the determined cDNA sequence for P263

10   SEQ ID NO: 156 is the determined cDNA sequence for P264

SEQ ID NO: 157 is the determined cDNA sequence for P266

SEQ ID NO: 158 is the determined cDNA sequence for P270

SEQ ID NO: 159 is the determined cDNA sequence for P272

SEQ ID NO: 160 is the determined cDNA sequence for P278

15   SEQ ID NO: 161 is the determined cDNA sequence for P105

SEQ ID NO: 162 is the determined cDNA sequence for P107

SEQ ID NO: 163 is the determined cDNA sequence for P137

SEQ ID NO: 164 is the determined cDNA sequence for P194

SEQ ID NO: 165 is the determined cDNA sequence for P195

20   SEQ ID NO: 166 is the determined cDNA sequence for P196

SEQ ID NO: 167 is the determined cDNA sequence for P220

SEQ ID NO: 168 is the determined cDNA sequence for P234

SEQ ID NO: 169 is the determined cDNA sequence for P235

SEQ ID NO: 170 is the determined cDNA sequence for P243

25   SEQ ID NO: 171 is the determined cDNA sequence for P703P-DE1

SEQ ID NO: 172 is the predicted amino acid sequence for P703P-DE1

SEQ ID NO: 173 is the determined cDNA sequence for P703P-DE2

SEQ ID NO: 174 is the determined cDNA sequence for P703P-DE6

SEQ ID NO: 175 is the determined cDNA sequence for P703P-DE13

30   SEQ ID NO: 176 is the predicted amino acid sequence for P703P-DE13

16

SEQ ID NO: 177 is the determined cDNA sequence for P703P-DE14

SEQ ID NO: 178 is the predicted amino acid sequence for P703P-DE14

SEQ ID NO: 179 is the determined extended cDNA sequence for 1G-4736

5   SEQ ID NO: 180 is the determined extended cDNA sequence for 1G-4738

SEQ ID NO: 181 is the determined extended cDNA sequence for 1G-4741

SEQ ID NO: 182 is the determined extended cDNA sequence for 1G-10 4744

SEQ ID NO: 183 is the determined extended cDNA sequence for 1H-4774

SEQ ID NO: 184 is the determined extended cDNA sequence for 1H-4781

15   SEQ ID NO: 185 is the determined extended cDNA sequence for 1H-4785

SEQ ID NO: 186 is the determined extended cDNA sequence for 1H-4787

SEQ ID NO: 187 is the determined extended cDNA sequence for 1H-20 4796

SEQ ID NO: 188 is the determined extended cDNA sequence for 1I-4807

SEQ ID NO: 189 is the determined 3' cDNA sequence for 1I-4810

SEQ ID NO: 190 is the determined 3' cDNA sequence for 1I-4811

25   SEQ ID NO: 191 is the determined extended cDNA sequence for 1J-4876

SEQ ID NO: 192 is the determined extended cDNA sequence for 1K-4884

SEQ ID NO: 193 is the determined extended cDNA sequence for 1K-30 4896

17

SEQ ID NO: 194 is the determined extended cDNA sequence for 1G-4761

SEQ ID NO: 195 is the determined extended cDNA sequence for 1G-4762

SEQ ID NO: 196 is the determined extended cDNA sequence for 1H-4766

SEQ ID NO: 197 is the determined 3' cDNA sequence for 1H-4770

SEQ ID NO: 198 is the determined 3' cDNA sequence for 1H-4771

SEQ ID NO: 199 is the determined extended cDNA sequence for 1H-4772

SEQ ID NO: 200 is the determined extended cDNA sequence for 1D-4309

SEQ ID NO: 201 is the determined extended cDNA sequence for 1D.1-4278

SEQ ID NO: 202 is the determined extended cDNA sequence for 1D-4288

SEQ ID NO: 203 is the determined extended cDNA sequence for 1D-4283

SEQ ID NO: 204 is the determined extended cDNA sequence for 1D-4304

SEQ ID NO: 205 is the determined extended cDNA sequence for 1D-4296

SEQ ID NO: 206 is the determined extended cDNA sequence for 1D-4280

SEQ ID NO: 207 is the determined cDNA sequence for 10-d8fwd

SEQ ID NO: 208 is the determined cDNA sequence for 10-H10con

SEQ ID NO: 209 is the determined cDNA sequence for 11-C8rev

SEQ ID NO: 210 is the determined cDNA sequence for 7.g6fwd

SEQ ID NO: 211 is the determined cDNA sequence for 7.g6rev

SEQ ID NO: 212 is the determined cDNA sequence for 8-b5fwd

18

SEQ ID NO: 213 is the determined cDNA sequence for 8-b5rev

SEQ ID NO: 214 is the determined cDNA sequence for 8-b6fwd

SEQ ID NO: 215 is the determined cDNA sequence for 8-b6 rev

SEQ ID NO: 216 is the determined cDNA sequence for 8-d4fwd

5   SEQ ID NO: 217 is the determined cDNA sequence for 8-d9rev

SEQ ID NO: 218 is the determined cDNA sequence for 8-g3fwd

SEQ ID NO: 219 is the determined cDNA sequence for 8-g3rev

SEQ ID NO: 220 is the determined cDNA sequence for 8-h11rev

SEQ ID NO: 221 is the determined cDNA sequence for g-f12fwd

10   SEQ ID NO: 222 is the determined cDNA sequence for g-f3rev

SEQ ID NO: 223 is the determined cDNA sequence for P509S

SEQ ID NO: 224 is the determined cDNA sequence for P510S

SEQ ID NO: 225 is the determined cDNA sequence for P703DE5

SEQ ID NO: 226 is the determined cDNA sequence for 9-A11

15   SEQ ID NO: 227 is the determined cDNA sequence for 8-C6

SEQ ID NO: 228 is the determined cDNA sequence for 8-H7

SEQ ID NO: 229 is the determined cDNA sequence for JPTPN13

SEQ ID NO: 230 is the determined cDNA sequence for JPTPN14

SEQ ID NO: 231 is the determined cDNA sequence for JPTPN23

20   SEQ ID NO: 232 is the determined cDNA sequence for JPTPN24

SEQ ID NO: 233 is the determined cDNA sequence for JPTPN25

SEQ ID NO: 234 is the determined cDNA sequence for JPTPN30

SEQ ID NO: 235 is the determined cDNA sequence for JPTPN34

SEQ ID NO: 236 is the determined cDNA sequence for PTPN35

25   SEQ ID NO: 237 is the determined cDNA sequence for JPTPN36

SEQ ID NO: 238 is the determined cDNA sequence for JPTPN38

SEQ ID NO: 239 is the determined cDNA sequence for JPTPN39

SEQ ID NO: 240 is the determined cDNA sequence for JPTPN40

SEQ ID NO: 241 is the determined cDNA sequence for JPTPN41

30   SEQ ID NO: 242 is the determined cDNA sequence for JPTPN42

19

SEQ ID NO: 243 is the determined cDNA sequence for JPTPN45

SEQ ID NO: 244 is the determined cDNA sequence for JPTPN46

SEQ ID NO: 245 is the determined cDNA sequence for JPTPN51

SEQ ID NO: 246 is the determined cDNA sequence for JPTPN56

5   SEQ ID NO: 247 is the determined cDNA sequence for PTPN64

SEQ ID NO: 248 is the determined cDNA sequence for JPTPN65

SEQ ID NO: 249 is the determined cDNA sequence for JPTPN67

SEQ ID NO: 250 is the determined cDNA sequence for JPTPN76

SEQ ID NO: 251 is the determined cDNA sequence for JPTPN84

10   SEQ ID NO: 252 is the determined cDNA sequence for JPTPN85

SEQ ID NO: 253 is the determined cDNA sequence for JPTPN86

SEQ ID NO: 254 is the determined cDNA sequence for JPTPN87

SEQ ID NO: 255 is the determined cDNA sequence for JPTPN88

SEQ ID NO: 256 is the determined cDNA sequence for JP1F1

15   SEQ ID NO: 257 is the determined cDNA sequence for JP1F2

SEQ ID NO: 258 is the determined cDNA sequence for JP1C2

SEQ ID NO: 259 is the determined cDNA sequence for JP1B1

SEQ ID NO: 260 is the determined cDNA sequence for JP1B2

SEQ ID NO: 261 is the determined cDNA sequence for JP1D3

20   SEQ ID NO: 262 is the determined cDNA sequence for JP1A4

SEQ ID NO: 263 is the determined cDNA sequence for JP1F5

SEQ ID NO: 264 is the determined cDNA sequence for JP1E6

SEQ ID NO: 265 is the determined cDNA sequence for JP1D6

SEQ ID NO: 266 is the determined cDNA sequence for JP1B5

25   SEQ ID NO: 267 is the determined cDNA sequence for JP1A6

SEQ ID NO: 268 is the determined cDNA sequence for JP1E8

SEQ ID NO: 269 is the determined cDNA sequence for JP1D7

SEQ ID NO: 270 is the determined cDNA sequence for JP1D9

SEQ ID NO: 271 is the determined cDNA sequence for JP1C10

30   SEQ ID NO: 272 is the determined cDNA sequence for JP1A9

20

SEQ ID NO: 273 is the determined cDNA sequence for JP1F12

SEQ ID NO: 274 is the determined cDNA sequence for JP1E12

SEQ ID NO: 275 is the determined cDNA sequence for JP1D11

SEQ ID NO: 276 is the determined cDNA sequence for JP1C11

5   SEQ ID NO: 277 is the determined cDNA sequence for JP1C12

SEQ ID NO: 278 is the determined cDNA sequence for JP1B12

SEQ ID NO: 279 is the determined cDNA sequence for JP1A12

SEQ ID NO: 280 is the determined cDNA sequence for JP8G2

SEQ ID NO: 281 is the determined cDNA sequence for JP8H1

10   SEQ ID NO: 282 is the determined cDNA sequence for JP8H2

SEQ ID NO: 283 is the determined cDNA sequence for JP8A3

SEQ ID NO: 284 is the determined cDNA sequence for JP8A4

SEQ ID NO: 285 is the determined cDNA sequence for JP8C3

SEQ ID NO: 286 is the determined cDNA sequence for JP8G4

15   SEQ ID NO: 287 is the determined cDNA sequence for JP8B6

SEQ ID NO: 288 is the determined cDNA sequence for JP8D6

SEQ ID NO: 289 is the determined cDNA sequence for JP8F5

SEQ ID NO: 290 is the determined cDNA sequence for JP8A8

SEQ ID NO: 291 is the determined cDNA sequence for JP8C7

20   SEQ ID NO: 292 is the determined cDNA sequence for JP8D7

SEQ ID NO: 293 is the determined cDNA sequence for P8D8

SEQ ID NO: 294 is the determined cDNA sequence for JP8E7

SEQ ID NO: 295 is the determined cDNA sequence for JP8F8

SEQ ID NO: 296 is the determined cDNA sequence for JP8G8

25   SEQ ID NO: 297 is the determined cDNA sequence for JP8B10

SEQ ID NO: 298 is the determined cDNA sequence for JP8C10

SEQ ID NO: 299 is the determined cDNA sequence for JP8E9

SEQ ID NO: 300 is the determined cDNA sequence for JP8E10

SEQ ID NO: 301 is the determined cDNA sequence for JP8F9

30   SEQ ID NO: 302 is the determined cDNA sequence for JP8H9

SEQ ID NO: 303 is the determined cDNA sequence for JP8C12

SEQ ID NO: 304 is the determined cDNA sequence for JP8E11

SEQ ID NO: 305 is the determined cDNA sequence for JP8E12

SEQ ID NO: 306 is the amino acid sequence for the peptide PS2#12

5   SEQ ID NO: 307 is the determined cDNA sequence for P711P

SEQ ID NO: 308 is the determined cDNA sequence for P712P

SEQ ID NO: 309 is the determined cDNA sequence for CLONE23

SEQ ID NO: 310 is the determined cDNA sequence for P774P

SEQ ID NO: 311 is the determined cDNA sequence for P775P

10   SEQ ID NO: 312 is the determined cDNA sequence for P715P

SEQ ID NO: 313 is the determined cDNA sequence for P710P

SEQ ID NO: 314 is the determined cDNA sequence for P767P

SEQ ID NO: 315 is the determined cDNA sequence for P768P

SEQ ID NO: 316-325 are the determined cDNA sequences of previously

15   isolated genes

SEQ ID NO: 326 is the determined cDNA sequence for P703PDE5

SEQ ID NO: 327 is the predicted amino acid sequence for P703PDE5

SEQ ID NO: 328 is the determined cDNA sequence for P703P6.26

SEQ ID NO: 329 is the predicted amino acid sequence for P703P6.26

20   SEQ ID NO: 330 is the determined cDNA sequence for P703PX-23

SEQ ID NO: 331 is the predicted amino acid sequence for P703PX-23

SEQ ID NO: 332 is the determined full length cDNA sequence for

P509S

SEQ ID NO: 333 is the determined extended cDNA sequence for P707P

25   (also referred to as 11-C9)

SEQ ID NO: 334 is the determined cDNA sequence for P714P

SEQ ID NO: 335 is the determined cDNA sequence for P705P (also

referred to as 9-F3)

SEQ ID NO: 336 is the predicted amino acid sequence for P705P

30   SEQ ID NO: 337 is the amino acid sequence of the peptide P1S#10

22

SEQ ID NO: 338 is the amino acid sequence of the peptide p5

SEQ ID NO: 339 is the predicted amino acid sequence of P509S

SEQ ID NO: 340 is the determined cDNA sequence for P778P

SEQ ID NO: 341 is the determined cDNA sequence for P786P

5   SEQ ID NO: 342 is the determined cDNA sequence for P789P

SEQ ID NO: 343 is the determined cDNA sequence for a clone showing
homology to Homo sapiens MM46 mRNA

SEQ ID NO: 344 is the determined cDNA sequence for a clone showing
homology to Homo sapiens TNF-alpha stimulated ABC protein (ABC50) mRNA

10   SEQ ID NO: 345 is the determined cDNA sequence for a clone showing
homology to Homo sapiens mRNA for E-cadherin

SEQ ID NO: 346 is the determined cDNA sequence for a clone showing
homology to Human nuclear-encoded mitochondrial serine hydroxymethyltransferase
(SHMT)

15   SEQ ID NO: 347 is the determined cDNA sequence for a clone showing
homology to Homo sapiens natural resistance-associated macrophage protein2
(NRAMP2)

SEQ ID NO: 348 is the determined cDNA sequence for a clone showing
homology to Homo sapiens phosphoglucomutase-related protein (PGMRP)

20   SEQ ID NO: 349 is the determined cDNA sequence for a clone showing
homology to Human mRNA for proteosome subunit p40

SEQ ID NO: 350 is the determined cDNA sequence for P777P

SEQ ID NO: 351 is the determined cDNA sequence for P779P

SEQ ID NO: 352 is the determined cDNA sequence for P790P

25   SEQ ID NO: 353 is the determined cDNA sequence for P784P

SEQ ID NO: 354 is the determined cDNA sequence for P776P

SEQ ID NO: 355 is the determined cDNA sequence for P780P

SEQ ID NO: 356 is the determined cDNA sequence for P544S

SEQ ID NO: 357 is the determined cDNA sequence for P745S

30   SEQ ID NO: 358 is the determined cDNA sequence for P782P

SEQ ID NO: 359 is the determined cDNA sequence for P783P

SEQ ID NO: 360 is the determined cDNA sequence for unknown 17984

SEQ ID NO: 361 is the determined cDNA sequence for P787P

SEQ ID NO: 362 is the determined cDNA sequence for P788P

5   SEQ ID NO: 363 is the determined cDNA sequence for unknown 17994

SEQ ID NO: 364 is the determined cDNA sequence for P781P

SEQ ID NO: 365 is the determined cDNA sequence for P785P

SEQ ID NO: 366-375 are the determined cDNA sequences for splice variants of B305D.

10   SEQ ID NO: 376 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 366.

SEQ ID NO: 377 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 372.

SEQ ID NO: 378 is the predicted amino acid sequence encoded by the 15 sequence of SEQ ID NO: 373.

SEQ ID NO: 379 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 374.

SEQ ID NO: 380 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 375.

20   SEQ ID NO: 381 is the determined cDNA sequence for B716P.

SEQ ID NO: 382 is the determined full-length cDNA sequence for P711P.

SEQ ID NO: 383 is the predicted amino acid sequence for P711P.

SEQ ID NO: 384 is the cDNA sequence for P1000C.

25   SEQ ID NO: 385 is the cDNA sequence for CGI-82.

SEQ ID NO:386 is the cDNA sequence for 23320.

SEQ ID NO:387 is the cDNA sequence for CGI-69.

SEQ ID NO:388 is the cDNA sequence for L-iditol-2-dehydrogenase.

SEQ ID NO:389 is the cDNA sequence for 23379.

30   SEQ ID NO:390 is the cDNA sequence for 23381.

SEQ ID NO:391 is the cDNA sequence for KIAA0122.

SEQ ID NO:392 is the cDNA sequence for 23399.

SEQ ID NO:393 is the cDNA sequence for a previously identified gene.

SEQ ID NO:394 is the cDNA sequence for HCLBP.

SEQ ID NO:395 is the cDNA sequence for transglutaminase.

SEQ ID NO:396 is the cDNA sequence for a previously identified gene.

SEQ ID NO:397 is the cDNA sequence for PAP.

SEQ ID NO:398 is the cDNA sequence for Ets transcription factor
PDEF.

SEQ ID NO:399 is the cDNA sequence for hTGR.

SEQ ID NO:400 is the cDNA sequence for KIAA0295.

SEQ ID NO:401 is the cDNA sequence for 22545.

SEQ ID NO:402 is the cDNA sequence for 22547.

SEQ ID NO:403 is the cDNA sequence for 22548.

SEQ ID NO:404 is the cDNA sequence for 22550.

SEQ ID NO:405 is the cDNA sequence for 22551.

SEQ ID NO:406 is the cDNA sequence for 22552.

SEQ ID NO:407 is the cDNA sequence for 22553 (also known as
P1020C).

SEQ ID NO:408 is the cDNA sequence for 22558.

SEQ ID NO:409 is the cDNA sequence for 22562.

SEQ ID NO:410 is the cDNA sequence for 22565.

SEQ ID NO:411 is the cDNA sequence for 22567.

SEQ ID NO:412 is the cDNA sequence for 22568.

SEQ ID NO:413 is the cDNA sequence for 22570.

SEQ ID NO:414 is the cDNA sequence for 22571.

SEQ ID NO:415 is the cDNA sequence for 22572.

SEQ ID NO:416 is the cDNA sequence for 22573.

SEQ ID NO:417 is the cDNA sequence for 22573.

SEQ ID NO:418 is the cDNA sequence for 22575.

25

SEQ ID NO:419 is the cDNA sequence for 22580.

SEQ ID NO:420 is the cDNA sequence for 22581.

SEQ ID NO:421 is the cDNA sequence for 22582.

SEQ ID NO:422 is the cDNA sequence for 22583.

5   SEQ ID NO:423 is the cDNA sequence for 22584.

SEQ ID NO:424 is the cDNA sequence for 22585.

SEQ ID NO:425 is the cDNA sequence for 22586.

SEQ ID NO:426 is the cDNA sequence for 22587.

SEQ ID NO:427 is the cDNA sequence for 22588.

10   SEQ ID NO:428 is the cDNA sequence for 22589.

SEQ ID NO:429 is the cDNA sequence for 22590.

SEQ ID NO:430 is the cDNA sequence for 22591.

SEQ ID NO:431 is the cDNA sequence for 22592.

SEQ ID NO:432 is the cDNA sequence for 22593.

15   SEQ ID NO:433 is the cDNA sequence for 22594.

SEQ ID NO:434 is the cDNA sequence for 22595.

SEQ ID NO:435 is the cDNA sequence for 22596.

SEQ ID NO:436 is the cDNA sequence for 22847.

SEQ ID NO:437 is the cDNA sequence for 22848.

20   SEQ ID NO:438 is the cDNA sequence for 22849.

SEQ ID NO:439 is the cDNA sequence for 22851.

SEQ ID NO:440 is the cDNA sequence for 22852.

SEQ ID NO:441 is the cDNA sequence for 22853.

SEQ ID NO:442 is the cDNA sequence for 22854.

25   SEQ ID NO:443 is the cDNA sequence for 22855.

SEQ ID NO:444 is the cDNA sequence for 22856.

SEQ ID NO:445 is the cDNA sequence for 22857.

SEQ ID NO:446 is the cDNA sequence for 23601.

SEQ ID NO:447 is the cDNA sequence for 23602.

30   SEQ ID NO:448 is the cDNA sequence for 23605.

26

SEQ ID NO:449 is the cDNA sequence for 23606.

SEQ ID NO:450 is the cDNA sequence for 23612.

SEQ ID NO:451 is the cDNA sequence for 23614.

SEQ ID NO:452 is the cDNA sequence for 23618.

5   SEQ ID NO:453 is the cDNA sequence for 23622.

SEQ ID NO:454 is the cDNA sequence for folate hydrolase.

SEQ ID NO:455 is the cDNA sequence for LIM protein.

SEQ ID NO:456 is the cDNA sequence for a known gene.

SEQ ID NO:457 is the cDNA sequence for a known gene.

10   SEQ ID NO:458 is the cDNA sequence for a previously identified gene.

SEQ ID NO:459 is the cDNA sequence for 23045.

SEQ ID NO:460 is the cDNA sequence for 23032.

SEQ ID NO:461 is the cDNA sequence for clone 23054.

SEQ ID NO:462-467 are cDNA sequences for known genes.

15   SEQ ID NO:468-471 are cDNA sequences for P710P.

SEQ ID NO:472 is a cDNA sequence for P1001C.

SEQ ID NO: 473 is the determined cDNA sequence for a first splice
variant of P775P (referred to as 27505).

SEQ ID NO: 474 is the determined cDNA sequence for a second splice
20 variant of P775P (referred to as 19947).

SEQ ID NO: 475 is the determined cDNA sequence for a third splice
variant of P775P (referred to as 19941).

SEQ ID NO: 476 is the determined cDNA sequence for a fourth splice
variant of P775P (referred to as 19937).

25   SEQ ID NO: 477 is a first predicted amino acid sequence encoded by the
sequence of SEQ ID NO: 474.

SEQ ID NO: 478 is a second predicted amino acid sequence encoded by
the sequence of SEQ ID NO: 474.

SEQ ID NO: 479 is the predicted amino acid sequence encoded by the
30 sequence of SEQ ID NO: 475.

27

SEQ ID NO: 480 is a first predicted amino acid sequence encoded by the sequence of SEQ ID NO: 473.

SEQ ID NO: 481 is a second predicted amino acid sequence encoded by the sequence of SEQ ID NO: 473.

SEQ ID NO: 482 is a third predicted amino acid sequence encoded by the sequence of SEQ ID NO: 473.

SEQ ID NO: 483 is a fourth predicted amino acid sequence encoded by the sequence of SEQ ID NO: 473.

SEQ ID NO: 484 is the first 30 amino acids of the *M. tuberculosis* antigen Ra12.

SEQ ID NO: 485 is the PCR primer AW025.

SEQ ID NO: 486 is the PCR primer AW003.

SEQ ID NO: 487 is the PCR primer AW027.

SEQ ID NO: 488 is the PCR primer AW026.

SEQ ID NO: 489-501 are peptides employed in epitope mapping studies.

SEQ ID NO: 502 is the determined cDNA sequence of the complementarity determining region for the anti-P503S monoclonal antibody 20D4.

SEQ ID NO: 503 is the determined cDNA sequence of the complementarity determining region for the anti-P503S monoclonal antibody JA1.

SEQ ID NO: 504 & 505 are peptides employed in epitope mapping studies.

SEQ ID NO: 506 is the determined cDNA sequence of the complementarity determining region for the anti-P703P monoclonal antibody 8H2.

SEQ ID NO: 507 is the determined cDNA sequence of the complementarity determining region for the anti-P703P monoclonal antibody 7H8.

SEQ ID NO: 508 is the determined cDNA sequence of the complementarity determining region for the anti-P703P monoclonal antibody 2D4.

SEQ ID NO: 509-522 are peptides employed in epitope mapping studies.

SEQ ID NO: 523 is a mature form of P703P used to raise antibodies against P703P.

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SEQ ID NO: 524 is the putative full-length cDNA sequence of P703P.

SEQ ID NO: 525 is the predicted amino acid sequence encoded by SEQ ID NO: 524.

SEQ ID NO: 526 is the full-length cDNA sequence for P790P.

SEQ ID NO: 527 is the predicted amino acid sequence for P790P.

SEQ ID NO: 528 & 529 are PCR primers.

SEQ ID NO: 530 is the cDNA sequence of a splice variant of SEQ ID NO: 366.

SEQ ID NO: 531 is the cDNA sequence of the open reading frame of SEQ ID NO: 530.

SEQ ID NO: 532 is the predicted amino acid encoded by the sequence of SEQ ID NO: 531.

SEQ ID NO: 533 is the DNA sequence of a putative ORF of P775P.

SEQ ID NO: 534 is the predicted amino acid sequence encoded by SEQ ID NO: 533.

SEQ ID NO: 535 is a first full-length cDNA sequence for P510S.

SEQ ID NO: 536 is a second full-length cDNA sequence for P510S.

SEQ ID NO: 537 is the predicted amino acid sequence encoded by SEQ ID NO: 535.

SEQ ID NO: 538 is the predicted amino acid sequence encoded by SEQ ID NO: 536.

SEQ ID NO: 539 is the peptide P501S-370.

SEQ ID NO: 540 is the peptide P501S-376.

SEQ ID NO: 541-551 are epitopes of P501S.

SEQ ID NO: 552 is an extended cDNA sequence for P712P.

SEQ ID NO: 553-568 are the amino acid sequences encoded by predicted open reading frames within SEQ ID NO: 552.

SEQ ID NO: 569 is an extended cDNA sequence for P776P.

SEQ ID NO: 570 is the determined cDNA sequence for a splice variant of P776P referred to as contig 6.

29

SEQ ID NO: 571 is the determined cDNA sequence for a splice variant of P776P referred to as contig 7.

SEQ ID NO: 572 is the determined cDNA sequence for a splice variant of P776P referred to as contig 14.

SEQ ID NO: 573 is the amino acid sequence encoded by a first predicted ORF of SEQ ID NO: 570.

SEQ ID NO: 574 is the amino acid sequence encoded by a second predicted ORF of SEQ ID NO: 570.

SEQ ID NO: 575 is the amino acid sequence encoded by a predicted ORF of SEQ ID NO: 571.

SEQ ID NO: 576-586 are amino acid sequences encoded by predicted ORFs of SEQ ID NO: 569.

SEQ ID NO: 587 is a DNA consensus sequence of the sequences of P767P and P777P.

SEQ ID NO: 588-590 are amino acid sequences encoded by predicted ORFs of SEQ ID NO: 587.

SEQ ID NO: 591 is an extended cDNA sequence for P1020C.

SEQ ID NO: 592 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: P1020C.

SEQ ID NO: 593 is a splice variant of P775P referred to as 50748.

SEQ ID NO: 594 is a splice variant of P775P referred to as 50717.SEQ ID NO: 595 is a splice variant of P775P referred to as 45985.

SEQ ID NO: 596 is a splice variant of P775P referred to as 38769.

SEQ ID NO: 597 is a splice variant of P775P referred to as 37922.

SEQ ID NO: 598 is a splice variant of P510S referred to as 49274.

SEQ ID NO: 599 is a splice variant of P510S referred to as 39487.

SEQ ID NO: 600 is a splice variant of P504S referred to as 5167.16.

SEQ ID NO: 601 is a splice variant of P504S referred to as 5167.1.

SEQ ID NO: 602 is a splice variant of P504S referred to as 5163.46.

SEQ ID NO: 603 is a splice variant of P504S referred to as 5163.42.

30

SEQ ID NO: 604 is a splice variant of P504S referred to as 5163.34.

SEQ ID NO: 605 is a splice variant of P504S referred to as 5163.17.

SEQ ID NO: 606 is a splice variant of P501S referred to as 10640.

SEQ ID NO: 607-615 are the sequences of PCR primers.

SEQ ID NO: 616 is the determined cDNA sequence of a fusion of P703P and PSA.

SEQ ID NO: 617 is the amino acid sequence of the fusion of P703P and PSA.

SEQ ID NO: 618-689 are determined cDNA sequences of prostate-specific clones.

SEQ ID NO: 690 is the cDNA sequence of the gene DD3.

SEQ ID NO: 691-697 are determined cDNA sequences of prostate-specific clones.

SEQ ID NO: 698 is an extended cDNA sequence for P714P.

SEQ ID NO: 699-701 are the cDNA sequences for splice variants of P704P.

SEQ ID NO: 702 is the cDNA sequence of a spliced variant of P553S referred to as P553S-14.

SEQ ID NO: 703 is the cDNA sequence of a spliced variant of P553S referred to as P553S-12.

SEQ ID NO: 704 is the cDNA sequence of a spliced variant of P553S referred to as P553S-10.

SEQ ID NO: 705 is the cDNA sequence of a spliced variant of P553S referred to as P553S-6.

SEQ ID NO: 706 is the amino acid sequence encoded by SEQ ID NO: 705.

SEQ ID NO: 707 is the amino acid sequence encoded by SEQ ID NO: 702 SEQ ID NO: 708 is a second amino acid sequence encoded by SEQ ID NO: 702.

SEQ ID NO: 709-772 are determined cDNA sequences of prostate-specific clones.

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SEQ ID NO: 773 is a first full-length cDNA sequence for prostate-specific transglutaminase gene (also referred to herein as P558S).

SEQ ID NO: 774 is a second full-length cDNA sequence for prostate-specific transglutaminase gene.

5   SEQ ID NO: 775 is the amino acid sequence encoded by the sequence of SEQ ID NO: 773.

SEQ ID NO: 776 is the amino acid sequence encoded by the sequence of SEQ ID NO: 774.

SEQ ID NO: 777 is the full-length cDNA sequence for P788P.

10   SEQ ID NO: 778 is the amino acid sequence encoded by SEQ ID NO: 777.

SEQ ID NO: 779 is the determined cDNA sequence for a polymorphic variant of P788P.

SEQ ID NO: 780 is the amino acid sequence encoded by SEQ ID NO: 15   779.

SEQ ID NO: 781 is the amino acid sequence of peptide 4 from P703P.

SEQ ID NO: 782 is the cDNA sequence that encodes peptide 4 from P703P.

SEQ ID NO: 783-798 are the cDNA sequence encoding epitopes of 20   P703P.

SEQ ID NO: 799-814 are the amino acid sequences of epitopes of P703P.

SEQ ID NO: 815 and 816 are PCR primers.

SEQ ID NO: 817 is the cDNA sequence encoding an N-terminal portion 25   of P788P expressed in *E. coli*.

SEQ ID NO: 818 is the amino acid sequence of the N-terminal portion of P788P expressed in *E. coli*.

SEQ ID NO: 819 is the amino acid sequence of the *M. tuberculosis* antigen Ra12.

30   SEQ ID NO: 820 and 821 are PCR primers.

32

SEQ ID NO: 822 is the cDNA sequence for the Ra12-P510S-C construct.

SEQ ID NO: 823 is the cDNA sequence for the P510S-C construct.

SEQ ID NO: 824 is the cDNA sequence for the P510S-E3 construct.

SEQ ID NO: 825 is the amino acid sequence for the Ra12-P510S-C construct.

SEQ ID NO: 826 is the amino acid sequence for the P510S-C construct.

SEQ ID NO: 827 is the amino acid sequence for the P510S-E3 construct.

SEQ ID NO: 828-833 are PCR primers.

SEQ ID NO: 834 is the cDNA sequence of the construct Ra12-P775P-ORF3.

SEQ ID NO: 835 is the amino acid sequence of the construct Ra12-P775P-ORF3.

SEQ ID NO: 836 and 837 are PCR primers.

SEQ ID NO: 838 is the determined amino acid sequence for a P703P His tag fusion protein.

SEQ ID NO: 839 is the determined cDNA sequence for a P703P His tag fusion protein.

SEQ ID NO: 840 and 841 are PCR primers.

SEQ ID NO: 842 is the determined amino acid sequence for a P705P His tag fusion protein.

SEQ ID NO: 843 is the determined cDNA sequence for a P705P His tag fusion protein.

SEQ ID NO: 844 and 845 are PCR primers.

SEQ ID NO: 846 is the determined amino acid sequence for a P711P His tag fusion protein.

SEQ ID NO: 847 is the determined cDNA sequence for a P711P His tag fusion protein.

SEQ ID NO: 848 is the amino acid sequence of the *M. tuberculosis* antigen Ra12.

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SEQ ID NO: 849 and 850 are PCR primers.

SEQ ID NO: 851 is the determined cDNA sequence for the construct Ra12-P501S-E2.

SEQ ID NO: 852 is the determined amino acid sequence for the construct Ra12-P501S-E2.

SEQ ID NO: 853 is the amino acid sequence for an epitope of P501S.

SEQ ID NO: 854 is the DNA sequence encoding SEQ ID NO: 853.

SEQ ID NO: 855 is the amino acid sequence for an epitope of P501S.

SEQ ID NO: 856 is the DNA sequence encoding SEQ ID NO: 855.

SEQ ID NO: 857 is a peptide employed in epitope mapping studies.

SEQ ID NO: 858 is the amino acid sequence for an epitope of P501S.

SEQ ID NO: 859 is the DNA sequence encoding SEQ ID NO: 858.

SEQ ID NO: 860-862 are the amino acid sequences for CD4 epitopes of P501S.

SEQ ID NO: 863-865 are the DNA sequences encoding the sequences of SEQ ID NO: 860-862.

SEQ ID NO: 866-877 are the amino acid sequences for putative CTL epitopes of P703P.

SEQ ID NO: 878 is the full-length cDNA sequence for P789P.

SEQ ID NO: 879 is the amino acid sequence encoded by SEQ ID NO: 878.

SEQ ID NO: 880 is the determined full-length cDNA sequence for the splice variant of P776P referred to as contig 6.

SEQ ID NO: 881-882 are determined full-length cDNA sequences for the splice variant of P776P referred to as contig 7.

SEQ ID NO: 883-887 are amino acid sequences encoded by SEQ ID NO: 880.

SEQ ID NO: 888-893 are amino acid sequences encoded by the splice variant of P776P referred to as contig 7.

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SEQ ID NO: 894 is the full-length cDNA sequence for human transmembrane protease serine 2.

SEQ ID NO: 895 is the amino acid sequence encoded by SEQ ID NO: 894.

SEQ ID NO: 896 is the cDNA sequence encoding the first 209 amino acids of human transmembrane protease serine 2.

SEQ ID NO: 897 is the first 209 amino acids of human transmembrane protease serine 2.

SEQ ID NO: 898 is the amino acid sequence of peptide 296-322 of P501S.

SEQ ID NO: 899-902 are PCR primers.

SEQ ID NO: 903 is the determined cDNA sequence of the Vb chain of a T cell receptor for the P501S-specific T cell clone 4E5.

SEQ ID NO: 904 is the determined cDNA sequence of the Va chain of a T cell receptor for the P501S-specific T cell clone 4E5.

SEQ ID NO: 905 is the amino acid sequence encoded by SEQ ID NO 903.

SEQ ID NO: 906 is the amino acid sequence encoded by SEQ ID NO 904.

SEQ ID NO: 907 is the full-length open reading frame for P768P including stop codon.

SEQ ID NO: 908 is the full-length open reading frame for P768P without stop codon.

SEQ ID NO: 909 is the amino acid sequence encoded by SEQ ID NO: 908.

SEQ ID NO: 910-915 are the amino acid sequences for predicted domains of P768P.

SEQ ID NO: 916 is the full-length cDNA sequence of P835P.

SEQ ID NO: 917 is the cDNA sequence of the previously identified clone FLJ13581.

SEQ ID NO: 918 is the cDNA sequence of the open reading frame for P835P with stop codon.

SEQ ID NO: 919 is the cDNA sequence of the open reading frame for P835P without stop codon.

5   SEQ ID NO: 920 is the full-length amino acid sequence for P835P.

SEQ ID NO: 921-928 are the amino acid sequences of extracellular and intracellular domains of P835P.

SEQ ID NO: 929 is the full-length cDNA sequence for P1000C.

SEQ ID NO: 930 is the cDNA sequence of the open reading frame for

10   P1000C, including stop codon.

SEQ ID NO: 931 is the cDNA sequence of the open reading frame for P1000C, without stop codon.

SEQ ID NO: 932 is the full-length amino acid sequence for P1000C.

SEQ ID NO: 933 is amino acids 1-100 of SEQ ID NO: 932.

15   SEQ ID NO: 934 is amino acids 100-492 of SEQ ID NO: 932.

SEQ ID NO: 935-937 are PCR primers.

SEQ ID NO: 938 is the cDNA sequence of the expressed full-length P767P coding region.

SEQ ID NO: 939 is the cDNA sequence of an expressed truncated P767P

20   coding region.

SEQ ID NO: 940 is the amino acid sequence encoded by SEQ ID NO: 939.

SEQ ID NO: 941 is the amino acid sequence encoded by SEQ ID NO: 938.

25   SEQ ID NO: 942 is the DNA sequence of a CD4 epitope of P703P.

SEQ ID NO: 943 is the amino acid sequence of a CD4 epitope of P703P.

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DETAILED DESCRIPTION OF THE INVENTION

The present invention is directed generally to compositions and their use in the therapy and diagnosis of cancer, particularly prostate cancer. As described further below, illustrative compositions of the present invention include, but are not restricted

5   to, polypeptides, particularly immunogenic polypeptides, polynucleotides encoding such polypeptides, antibodies and other binding agents, antigen presenting cells (APCs) and immune system cells (*e.g.,* T cells).

The practice of the present invention will employ, unless indicated specifically to the contrary, conventional methods of virology, immunology,

10   microbiology, molecular biology and recombinant DNA techniques within the skill of the art, many of which are described below for the purpose of illustration. Such techniques are explained fully in the literature. See, *e.g.,* Sambrook, et al. Molecular Cloning: A Laboratory Manual (2nd Edition, 1989); Maniatis et al. Molecular Cloning: A Laboratory Manual (1982); DNA Cloning: A Practical Approach, vol. I & II (D.

15   Glover, ed.); Oligonucleotide Synthesis (N. Gait, ed., 1984); Nucleic Acid Hybridization (B. Hames & S. Higgins, eds., 1985); Transcription and Translation (B. Hames & S. Higgins, eds., 1984); Animal Cell Culture (R. Freshney, ed., 1986); Perbal, A Practical Guide to Molecular Cloning (1984).

All publications, patents and patent applications cited herein, whether

20   supra or infra, are hereby incorporated by reference in their entirety.

As used in this specification and the appended claims, the singular forms "a," "an" and "the" include plural references unless the content clearly dictates otherwise.

Polypeptide Compositions

25   As used herein, the term "polypeptide" " is used in its conventional meaning, *i.e.,* as a sequence of amino acids. The polypeptides are not limited to a specific length of the product; thus, peptides, oligopeptides, and proteins are included within the definition of polypeptide, and such terms may be used interchangeably herein unless specifically indicated otherwise. This term also does not refer to or exclude post-

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expression modifications of the polypeptide, for example, glycosylations, acetylations, phosphorylations and the like, as well as other modifications known in the art, both naturally occurring and non-naturally occurring. A polypeptide may be an entire protein, or a subsequence thereof. Particular polypeptides of interest in the context of

5   this invention are amino acid subsequences comprising epitopes, *i.e.*, antigenic determinants substantially responsible for the immunogenic properties of a polypeptide and being capable of evoking an immune response.

Particularly illustrative polypeptides of the present invention comprise those encoded by a polynucleotide sequence set forth in any one of SEQ ID NOs: 1-111,

10   115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-705, 709-774, 777, 789, 817, 823, 824, 878, 880-882, 894, 896, 907, 908, 916-919, 929-931, 938, 939 and 942, or a sequence that hybridizes under moderately stringent conditions, or, alternatively, under highly stringent conditions, to a polynucleotide

15   sequence set forth in any one of SEQ ID NOs: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-705, 709-774, 777, 789, 817, 823, 824, 878, 880-882, 894, 896, 907, 908, 916-919, 929-931, 938, 939 and 942. In specific embodiments, the polypeptides of the invention comprise amino acid sequences as set

20   forth in any one of SEQ ID NO: 112-114, 172, 176, 178, 327, 329, 331, 336, 339, 376-380, 383, 477-483, 496, 504, 505, 519, 520, 522, 525, 527, 532, 534, 537-551, 553-568, 573-586, 588-590, 592, 706-708, 775, 776, 778, 780, 781, 811, 814, 818, 826, 827, 853, 855, 858, 860-862, 866-877, 879, 883-893, 895, 897, 898, 909-915, 920-928, 932-934, 940, 941 and 943.

25   The polypeptides of the present invention are sometimes herein referred to as prostate-specific proteins or prostate-specific polypeptides, as an indication that their identification has been based at least in part upon their increased levels of expression in prostate tissue samples. Thus, a "prostate-specific polypeptide" or "prostate-specific protein," refers generally to a polypeptide sequence of the present

30   invention, or a polynucleotide sequence encoding such a polypeptide, that is expressed

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in a substantial proportion of prostate tissue samples, for example preferably greater than about 20%, more preferably greater than about 30%, and most preferably greater than about 50% or more of prostate tissue samples tested, at a level that is at least two fold, and preferably at least five fold, greater than the level of expression in other

5 · normal tissues, as determined using a representative assay provided herein. A prostate-specific polypeptide sequence of the invention, based upon its increased level of expression in tumor cells, has particular utility both as a diagnostic marker as well as a therapeutic target, as further described below.

In certain preferred embodiments, the polypeptides of the invention are

10 immunogenic, *i.e.*, they react detectably within an immunoassay (such as an ELISA or T-cell stimulation assay) with antisera and/or T-cells from a patient with prostate cancer. Screening for immunogenic activity can be performed using techniques well known to the skilled artisan. For example, such screens can be performed using methods such as those described in Harlow and Lane, *Antibodies: A Laboratory*

15 *Manual,* Cold Spring Harbor Laboratory, 1988. In one illustrative example, a polypeptide may be immobilized on a solid support and contacted with patient sera to allow binding of antibodies within the sera to the immobilized polypeptide. Unbound sera may then be removed and bound antibodies detected using, for example, ^{125}I-labeled Protein A.

20 As would be recognized by the skilled artisan, immunogenic portions of the polypeptides disclosed herein are also encompassed by the present invention. An "immunogenic portion," as used herein, is a fragment of an immunogenic polypeptide of the invention that itself is immunologically reactive (*i.e.,* specifically binds) with the B-cells and/or T-cell surface antigen receptors that recognize the polypeptide.

25 Immunogenic portions may generally be identified using well known techniques, such as those summarized in Paul, *Fundamental Immunology*, 3rd ed., 243-247 (Raven Press, 1993) and references cited therein. Such techniques include screening polypeptides for the ability to react with antigen-specific antibodies, antisera and/or T-cell lines or clones. As used herein, antisera and antibodies are "antigen-specific" if they

30 specifically bind to an antigen (*i.e.,* they react with the protein in an ELISA or other

immunoassay, and do not react detectably with unrelated proteins). Such antisera and antibodies may be prepared as described herein, and using well-known techniques.

In one preferred embodiment, an immunogenic portion of a polypeptide of the present invention is a portion that reacts with antisera and/or T-cells at a level that

5 is not substantially less than the reactivity of the full-length polypeptide (*e.g.*, in an ELISA and/or T-cell reactivity assay). Preferably, the level of immunogenic activity of the immunogenic portion is at least about 50%, preferably at least about 70% and most preferably greater than about 90% of the immunogenicity for the full-length polypeptide. In some instances, preferred immunogenic portions will be identified that

10 have a level of immunogenic activity greater than that of the corresponding full-length polypeptide, *e.g.*, having greater than about 100% or 150% or more immunogenic activity.

In certain other embodiments, illustrative immunogenic portions may include peptides in which an N-terminal leader sequence and/or transmembrane domain

15 has been deleted. Other illustrative immunogenic portions will contain a small N- and/or C-terminal deletion (*e.g.*, 1-30 amino acids, preferably 5-15 amino acids), relative to the mature protein.

In another embodiment, a polypeptide composition of the invention may also comprise one or more polypeptides that are immunologically reactive with T cells

20 and/or antibodies generated against a polypeptide of the invention, particularly a polypeptide having an amino acid sequence disclosed herein, or to an immunogenic fragment or variant thereof.

In another embodiment of the invention, polypeptides are provided that comprise one or more polypeptides that are capable of eliciting T cells and/or antibodies

25 that are immunologically reactive with one or more polypeptides described herein, or one or more polypeptides encoded by contiguous nucleic acid sequences contained in the polynucleotide sequences disclosed herein, or immunogenic fragments or variants thereof, or to one or more nucleic acid sequences which hybridize to one or more of these sequences under conditions of moderate to high stringency.

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The present invention, in another aspect, provides polypeptide fragments comprising at least about 5, 10, 15, 20, 25, 50, or 100 contiguous amino acids, or more, including all intermediate lengths, of a polypeptide composition set forth herein, such as those set forth in SEQ ID NO: 112-114, 172, 176, 178, 327, 329, 331, 336, 339, 376-
5   380, 383, 477-483, 496, 504, 505, 519, 520, 522, 525, 527, 532, 534, 537-551, 553-568, 573-586, 588-590, 592, 706-708, 775, 776, 778, 780, 781, 811, 814, 818, 826, 827, 853, 855, 858, 860-862, 866-877, 879, 883-893, 895, 897, 898, 909-915, 920-928, 932-934, 940, 941 and 943, or those encoded by a polynucleotide sequence set forth in a sequence of SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-
10   335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-705, 709-774, 777, 789, 817, 823, 824, 878, 880-882, 894, 896, 907, 908, 916-919, 929-931, 938, 939 and 942.

In another aspect, the present invention provides variants of the polypeptide compositions described herein.   Polypeptide variants generally
15   encompassed by the present invention will typically exhibit at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% or more identity (determined as described below), along its length, to a polypeptide sequence set forth herein.

In one preferred embodiment, the polypeptide fragments and variants
20   provided by the present invention are immunologically reactive with an antibody and/or T-cell that reacts with a full-length polypeptide specifically set forth herein.

In another preferred embodiment, the polypeptide fragments and variants provided by the present invention exhibit a level of immunogenic activity of at least about 50%, preferably at least about 70%, and most preferably at least about 90% or
25   more of that exhibited by a full-length polypeptide sequence specifically set forth herein.

A polypeptide "variant," as the term is used herein, is a polypeptide that typically differs from a polypeptide specifically disclosed herein in one or more substitutions, deletions, additions and/or insertions.   Such variants may be naturally
30   occurring or may be synthetically generated, for example, by modifying one or more of

the above polypeptide sequences of the invention and evaluating their immunogenic activity as described herein using any of a number of techniques well known in the art.

For example, certain illustrative variants of the polypeptides of the invention include those in which one or more portions, such as an N-terminal leader sequence or transmembrane domain, have been removed. Other illustrative variants include variants in which a small portion (e.g., 1-30 amino acids, preferably 5-15 amino acids) has been removed from the N- and/or C-terminal of the mature protein.

In many instances, a variant will contain conservative substitutions. A "conservative substitution" is one in which an amino acid is substituted for another amino acid that has similar properties, such that one skilled in the art of peptide chemistry would expect the secondary structure and hydropathic nature of the polypeptide to be substantially unchanged. As described above, modifications may be made in the structure of the polynucleotides and polypeptides of the present invention and still obtain a functional molecule that encodes a variant or derivative polypeptide with desirable characteristics, e.g., with immunogenic characteristics. When it is desired to alter the amino acid sequence of a polypeptide to create an equivalent, or even an improved, immunogenic variant or portion of a polypeptide of the invention, one skilled in the art will typically change one or more of the codons of the encoding DNA sequence according to Table 1.

For example, certain amino acids may be substituted for other amino acids in a protein structure without appreciable loss of interactive binding capacity with structures such as, for example, antigen-binding regions of antibodies or binding sites on substrate molecules. Since it is the interactive capacity and nature of a protein that defines that protein's biological functional activity, certain amino acid sequence substitutions can be made in a protein sequence, and, of course, its underlying DNA coding sequence, and nevertheless obtain a protein with like properties. It is thus contemplated that various changes may be made in the peptide sequences of the disclosed compositions, or corresponding DNA sequences which encode said peptides without appreciable loss of their biological utility or activity.

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TABLE 1

Amino Acids			Codons					
Alanine	Ala	A	GCA	GCC	GCG	GCU		
Cysteine	Cys	C	UGC	UGU				
Aspartic acid	Asp	D	GAC	GAU				
Glutamic acid	Glu	E	GAA	GAG				
Phenylalanine	Phe	F	UUC	UUU				
Glycine	Gly	G	GGA	GGC	GGG	GGU		
Histidine	His	H	CAC	CAU				
Isoleucine	Ile	I	AUA	AUC	AUU			
Lysine	Lys	K	AAA	AAG				
Leucine	Leu	L	UUA	UUG	CUA	CUC	CUG	CUU
Methionine	Met	M	AUG					
Asparagine	Asn	N	AAC	AAU				
Proline	Pro	P	CCA	CCC	CCG	CCU		
Glutamine	Gln	Q	CAA	CAG				
Arginine	Arg	R	AGA	AGG	CGA	CGC	CGG	CGU
Serine	Ser	S	AGC	AGU	UCA	UCC	UCG	UCU
Threonine	Thr	T	ACA	ACC	ACG	ACU		
Valine	Val	V	GUA	GUC	GUG	GUU		
Tryptophan	Trp	W	UGG					
Tyrosine	Tyr	Y	UAC	UAU				

     In making such changes, the hydropathic index of amino acids may be

5   considered. The importance of the hydropathic amino acid index in conferring interactive biologic function on a protein is generally understood in the art (Kyte and Doolittle, 1982, incorporated herein by reference). It is accepted that the relative hydropathic character of the amino acid contributes to the secondary structure of the resultant protein, which in turn defines the interaction of the protein with other

10 molecules, for example, enzymes, substrates, receptors, DNA, antibodies, antigens, and the like. Each amino acid has been assigned a hydropathic index on the basis of its

hydrophobicity and charge characteristics (Kyte and Doolittle, 1982). These values are: isoleucine (+4.5); valine (+4.2); leucine (+3.8); phenylalanine (+2.8); cysteine/cystine (+2.5); methionine (+1.9); alanine (+1.8); glycine (-0.4); threonine (-0.7); serine (-0.8); tryptophan (-0.9); tyrosine (-1.3); proline (-1.6); histidine (-3.2); glutamate (-3.5);

5   glutamine (-3.5); aspartate (-3.5); asparagine (-3.5); lysine (-3.9); and arginine (-4.5).

It is known in the art that certain amino acids may be substituted by other amino acids having a similar hydropathic index or score and still result in a protein with similar biological activity, *i.e.* still obtain a biological functionally equivalent protein. In making such changes, the substitution of amino acids whose hydropathic indices are

10 within ±2 is preferred, those within ±1 are particularly preferred, and those within ±0.5 are even more particularly preferred. It is also understood in the art that the substitution of like amino acids can be made effectively on the basis of hydrophilicity. U. S. Patent 4,554,101 (specifically incorporated herein by reference in its entirety), states that the greatest local average hydrophilicity of a protein, as governed by the hydrophilicity of

15 its adjacent amino acids, correlates with a biological property of the protein.

As detailed in U. S. Patent 4,554,101, the following hydrophilicity values have been assigned to amino acid residues: arginine (+3.0); lysine (+3.0); aspartate (+3.0 ± 1); glutamate (+3.0 ± 1); serine (+0.3); asparagine (+0.2); glutamine (+0.2); glycine (0); threonine (-0.4); proline (-0.5 ± 1); alanine (-0.5); histidine (-0.5); cysteine

20 (-1.0); methionine (-1.3); valine (-1.5); leucine (-1.8); isoleucine (-1.8); tyrosine (-2.3); phenylalanine (-2.5); tryptophan (-3.4). It is understood that an amino acid can be substituted for another having a similar hydrophilicity value and still obtain a biologically equivalent, and in particular, an immunologically equivalent protein. In such changes, the substitution of amino acids whose hydrophilicity values are within ±2

25 is preferred, those within ±1 are particularly preferred, and those within ±0.5 are even more particularly preferred.

As outlined above, amino acid substitutions are generally therefore based on the relative similarity of the amino acid side-chain substituents, for example, their hydrophobicity, hydrophilicity, charge, size, and the like. Exemplary substitutions that

30 take various of the foregoing characteristics into consideration are well known to those

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of skill in the art and include: arginine and lysine; glutamate and aspartate; serine and threonine; glutamine and asparagine; and valine, leucine and isoleucine.

In addition, any polynucleotide may be further modified to increase stability *in vivo*. Possible modifications include, but are not limited to, the addition of 5 flanking sequences at the 5' and/or 3' ends; the use of phosphorothioate or 2' O-methyl rather than phosphodiesterase linkages in the backbone; and/or the inclusion of nontraditional bases such as inosine, queosine and wybutosine, as well as acetyl-methyl-, thio- and other modified forms of adenine, cytidine, guanine, thymine and uridine.

10   Amino acid substitutions may further be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity and/or the amphipathic nature of the residues. For example, negatively charged amino acids include aspartic acid and glutamic acid; positively charged amino acids include lysine and arginine; and amino acids with uncharged polar head groups having similar hydrophilicity values 15 include leucine, isoleucine and valine; glycine and alanine; asparagine and glutamine; and serine, threonine, phenylalanine and tyrosine. Other groups of amino acids that may represent conservative changes include: (1) ala, pro, gly, glu, asp, gln, asn, ser, thr; (2) cys, ser, tyr, thr; (3) val, ile, leu, met, ala, phe; (4) lys, arg, his; and (5) phe, tyr, trp, his. A variant may also, or alternatively, contain nonconservative changes. In a 20 preferred embodiment, variant polypeptides differ from a native sequence by substitution, deletion or addition of five amino acids or fewer. Variants may also (or alternatively) be modified by, for example, the deletion or addition of amino acids that have minimal influence on the immunogenicity, secondary structure and hydropathic nature of the polypeptide.

25   As noted above, polypeptides may comprise a signal (or leader) sequence at the N-terminal end of the protein, which co-translationally or post-translationally directs transfer of the protein. The polypeptide may also be conjugated to a linker or other sequence for ease of synthesis, purification or identification of the polypeptide (*e.g.*, poly-His), or to enhance binding of the polypeptide to a solid support. For 30 example, a polypeptide may be conjugated to an immunoglobulin Fc region.

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When comparing polypeptide sequences, two sequences are said to be "identical" if the sequence of amino acids in the two sequences is the same when aligned for maximum correspondence, as described below. Comparisons between two sequences are typically performed by comparing the sequences over a comparison window to identify and compare local regions of sequence similarity. A "comparison window" as used herein, refers to a segment of at least about 20 contiguous positions, usually 30 to about 75, 40 to about 50, in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned.

Optimal alignment of sequences for comparison may be conducted using the Megalign program in the Lasergene suite of bioinformatics software (DNASTAR, Inc., Madison, WI), using default parameters. This program embodies several alignment schemes described in the following references: Dayhoff, M.O. (1978) A model of evolutionary change in proteins – Matrices for detecting distant relationships. In Dayhoff, M.O. (ed.) Atlas of Protein Sequence and Structure, National Biomedical Research Foundation, Washington DC Vol. 5, Suppl. 3, pp. 345-358; Hein J. (1990) Unified Approach to Alignment and Phylogenes pp. 626-645 *Methods in Enzymology* vol. 183, Academic Press, Inc., San Diego, CA; Higgins, D.G. and Sharp, P.M. (1989) *CABIOS* 5:151-153; Myers, E.W. and Muller W. (1988) *CABIOS* 4:11-17; Robinson, E.D. (1971) *Comb. Theor 11*:105; Santou, N. Nes, M. (1987) *Mol. Biol. Evol. 4*:406-425; Sneath, P.H.A. and Sokal, R.R. (1973) *Numerical Taxonomy – the Principles and Practice of Numerical Taxonomy*, Freeman Press, San Francisco, CA; Wilbur, W.J. and Lipman, D.J. (1983) *Proc. Natl. Acad., Sci. USA 80*:726-730.

Alternatively, optimal alignment of sequences for comparison may be conducted by the local identity algorithm of Smith and Waterman (1981) *Add. APL. Math 2*:482, by the identity alignment algorithm of Needleman and Wunsch (1970) *J. Mol. Biol.* 48:443, by the search for similarity methods of Pearson and Lipman (1988) *Proc. Natl. Acad. Sci. USA* 85: 2444, by computerized implementations of these algorithms (GAP, BESTFIT, BLAST, FASTA, and TFASTA in the Wisconsin Genetics

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Software Package, Genetics Computer Group (GCG), 575 Science Dr., Madison, WI),
or by inspection.

One preferred example of algorithms that are suitable for determining
percent sequence identity and sequence similarity are the BLAST and BLAST 2.0
5   algorithms, which are described in Altschul et al. (1977) *Nucl. Acids Res.* 25:3389-3402
and Altschul et al. (1990) *J. Mol. Biol.* 215:403-410, respectively. BLAST and BLAST
2.0 can be used, for example with the parameters described herein, to determine percent
sequence identity for the polynucleotides and polypeptides of the invention. Software
for performing BLAST analyses is publicly available through the National Center for
10   Biotechnology Information. For amino acid sequences, a scoring matrix can be used to
calculate the cumulative score. Extension of the word hits in each direction are halted
when: the cumulative alignment score falls off by the quantity X from its maximum
achieved value; the cumulative score goes to zero or below, due to the accumulation of
one or more negative-scoring residue alignments; or the end of either sequence is
15   reached. The BLAST algorithm parameters W, T and X determine the sensitivity and
speed of the alignment.

In one preferred approach, the "percentage of sequence identity" is
determined by comparing two optimally aligned sequences over a window of
comparison of at least 20 positions, wherein the portion of the polypeptide sequence in
20   the comparison window may comprise additions or deletions (*i.e.,* gaps) of 20 percent
or less, usually 5 to 15 percent, or 10 to 12 percent, as compared to the reference
sequences (which does not comprise additions or deletions) for optimal alignment of the
two sequences. The percentage is calculated by determining the number of positions at
which the identical amino acid residue occurs in both sequences to yield the number of
25   matched positions, dividing the number of matched positions by the total number of
positions in the reference sequence (*i.e.,* the window size) and multiplying the results by
100 to yield the percentage of sequence identity.

Within other illustrative embodiments, a polypeptide may be a fusion
polypeptide that comprises multiple polypeptides as described herein, or that comprises
30   at least one polypeptide as described herein and an unrelated sequence, such as a known

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tumor protein. A fusion partner may, for example, assist in providing T helper epitopes (an immunological fusion partner), preferably T helper epitopes recognized by humans, or may assist in expressing the protein (an expression enhancer) at higher yields than the native recombinant protein. Certain preferred fusion partners are both immunological

5   and expression enhancing fusion partners. Other fusion partners may be selected so as to increase the solubility of the polypeptide or to enable the polypeptide to be targeted to desired intracellular compartments. Still further fusion partners include affinity tags, which facilitate purification of the polypeptide.

Fusion polypeptides may generally be prepared using standard

10   techniques, including chemical conjugation. Preferably, a fusion polypeptide is expressed as a recombinant polypeptide, allowing the production of increased levels, relative to a non-fused polypeptide, in an expression system. Briefly, DNA sequences encoding the polypeptide components may be assembled separately, and ligated into an appropriate expression vector. The 3' end of the DNA sequence encoding one

15   polypeptide component is ligated, with or without a peptide linker, to the 5' end of a DNA sequence encoding the second polypeptide component so that the reading frames of the sequences are in phase. This permits translation into a single fusion polypeptide that retains the biological activity of both component polypeptides.

A peptide linker sequence may be employed to separate the first and

20   second polypeptide components by a distance sufficient to ensure that each polypeptide folds into its secondary and tertiary structures. Such a peptide linker sequence is incorporated into the fusion polypeptide using standard techniques well known in the art. Suitable peptide linker sequences may be chosen based on the following factors: (1) their ability to adopt a flexible extended conformation; (2) their inability to adopt a

25   secondary structure that could interact with functional epitopes on the first and second polypeptides; and (3) the lack of hydrophobic or charged residues that might react with the polypeptide functional epitopes. Preferred peptide linker sequences contain Gly, Asn and Ser residues. Other near neutral amino acids, such as Thr and Ala may also be used in the linker sequence. Amino acid sequences which may be usefully employed as

30   linkers include those disclosed in Maratea et al., *Gene* 40:39-46, 1985; Murphy et al.,

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Proc. Natl. Acad. Sci. USA 83:8258-8262, 1986; U.S. Patent No. 4,935,233 and U.S. Patent No. 4,751,180. The linker sequence may generally be from 1 to about 50 amino acids in length. Linker sequences are not required when the first and second polypeptides have non-essential N-terminal amino acid regions that can be used to
5   separate the functional domains and prevent steric interference.

The ligated DNA sequences are operably linked to suitable transcriptional or translational regulatory elements. The regulatory elements responsible for expression of DNA are located only 5' to the DNA sequence encoding the first polypeptides. Similarly, stop codons required to end translation and
10   transcription termination signals are only present 3' to the DNA sequence encoding the second polypeptide.

The fusion polypeptide can comprise a polypeptide as described herein together with an unrelated immunogenic protein, such as an immunogenic protein capable of eliciting a recall response. Examples of such proteins include tetanus,
15   tuberculosis and hepatitis proteins (*see*, for example, Stoute et al. *New Engl. J. Med.*, *336*:86-91, 1997).

In one preferred embodiment, the immunological fusion partner is derived from a Mycobacterium sp., such as a *Mycobacterium tuberculosis*-derived Ra12 fragment. Ra12 compositions and methods for their use in enhancing the expression
20   and/or immunogenicity of heterologous polynucleotide/polypeptide sequences is described in U.S. Patent Application 60/158,585, the disclosure of which is incorporated herein by reference in its entirety. Briefly, Ra12 refers to a polynucleotide region that is a subsequence of a *Mycobacterium tuberculosis* MTB32A nucleic acid. MTB32A is a serine protease of 32 KD molecular weight encoded by a gene in virulent
25   and avirulent strains of *M. tuberculosis*. The nucleotide sequence and amino acid sequence of MTB32A have been described (for example, U.S. Patent Application 60/158,585; see also, Skeiky *et al., Infection and Immun.* (1999) 67:3998-4007, incorporated herein by reference). C-terminal fragments of the MTB32A coding sequence express at high levels and remain as a soluble polypeptides throughout the
30   purification process. Moreover, Ra12 may enhance the immunogenicity of heterologous

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immunogenic polypeptides with which it is fused.   One preferred Ra12 fusion polypeptide comprises a 14 KD C-terminal fragment corresponding to amino acid residues 192 to 323 of MTB32A.   Other preferred Ra12 polynucleotides generally comprise at least about 15 consecutive nucleotides, at least about 30 nucleotides, at least

5   about 60 nucleotides, at least about 100 nucleotides, at least about 200 nucleotides, or at least about 300 nucleotides that encode a portion of a Ra12 polypeptide.   Ra12 polynucleotides may comprise a native sequence (*i.e.,* an endogenous sequence that encodes a Ra12 polypeptide or a portion thereof) or may comprise a variant of such a sequence.   Ra12 polynucleotide variants may contain one or more substitutions,

10   additions, deletions and/or insertions such that the biological activity of the encoded fusion polypeptide is not substantially diminished, relative to a fusion polypeptide comprising a native Ra12 polypeptide.   Variants preferably exhibit at least about 70% identity, more preferably at least about 80% identity and most preferably at least about 90% identity to a polynucleotide sequence that encodes a native Ra12 polypeptide or a

15   portion thereof.

Within other preferred embodiments, an immunological fusion partner is derived from protein D, a surface protein of the gram-negative bacterium Haemophilus influenza B (WO 91/18926).   Preferably, a protein D derivative comprises approximately the first third of the protein (*e.g.,* the first N-terminal 100-110 amino

20   acids), and a protein D derivative may be lipidated.   Within certain preferred embodiments, the first 109 residues of a Lipoprotein D fusion partner is included on the N-terminus to provide the polypeptide with additional exogenous T-cell epitopes and to increase the expression level in *E. coli* (thus functioning as an expression enhancer). The lipid tail ensures optimal presentation of the antigen to antigen presenting cells.

25   Other fusion partners include the non-structural protein from influenzae virus, NS1 (hemaglutinin).   Typically, the N-terminal 81 amino acids are used, although different fragments that include T-helper epitopes may be used.

In another embodiment, the immunological fusion partner is the protein known as LYTA, or a portion thereof (preferably a C-terminal portion).   LYTA is

30   derived from *Streptococcus pneumoniae,* which synthesizes an N-acetyl-L-alanine

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amidase known as amidase LYTA (encoded by the LytA gene; *Gene 43*:265-292, 1986). LYTA is an autolysin that specifically degrades certain bonds in the peptidoglycan backbone. The C-terminal domain of the LYTA protein is responsible for the affinity to the choline or to some choline analogues such as DEAE. This property has been

5   exploited for the development of *E. coli* C-LYTA expressing plasmids useful for expression of fusion proteins. Purification of hybrid proteins containing the C-LYTA fragment at the amino terminus has been described (*see Biotechnology 10*:795-798, 1992). Within a preferred embodiment, a repeat portion of LYTA may be incorporated into a fusion polypeptide. A repeat portion is found in the C-terminal region starting at

10 residue 178. A particularly preferred repeat portion incorporates residues 188-305.

Yet another illustrative embodiment involves fusion polypeptides, and the polynucleotides encoding them, wherein the fusion partner comprises a targeting signal capable of directing a polypeptide to the endosomal/lysosomal compartment, as described in U.S. Patent No. 5,633,234. An immunogenic polypeptide of the invention,

15 when fused with this targeting signal, will associate more efficiently with MHC class II molecules and thereby provide enhanced in vivo stimulation of $CD4^+$ T-cells specific for the polypeptide.

Polypeptides of the invention are prepared using any of a variety of well known synthetic and/or recombinant techniques, the latter of which are further

20 described below. Polypeptides, portions and other variants generally less than about 150 amino acids can be generated by synthetic means, using techniques well known to those of ordinary skill in the art. In one illustrative example, such polypeptides are synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a

25 growing amino acid chain. *See* Merrifield, *J. Am. Chem. Soc. 85*:2149-2146, 1963. Equipment for automated synthesis of polypeptides is commercially available from suppliers such as Perkin Elmer/Applied BioSystems Division (Foster City, CA), and may be operated according to the manufacturer's instructions.

In general, polypeptide compositions (including fusion polypeptides) of

30 the invention are isolated. An "isolated" polypeptide is one that is removed from its

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original environment. For example, a naturally-occurring protein or polypeptide is isolated if it is separated from some or all of the coexisting materials in the natural system. Preferably, such polypeptides are also purified, *e.g.*, are at least about 90% pure, more preferably at least about 95% pure and most preferably at least about 99%
5   pure.

Polynucleotide Compositions

The present invention, in other aspects, provides polynucleotide compositions. The terms "DNA" and "polynucleotide" are used essentially interchangeably herein to refer to a DNA molecule that has been isolated free of total
10   genomic DNA of a particular species. "Isolated," as used herein, means that a polynucleotide is substantially away from other coding sequences, and that the DNA molecule does not contain large portions of unrelated coding DNA, such as large chromosomal fragments or other functional genes or polypeptide coding regions. Of course, this refers to the DNA molecule as originally isolated, and does not exclude
15   genes or coding regions later added to the segment by the hand of man.

As will be understood by those skilled in the art, the polynucleotide compositions of this invention can include genomic sequences, extra-genomic and plasmid-encoded sequences and smaller engineered gene segments that express, or may be adapted to express, proteins, polypeptides, peptides and the like. Such segments may
20   be naturally isolated, or modified synthetically by the hand of man.

As will be also recognized by the skilled artisan, polynucleotides of the invention may be single-stranded (coding or antisense) or double-stranded, and may be DNA (genomic, cDNA or synthetic) or RNA molecules. RNA molecules may include HnRNA molecules, which contain introns and correspond to a DNA molecule in a one-
25   to-one manner, and mRNA molecules, which do not contain introns. Additional coding or non-coding sequences may, but need not, be present within a polynucleotide of the present invention, and a polynucleotide may, but need not, be linked to other molecules and/or support materials.

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Polynucleotides may comprise a native sequence (*i.e.*, an endogenous sequence that encodes a polypeptide/protein of the invention or a portion thereof) or may comprise a sequence that encodes a variant or derivative, preferably an immunogenic variant or derivative, of such a sequence.

5   Therefore, according to another aspect of the present invention, polynucleotide compositions are provided that comprise some or all of a polynucleotide sequence set forth in any one of SEQ ID NOs: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-705, 709-774, 777, 789, 817, 823, 10   824, 878, 880-882, 894, 896, 907, 908, 916-919, 929-931, 938, 939 and 942, complements of a polynucleotide sequence set forth in any one of SEQ ID NOs: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-705, 709-774, 777, 789, 817, 823, 824, 878, 880-882, 894, 896, 907, 908, 916-919, 929-15   931, 938, 939 and 942, and degenerate variants of a polynucleotide sequence set forth in any one of SEQ ID NOs: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-705, 709-774, 777, 789, 817, 823, 824, 878, 880-882, 894, 896, 907, 908, 916-919, 929-931, 938, 939 and 942.   In certain preferred 20   embodiments, the polynucleotide sequences set forth herein encode immunogenic polypeptides, as described above.

In other related embodiments, the present invention provides polynucleotide variants having substantial identity to the sequences disclosed herein in SEQ ID NOs: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-25   335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-705, 709-774, 777, 789, 817, 823, 824, 878, 880-882, 894, 896, 907, 908, 916-919, 929-931, 938, 939 and 942, for example those comprising at least 70% sequence identity, preferably at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% or higher, sequence identity compared to a polynucleotide sequence of this 30   invention using the methods described herein, (*e.g.*, BLAST analysis using standard

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parameters, as described below). One skilled in this art will recognize that these values can be appropriately adjusted to determine corresponding identity of proteins encoded by two nucleotide sequences by taking into account codon degeneracy, amino acid similarity, reading frame positioning and the like.

5   Typically, polynucleotide variants will contain one or more substitutions, additions, deletions and/or insertions, preferably such that the immunogenicity of the polypeptide encoded by the variant polynucleotide is not substantially diminished relative to a polypeptide encoded by a polynucleotide sequence specifically set forth herein). The term "variants" should also be understood to encompasses homologous
10   genes of xenogenic origin.

In additional embodiments, the present invention provides polynucleotide fragments comprising various lengths of contiguous stretches of sequence identical to, or complementary to, one or more of the sequences disclosed herein. For example, polynucleotides are provided by this invention that comprise at
15   least about 10, 15, 20, 30, 40, 50, 75, 100, 150, 200, 300, 400, 500 or 1000 or more contiguous nucleotides of one or more of the sequences disclosed herein as well as all intermediate lengths there between. It will be readily understood that "intermediate lengths", in this context, means any length between the quoted values, such as 16, 17, 18, 19, etc.; 21, 22, 23, etc.; 30, 31, 32, etc.; 50, 51, 52, 53, etc.; 100, 101, 102, 103,
20   etc.; 150, 151, 152, 153, etc.; including all integers through 200-500; 500-1,000, and the like.

In another embodiment of the invention, polynucleotide compositions are provided that are capable of hybridizing under moderate to high stringency conditions to a polynucleotide sequence provided herein, or a fragment thereof, or a complementary
25   sequence thereof. Hybridization techniques are well known in the art of molecular biology. For purposes of illustration, suitable moderately stringent conditions for testing the hybridization of a polynucleotide of this invention with other polynucleotides include prewashing in a solution of 5 X SSC, 0.5% SDS, 1.0 mM EDTA (pH 8.0); hybridizing at 50°C-60°C, 5 X SSC, overnight; followed by washing twice at 65°C for
30   20 minutes with each of 2X, 0.5X and 0.2X SSC containing 0.1% SDS. One skilled in

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the art will understand that the stringency of hybridization can be readily manipulated, such as by altering the salt content of the hybridization solution and/or the temperature at which the hybridization is performed. For example, in another embodiment, suitable highly stringent hybridization conditions include those described above, with the

5   exception that the temperature of hybridization is increased, e.g., to 60-65°C or 65-70°C.

In certain preferred embodiments, the polynucleotides described above, e.g., polynucleotide variants, fragments and hybridizing sequences, encode polypeptides that are immunologically cross-reactive with a polypeptide sequence specifically set

10   forth herein. In other preferred embodiments, such polynucleotides encode polypeptides that have a level of immunogenic activity of at least about 50%, preferably at least about 70%, and more preferably at least about 90% of that for a polypeptide sequence specifically set forth herein.

The polynucleotides of the present invention, or fragments thereof,

15   regardless of the length of the coding sequence itself, may be combined with other DNA sequences, such as promoters, polyadenylation signals, additional restriction enzyme sites, multiple cloning sites, other coding segments, and the like, such that their overall length may vary considerably. It is therefore contemplated that a nucleic acid fragment of almost any length may be employed, with the total length preferably being limited by

20   the ease of preparation and use in the intended recombinant DNA protocol. For example, illustrative polynucleotide segments with total lengths of about 10,000, about 5000, about 3000, about 2,000, about 1,000, about 500, about 200, about 100, about 50 base pairs in length, and the like, (including all intermediate lengths) are contemplated to be useful in many implementations of this invention.

25   When comparing polynucleotide sequences, two sequences are said to be "identical" if the sequence of nucleotides in the two sequences is the same when aligned for maximum correspondence, as described below. Comparisons between two sequences are typically performed by comparing the sequences over a comparison window to identify and compare local regions of sequence similarity. A "comparison

30   window" as used herein, refers to a segment of at least about 20 contiguous positions,

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usually 30 to about 75, preferably 40 to about 50, in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned.

Optimal alignment of sequences for comparison may be conducted using the Megalign program in the Lasergene suite of bioinformatics software (DNASTAR, Inc., Madison, WI), using default parameters. This program embodies several alignment schemes described in the following references: Dayhoff, M.O. (1978) A model of evolutionary change in proteins – Matrices for detecting distant relationships. In Dayhoff, M.O. (ed.) Atlas of Protein Sequence and Structure, National Biomedical Research Foundation, Washington DC Vol. 5, Suppl. 3, pp. 345-358; Hein J. (1990) Unified Approach to Alignment and Phylogenes pp. 626-645 *Methods in Enzymology* vol. 183, Academic Press, Inc., San Diego, CA; Higgins, D.G. and Sharp, P.M. (1989) *CABIOS 5*:151-153; Myers, E.W. and Muller W. (1988) *CABIOS 4*:11-17; Robinson, E.D. (1971) *Comb. Theor 11*:105; Santou, N. Nes, M. (1987) *Mol. Biol. Evol. 4*:406-425; Sneath, P.H.A. and Sokal, R.R. (1973) *Numerical Taxonomy – the Principles and Practice of Numerical Taxonomy*, Freeman Press, San Francisco, CA; Wilbur, W.J. and Lipman, D.J. (1983) *Proc. Natl. Acad., Sci. USA 80*:726-730.

Alternatively, optimal alignment of sequences for comparison may be conducted by the local identity algorithm of Smith and Waterman (1981) *Add. APL. Math 2*:482, by the identity alignment algorithm of Needleman and Wunsch (1970) *J. Mol. Biol.* 48:443, by the search for similarity methods of Pearson and Lipman (1988) *Proc. Natl. Acad. Sci. USA* 85: 2444, by computerized implementations of these algorithms (GAP, BESTFIT, BLAST, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group (GCG), 575 Science Dr., Madison, WI), or by inspection.

One preferred example of algorithms that are suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul et al. (1977) *Nucl. Acids Res.* 25:3389-3402 and Altschul et al. (1990) *J. Mol. Biol.* 215:403-410, respectively. BLAST and BLAST 2.0 can be used, for example with the parameters described herein, to determine percent

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sequence identity for the polynucleotides of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information. In one illustrative example, cumulative scores can be calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always >0) and N (penalty score for mismatching residues; always <0). Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff and Henikoff (1989) *Proc. Natl. Acad. Sci. USA* 89:10915) alignments, (B) of 50, expectation (E) of 10, M=5, N=−4 and a comparison of both strands.

Preferably, the "percentage of sequence identity" is determined by comparing two optimally aligned sequences over a window of comparison of at least 20 positions, wherein the portion of the polynucleotide sequence in the comparison window may comprise additions or deletions (*i.e.*, gaps) of 20 percent or less, usually 5 to 15 percent, or 10 to 12 percent, as compared to the reference sequences (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid bases occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the reference sequence (*i.e.*, the window size) and multiplying the results by 100 to yield the percentage of sequence identity.

It will be appreciated by those of ordinary skill in the art that, as a result of the degeneracy of the genetic code, there are many nucleotide sequences that encode a polypeptide as described herein. Some of these polynucleotides bear minimal homology to the nucleotide sequence of any native gene. Nonetheless, polynucleotides that vary due to differences in codon usage are specifically contemplated by the present

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invention. Further, alleles of the genes comprising the polynucleotide sequences provided herein are within the scope of the present invention. Alleles are endogenous genes that are altered as a result of one or more mutations, such as deletions, additions and/or substitutions of nucleotides. The resulting mRNA and protein may, but need not,

5   have an altered structure or function. Alleles may be identified using standard techniques (such as hybridization, amplification and/or database sequence comparison).

Therefore, in another embodiment of the invention, a mutagenesis approach, such as site-specific mutagenesis, is employed for the preparation of immunogenic variants and/or derivatives of the polypeptides described herein. By this

10 approach, specific modifications in a polypeptide sequence can be made through mutagenesis of the underlying polynucleotides that encode them. These techniques provides a straightforward approach to prepare and test sequence variants, for example, incorporating one or more of the foregoing considerations, by introducing one or more nucleotide sequence changes into the polynucleotide.

15 Site-specific mutagenesis allows the production of mutants through the use of specific oligonucleotide sequences which encode the DNA sequence of the desired mutation, as well as a sufficient number of adjacent nucleotides, to provide a primer sequence of sufficient size and sequence complexity to form a stable duplex on both sides of the deletion junction being traversed. Mutations may be employed in a

20 selected polynucleotide sequence to improve, alter, decrease, modify, or otherwise change the properties of the polynucleotide itself, and/or alter the properties, activity, composition, stability, or primary sequence of the encoded polypeptide.

In certain embodiments of the present invention, the inventors contemplate the mutagenesis of the disclosed polynucleotide sequences to alter one or

25 more properties of the encoded polypeptide, such as the immunogenicity of a polypeptide vaccine. The techniques of site-specific mutagenesis are well-known in the art, and are widely used to create variants of both polypeptides and polynucleotides. For example, site-specific mutagenesis is often used to alter a specific portion of a DNA molecule. In such embodiments, a primer comprising typically about 14 to about 25

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nucleotides or so in length is employed, with about 5 to about 10 residues on both sides of the junction of the sequence being altered.

As will be appreciated by those of skill in the art, site-specific mutagenesis techniques have often employed a phage vector that exists in both a single stranded and double stranded form. Typical vectors useful in site-directed mutagenesis include vectors such as the M13 phage. These phage are readily commercially-available and their use is generally well-known to those skilled in the art. Double-stranded plasmids are also routinely employed in site directed mutagenesis that eliminates the step of transferring the gene of interest from a plasmid to a phage.

In general, site-directed mutagenesis in accordance herewith is performed by first obtaining a single-stranded vector or melting apart of two strands of a double-stranded vector that includes within its sequence a DNA sequence that encodes the desired peptide. An oligonucleotide primer bearing the desired mutated sequence is prepared, generally synthetically. This primer is then annealed with the single-stranded vector, and subjected to DNA polymerizing enzymes such as *E. coli* polymerase I Klenow fragment, in order to complete the synthesis of the mutation-bearing strand. Thus, a heteroduplex is formed wherein one strand encodes the original non-mutated sequence and the second strand bears the desired mutation. This heteroduplex vector is then used to transform appropriate cells, such as *E. coli* cells, and clones are selected which include recombinant vectors bearing the mutated sequence arrangement.

The preparation of sequence variants of the selected peptide-encoding DNA segments using site-directed mutagenesis provides a means of producing potentially useful species and is not meant to be limiting as there are other ways in which sequence variants of peptides and the DNA sequences encoding them may be obtained. For example, recombinant vectors encoding the desired peptide sequence may be treated with mutagenic agents, such as hydroxylamine, to obtain sequence variants. Specific details regarding these methods and protocols are found in the teachings of Maloy *et al.*, 1994; Segal, 1976; Prokop and Bajpai, 1991; Kuby, 1994; and Maniatis *et al.*, 1982, each incorporated herein by reference, for that purpose.

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As used herein, the term "oligonucleotide directed mutagenesis procedure" refers to template-dependent processes and vector-mediated propagation which result in an increase in the concentration of a specific nucleic acid molecule relative to its initial concentration, or in an increase in the concentration of a detectable

5   signal, such as amplification. As used herein, the term "oligonucleotide directed mutagenesis procedure" is intended to refer to a process that involves the template-dependent extension of a primer molecule. The term template dependent process refers to nucleic acid synthesis of an RNA or a DNA molecule wherein the sequence of the newly synthesized strand of nucleic acid is dictated by the well-known

10 rules of complementary base pairing (see, for example, Watson, 1987). Typically, vector mediated methodologies involve the introduction of the nucleic acid fragment into a DNA or RNA vector, the clonal amplification of the vector, and the recovery of the amplified nucleic acid fragment. Examples of such methodologies are provided by U. S. Patent No. 4,237,224, specifically incorporated herein by reference in its entirety.

15 In another approach for the production of polypeptide variants of the present invention, recursive sequence recombination, as described in U.S. Patent No. 5,837,458, may be employed. In this approach, iterative cycles of recombination and screening or selection are performed to "evolve" individual polynucleotide variants of the invention having, for example, enhanced immunogenic activity.

20 In other embodiments of the present invention, the polynucleotide sequences provided herein can be advantageously used as probes or primers for nucleic acid hybridization. As such, it is contemplated that nucleic acid segments that comprise a sequence region of at least about 15 contiguous nucleotides that has the same sequence as, or is complementary to, a 15 nucleotide long contiguous sequence

25 disclosed herein will find particular utility. Longer contiguous identical or complementary sequences, e.g., those of about 20, 30, 40, 50, 100, 200, 500, 1000 (including all intermediate lengths) and even up to full length sequences will also be of use in certain embodiments.

The ability of such nucleic acid probes to specifically hybridize to a

30 sequence of interest will enable them to be of use in detecting the presence of

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complementary sequences in a given sample. However, other uses are also envisioned, such as the use of the sequence information for the preparation of mutant species primers, or primers for use in preparing other genetic constructions.

Polynucleotide molecules having sequence regions consisting of contiguous nucleotide stretches of 10-14, 15-20, 30, 50, or even of 100-200 nucleotides or so (including intermediate lengths as well), identical or complementary to a polynucleotide sequence disclosed herein, are particularly contemplated as hybridization probes for use in, *e.g.*, Southern and Northern blotting. This would allow a gene product, or fragment thereof, to be analyzed, both in diverse cell types and also in various bacterial cells. The total size of fragment, as well as the size of the complementary stretch(es), will ultimately depend on the intended use or application of the particular nucleic acid segment. Smaller fragments will generally find use in hybridization embodiments, wherein the length of the contiguous complementary region may be varied, such as between about 15 and about 100 nucleotides, but larger contiguous complementarity stretches may be used, according to the length complementary sequences one wishes to detect.

The use of a hybridization probe of about 15-25 nucleotides in length allows the formation of a duplex molecule that is both stable and selective. Molecules having contiguous complementary sequences over stretches greater than 15 bases in length are generally preferred, though, in order to increase stability and selectivity of the hybrid, and thereby improve the quality and degree of specific hybrid molecules obtained. One will generally prefer to design nucleic acid molecules having gene-complementary stretches of 15 to 25 contiguous nucleotides, or even longer where desired.

Hybridization probes may be selected from any portion of any of the sequences disclosed herein. All that is required is to review the sequences set forth herein, or to any continuous portion of the sequences, from about 15-25 nucleotides in length up to and including the full length sequence, that one wishes to utilize as a probe or primer. The choice of probe and primer sequences may be governed by various

factors. For example, one may wish to employ primers from towards the termini of the total sequence.

Small polynucleotide segments or fragments may be readily prepared by, for example, directly synthesizing the fragment by chemical means, as is commonly practiced using an automated oligonucleotide synthesizer. Also, fragments may be obtained by application of nucleic acid reproduction technology, such as the PCR™ technology of U. S. Patent 4,683,202 (incorporated herein by reference), by introducing selected sequences into recombinant vectors for recombinant production, and by other recombinant DNA techniques generally known to those of skill in the art of molecular biology.

The nucleotide sequences of the invention may be used for their ability to selectively form duplex molecules with complementary stretches of the entire gene or gene fragments of interest. Depending on the application envisioned, one will typically desire to employ varying conditions of hybridization to achieve varying degrees of selectivity of probe towards target sequence. For applications requiring high selectivity, one will typically desire to employ relatively stringent conditions to form the hybrids, e.g., one will select relatively low salt and/or high temperature conditions, such as provided by a salt concentration of from about 0.02 M to about 0.15 M salt at temperatures of from about 50°C to about 70°C. Such selective conditions tolerate little, if any, mismatch between the probe and the template or target strand, and would be particularly suitable for isolating related sequences.

Of course, for some applications, for example, where one desires to prepare mutants employing a mutant primer strand hybridized to an underlying template, less stringent (reduced stringency) hybridization conditions will typically be needed in order to allow formation of the heteroduplex. In these circumstances, one may desire to employ salt conditions such as those of from about 0.15 M to about 0.9 M salt, at temperatures ranging from about 20°C to about 55°C. Cross-hybridizing species can thereby be readily identified as positively hybridizing signals with respect to control hybridizations. In any case, it is generally appreciated that conditions can be rendered more stringent by the addition of increasing amounts of formamide, which serves to

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destabilize the hybrid duplex in the same manner as increased temperature. Thus, hybridization conditions can be readily manipulated, and thus will generally be a method of choice depending on the desired results.

According to another embodiment of the present invention, polynucleotide compositions comprising antisense oligonucleotides are provided. Antisense oligonucleotides have been demonstrated to be effective and targeted inhibitors of protein synthesis, and, consequently, provide a therapeutic approach by which a disease can be treated by inhibiting the synthesis of proteins that contribute to the disease. The efficacy of antisense oligonucleotides for inhibiting protein synthesis is well established. For example, the synthesis of polygalactauronase and the muscarine type 2 acetylcholine receptor are inhibited by antisense oligonucleotides directed to their respective mRNA sequences (U. S. Patent 5,739,119 and U. S. Patent 5,759,829). Further, examples of antisense inhibition have been demonstrated with the nuclear protein cyclin, the multiple drug resistance gene (MDG1), ICAM-1, E-selectin, STK-1, striatal GABA$_A$ receptor and human EGF (Jaskulski *et al.*, Science. 1988 Jun 10;240(4858):1544-6; Vasanthakumar and Ahmed, Cancer Commun. 1989;1(4):225-32; Peris *et al.*, Brain Res Mol Brain Res. 1998 Jun 15;57(2):310-20; U. S. Patent 5,801,154; U.S. Patent 5,789,573; U. S. Patent 5,718,709 and U.S. Patent 5,610,288). Antisense constructs have also been described that inhibit and can be used to treat a variety of abnormal cellular proliferations, *e.g.* cancer (U. S. Patent 5,747,470; U. S. Patent 5,591,317 and U. S. Patent 5,783,683).

Therefore, in certain embodiments, the present invention provides oligonucleotide sequences that comprise all, or a portion of, any sequence that is capable of specifically binding to polynucleotide sequence described herein, or a complement thereof. In one embodiment, the antisense oligonucleotides comprise DNA or derivatives thereof. In another embodiment, the oligonucleotides comprise RNA or derivatives thereof. In a third embodiment, the oligonucleotides are modified DNAs comprising a phosphorothioated modified backbone. In a fourth embodiment, the oligonucleotide sequences comprise peptide nucleic acids or derivatives thereof. In each case, preferred compositions comprise a sequence region that is complementary,

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and more preferably substantially-complementary, and even more preferably, completely complementary to one or more portions of polynucleotides disclosed herein. Selection of antisense compositions specific for a given gene sequence is based upon analysis of the chosen target sequence and determination of secondary structure, T_m,

5   binding energy, and relative stability. Antisense compositions may be selected based upon their relative inability to form dimers, hairpins, or other secondary structures that would reduce or prohibit specific binding to the target mRNA in a host cell. Highly preferred target regions of the mRNA, are those which are at or near the AUG translation initiation codon, and those sequences which are substantially complementary

10   to 5' regions of the mRNA. These secondary structure analyses and target site selection considerations can be performed, for example, using v.4 of the OLIGO primer analysis software and/or the BLASTN 2.0.5 algorithm software (Altschul et al., Nucleic Acids Res. 1997 Sep 1;25(17):3389-402).

The use of an antisense delivery method employing a short peptide

15   vector, termed MPG (27 residues), is also contemplated. The MPG peptide contains a hydrophobic domain derived from the fusion sequence of HIV gp41 and a hydrophilic domain from the nuclear localization sequence of SV40 T-antigen (Morris et al., Nucleic Acids Res. 1997 Jul 15;25(14):2730-6). It has been demonstrated that several molecules of the MPG peptide coat the antisense oligonucleotides and can be delivered

20   into cultured mammalian cells in less than 1 hour with relatively high efficiency (90%). Further, the interaction with MPG strongly increases both the stability of the oligonucleotide to nuclease and the ability to cross the plasma membrane.

According to another embodiment of the invention, the polynucleotide compositions described herein are used in the design and preparation of ribozyme

25   molecules for inhibiting expression of the tumor polypeptides and proteins of the present invention in tumor cells. Ribozymes are RNA-protein complexes that cleave nucleic acids in a site-specific fashion. Ribozymes have specific catalytic domains that possess endonuclease activity (Kim and Cech, Proc Natl Acad Sci U S A. 1987 Dec;84(24):8788-92; Forster and Symons, Cell. 1987 Apr 24;49(2):211-20). For

30   example, a large number of ribozymes accelerate phosphoester transfer reactions with a

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high degree of specificity, often cleaving only one of several phosphoesters in an oligonucleotide substrate (Cech *et al.*, Cell. 1981 Dec;27(3 Pt 2):487-96; Michel and Westhof, J Mol Biol. 1990 Dec 5;216(3):585-610; Reinhold-Hurek and Shub, Nature. 1992 May 14;357(6374):173-6). This specificity has been attributed to the requirement

5   that the substrate bind via specific base-pairing interactions to the internal guide sequence ("IGS") of the ribozyme prior to chemical reaction.

Six basic varieties of naturally-occurring enzymatic RNAs are known presently. Each can catalyze the hydrolysis of RNA phosphodiester bonds *in trans* (and thus can cleave other RNA molecules) under physiological conditions. In general,

10 enzymatic nucleic acids act by first binding to a target RNA. Such binding occurs through the target binding portion of a enzymatic nucleic acid which is held in close proximity to an enzymatic portion of the molecule that acts to cleave the target RNA. Thus, the enzymatic nucleic acid first recognizes and then binds a target RNA through complementary base-pairing, and once bound to the correct site, acts enzymatically to

15 cut the target RNA. Strategic cleavage of such a target RNA will destroy its ability to direct synthesis of an encoded protein. After an enzymatic nucleic acid has bound and cleaved its RNA target, it is released from that RNA to search for another target and can repeatedly bind and cleave new targets.

The enzymatic nature of a ribozyme is advantageous over many

20 technologies, such as antisense technology (where a nucleic acid molecule simply binds to a nucleic acid target to block its translation) since the concentration of ribozyme necessary to affect a therapeutic treatment is lower than that of an antisense oligonucleotide. This advantage reflects the ability of the ribozyme to act enzymatically. Thus, a single ribozyme molecule is able to cleave many molecules of

25 target RNA. In addition, the ribozyme is a highly specific inhibitor, with the specificity of inhibition depending not only on the base pairing mechanism of binding to the target RNA, but also on the mechanism of target RNA cleavage. Single mismatches, or base-substitutions, near the site of cleavage can completely eliminate catalytic activity of a ribozyme. Similar mismatches in antisense molecules do not prevent their action

30 (Woolf *et al.*, Proc Natl Acad Sci U S A. 1992 Aug 15;89(16):7305-9). Thus, the

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specificity of action of a ribozyme is greater than that of an antisense oligonucleotide binding the same RNA site.

The enzymatic nucleic acid molecule may be formed in a hammerhead, hairpin, a hepatitis δ virus, group I intron or RNaseP RNA (in association with an RNA 5 guide sequence) or Neurospora VS RNA motif. Examples of hammerhead motifs are described by Rossi *et al.* Nucleic Acids Res. 1992 Sep 11;20(17):4559-65. Examples of hairpin motifs are described by Hampel *et al.* (Eur. Pat. Appl. Publ. No. EP 0360257), Hampel and Tritz, Biochemistry 1989 Jun 13;28(12):4929-33; Hampel *et al.*, Nucleic Acids Res. 1990 Jan 25;18(2):299-304 and U. S. Patent 5,631,359. An example of the 10 hepatitis δ virus motif is described by Perrotta and Been, Biochemistry. 1992 Dec 1;31(47):11843-52; an example of the RNaseP motif is described by Guerrier-Takada *et al.*, Cell. 1983 Dec;35(3 Pt 2):849-57; Neurospora VS RNA ribozyme motif is described by Collins (Saville and Collins, Cell. 1990 May 18;61(4):685-96; Saville and Collins, Proc Natl Acad Sci U S A. 1991 Oct 1;88(19):8826-30; Collins and Olive, 15 Biochemistry. 1993 Mar 23;32(11):2795-9); and an example of the Group I intron is described in (U. S. Patent 4,987,071). All that is important in an enzymatic nucleic acid molecule of this invention is that it has a specific substrate binding site which is complementary to one or more of the target gene RNA regions, and that it have nucleotide sequences within or surrounding that substrate binding site which impart an 20 RNA cleaving activity to the molecule. Thus the ribozyme constructs need not be limited to specific motifs mentioned herein.

Ribozymes may be designed as described in Int. Pat. Appl. Publ. No. WO 93/23569 and Int. Pat. Appl. Publ. No. WO 94/02595, each specifically incorporated herein by reference) and synthesized to be tested *in vitro* and *in vivo*, as 25 described. Such ribozymes can also be optimized for delivery. While specific examples are provided, those in the art will recognize that equivalent RNA targets in other species can be utilized when necessary.

Ribozyme activity can be optimized by altering the length of the ribozyme binding arms, or chemically synthesizing ribozymes with modifications that 30 prevent their degradation by serum ribonucleases (see *e.g.*, Int. Pat. Appl. Publ. No. WO

92/07065; Int. Pat. Appl. Publ. No. WO 93/15187; Int. Pat. Appl. Publ. No. WO 91/03162; Eur. Pat. Appl. Publ. No. 92110298.4; U. S. Patent 5,334,711; and Int. Pat. Appl. Publ. No. WO 94/13688, which describe various chemical modifications that can be made to the sugar moieties of enzymatic RNA molecules), modifications which

5   enhance their efficacy in cells, and removal of stem II bases to shorten RNA synthesis times and reduce chemical requirements.

Sullivan *et al.* (Int. Pat. Appl. Publ. No. WO 94/02595) describes the general methods for delivery of enzymatic RNA molecules. Ribozymes may be administered to cells by a variety of methods known to those familiar to the art,

10   including, but not restricted to, encapsulation in liposomes, by iontophoresis, or by incorporation into other vehicles, such as hydrogels, cyclodextrins, biodegradable nanocapsules, and bioadhesive microspheres. For some indications, ribozymes may be directly delivered *ex vivo* to cells or tissues with or without the aforementioned vehicles. Alternatively, the RNA/vehicle combination may be locally delivered by direct

15   inhalation, by direct injection or by use of a catheter, infusion pump or stent. Other routes of delivery include, but are not limited to, intravascular, intramuscular, subcutaneous or joint injection, aerosol inhalation, oral (tablet or pill form), topical, systemic, ocular, intraperitoneal and/or intrathecal delivery. More detailed descriptions of ribozyme delivery and administration are provided in Int. Pat. Appl. Publ. No. WO

20   94/02595 and Int. Pat. Appl. Publ. No. WO 93/23569, each specifically incorporated herein by reference.

Another means of accumulating high concentrations of a ribozyme(s) within cells is to incorporate the ribozyme-encoding sequences into a DNA expression vector. Transcription of the ribozyme sequences are driven from a promoter for

25   eukaryotic RNA polymerase I (pol I), RNA polymerase II (pol II), or RNA polymerase III (pol III). Transcripts from pol II or pol III promoters will be expressed at high levels in all cells; the levels of a given pol II promoter in a given cell type will depend on the nature of the gene regulatory sequences (enhancers, silencers, *etc.*) present nearby. Prokaryotic RNA polymerase promoters may also be used, providing that the

30   prokaryotic RNA polymerase enzyme is expressed in the appropriate cells Ribozymes

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expressed from such promoters have been shown to function in mammalian cells. Such transcription units can be incorporated into a variety of vectors for introduction into mammalian cells, including but not restricted to, plasmid DNA vectors, viral DNA vectors (such as adenovirus or adeno-associated vectors), or viral RNA vectors (such as retroviral, semliki forest virus, sindbis virus vectors).

In another embodiment of the invention, peptide nucleic acids (PNAs) compositions are provided. PNA is a DNA mimic in which the nucleobases are attached to a pseudopeptide backbone (Good and Nielsen, Antisense Nucleic Acid Drug Dev. 1997 7(4) 431-37). PNA is able to be utilized in a number methods that traditionally have used RNA or DNA. Often PNA sequences perform better in techniques than the corresponding RNA or DNA sequences and have utilities that are not inherent to RNA or DNA. A review of PNA including methods of making, characteristics of, and methods of using, is provided by Corey (*Trends Biotechnol* 1997 Jun;15(6):224-9). As such, in certain embodiments, one may prepare PNA sequences that are complementary to one or more portions of the ACE mRNA sequence, and such PNA compositions may be used to regulate, alter, decrease, or reduce the translation of ACE-specific mRNA, and thereby alter the level of ACE activity in a host cell to which such PNA compositions have been administered.

PNAs have 2-aminoethyl-glycine linkages replacing the normal phosphodiester backbone of DNA (Nielsen *et al.*, *Science* 1991 Dec 6;254(5037):1497-500; Hanvey *et al.*, Science. 1992 Nov 27;258(5087):1481-5; Hyrup and Nielsen, Bioorg Med Chem. 1996 Jan;4(1):5-23). This chemistry has three important consequences: firstly, in contrast to DNA or phosphorothioate oligonucleotides, PNAs are neutral molecules; secondly, PNAs are achiral, which avoids the need to develop a stereoselective synthesis; and thirdly, PNA synthesis uses standard Boc or Fmoc protocols for solid-phase peptide synthesis, although other methods, including a modified Merrifield method, have been used.

PNA monomers or ready-made oligomers are commercially available from PerSeptive Biosystems (Framingham, MA). PNA syntheses by either Boc or Fmoc protocols are straightforward using manual or automated protocols (Norton *et al.*,

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Bioorg Med Chem. 1995 Apr;3(4):437-45). The manual protocol lends itself to the production of chemically modified PNAs or the simultaneous synthesis of families of closely related PNAs.

As with peptide synthesis, the success of a particular PNA synthesis will depend on the properties of the chosen sequence. For example, while in theory PNAs can incorporate any combination of nucleotide bases, the presence of adjacent purines can lead to deletions of one or more residues in the product. In expectation of this difficulty, it is suggested that, in producing PNAs with adjacent purines, one should repeat the coupling of residues likely to be added inefficiently. This should be followed by the purification of PNAs by reverse-phase high-pressure liquid chromatography, providing yields and purity of product similar to those observed during the synthesis of peptides.

Modifications of PNAs for a given application may be accomplished by coupling amino acids during solid-phase synthesis or by attaching compounds that contain a carboxylic acid group to the exposed N-terminal amine. Alternatively, PNAs can be modified after synthesis by coupling to an introduced lysine or cysteine. The ease with which PNAs can be modified facilitates optimization for better solubility or for specific functional requirements. Once synthesized, the identity of PNAs and their derivatives can be confirmed by mass spectrometry. Several studies have made and utilized modifications of PNAs (for example, Norton et al., Bioorg Med Chem. 1995 Apr;3(4):437-45; Petersen et al., J Pept Sci. 1995 May-Jun;1(3):175-83; Orum et al., Biotechniques. 1995 Sep;19(3):472-80; Footer et al., Biochemistry. 1996 Aug 20;35(33):10673-9; Griffith et al., Nucleic Acids Res. 1995 Aug 11;23(15):3003-8; Pardridge et al., Proc Natl Acad Sci U S A. 1995 Jun 6;92(12):5592-6; Boffa et al., Proc Natl Acad Sci U S A. 1995 Mar 14;92(6):1901-5; Gambacorti-Passerini et al., Blood. 1996 Aug 15;88(4):1411-7; Armitage et al., Proc Natl Acad Sci U S A. 1997 Nov 11;94(23):12320-5; Seeger et al., Biotechniques. 1997 Sep;23(3):512-7). U.S. Patent No. 5,700,922 discusses PNA-DNA-PNA chimeric molecules and their uses in diagnostics, modulating protein in organisms, and treatment of conditions susceptible to therapeutics.

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Methods of characterizing the antisense binding properties of PNAs are discussed in Rose (Anal Chem. 1993 Dec 15;65(24):3545-9) and Jensen *et al.* (Biochemistry. 1997 Apr 22;36(16):5072-7). Rose uses capillary gel electrophoresis to determine binding of PNAs to their complementary oligonucleotide, measuring the
5   relative binding kinetics and stoichiometry. Similar types of measurements were made by Jensen *et al.* using BIAcore™ technology.

Other applications of PNAs that have been described and will be apparent to the skilled artisan include use in DNA strand invasion, antisense inhibition, mutational analysis, enhancers of transcription, nucleic acid purification, isolation of
10   transcriptionally active genes, blocking of transcription factor binding, genome cleavage, biosensors, *in situ* hybridization, and the like.

Polynucleotide Identification, Characterization and Expression

Polynucleotide compositions of the present invention may be identified, prepared and/or manipulated using any of a variety of well established techniques *(see*
15   generally, Sambrook et al., *Molecular Cloning: A Laboratory Manual,* Cold Spring Harbor Laboratories, Cold Spring Harbor, NY, 1989, and other like references). For example, a polynucleotide may be identified, as described in more detail below, by screening a microarray of cDNAs for tumor-associated expression (*i.e.,* expression that is at least two fold greater in a tumor than in normal tissue, as determined using a
20   representative assay provided herein). Such screens may be performed, for example, using the microarray technology of Affymetrix, Inc. (Santa Clara, CA) according to the manufacturer's instructions (and essentially as described by Schena et al., *Proc. Natl. Acad. Sci. USA 93*:10614-10619, 1996 and Heller et al., *Proc. Natl. Acad. Sci. USA 94*:2150-2155, 1997). Alternatively, polynucleotides may be amplified from cDNA
25   prepared from cells expressing the proteins described herein, such as tumor cells.

Many template dependent processes are available to amplify a target sequences of interest present in a sample. One of the best known amplification methods is the polymerase chain reaction (PCR™) which is described in detail in U.S. Patent Nos. 4,683,195, 4,683,202 and 4,800,159, each of which is incorporated herein by

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reference in its entirety. Briefly, in PCR™, two primer sequences are prepared which are complementary to regions on opposite complementary strands of the target sequence. An excess of deoxynucleoside triphosphates is added to a reaction mixture along with a DNA polymerase (*e.g.*, *Taq* polymerase). If the target sequence is present

5   in a sample, the primers will bind to the target and the polymerase will cause the primers to be extended along the target sequence by adding on nucleotides. By raising and lowering the temperature of the reaction mixture, the extended primers will dissociate from the target to form reaction products, excess primers will bind to the target and to the reaction product and the process is repeated. Preferably reverse

10   transcription and PCR™ amplification procedure may be performed in order to quantify the amount of mRNA amplified. Polymerase chain reaction methodologies are well known in the art.

Any of a number of other template dependent processes, many of which are variations of the PCR ™ amplification technique, are readily known and available in

15   the art. Illustratively, some such methods include the ligase chain reaction (referred to as LCR), described, for example, in Eur. Pat. Appl. Publ. No. 320,308 and U.S. Patent No. 4,883,750; Qbeta Replicase, described in PCT Intl. Pat. Appl. Publ. No. PCT/US87/00880; Strand Displacement Amplification (SDA) and Repair Chain Reaction (RCR). Still other amplification methods are described in Great Britain Pat.

20   Appl. No. 2 202 328, and in PCT Intl. Pat. Appl. Publ. No. PCT/US89/01025. Other nucleic acid amplification procedures include transcription-based amplification systems (TAS) (PCT Intl. Pat. Appl. Publ. No. WO 88/10315), including nucleic acid sequence based amplification (NASBA) and 3SR. Eur. Pat. Appl. Publ. No. 329,822 describes a nucleic acid amplification process involving cyclically synthesizing single-stranded

25   RNA ("ssRNA"), ssDNA, and double-stranded DNA (dsDNA). PCT Intl. Pat. Appl. Publ. No. WO 89/06700 describes a nucleic acid sequence amplification scheme based on the hybridization of a promoter/primer sequence to a target single-stranded DNA ("ssDNA") followed by transcription of many RNA copies of the sequence. Other amplification methods such as "RACE" (Frohman, 1990), and "one-sided PCR" (Ohara,

30   1989) are also well-known to those of skill in the art.

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An amplified portion of a polynucleotide of the present invention may be used to isolate a full length gene from a suitable library (*e.g.*, a tumor cDNA library) using well known techniques. Within such techniques, a library (cDNA or genomic) is screened using one or more polynucleotide probes or primers suitable for amplification.

5   Preferably, a library is size-selected to include larger molecules. Random primed libraries may also be preferred for identifying 5' and upstream regions of genes. Genomic libraries are preferred for obtaining introns and extending 5' sequences.

For hybridization techniques, a partial sequence may be labeled (*e.g.*, by nick-translation or end-labeling with ^{32}P) using well known techniques. A bacterial or

10   bacteriophage library is then generally screened by hybridizing filters containing denatured bacterial colonies (or lawns containing phage plaques) with the labeled probe (*see* Sambrook et al., *Molecular Cloning: A Laboratory Manual,* Cold Spring Harbor Laboratories, Cold Spring Harbor, NY, 1989). Hybridizing colonies or plaques are selected and expanded, and the DNA is isolated for further analysis. cDNA clones may

15   be analyzed to determine the amount of additional sequence by, for example, PCR using a primer from the partial sequence and a primer from the vector. Restriction maps and partial sequences may be generated to identify one or more overlapping clones. The complete sequence may then be determined using standard techniques, which may involve generating a series of deletion clones. The resulting overlapping sequences can

20   then assembled into a single contiguous sequence. A full length cDNA molecule can be generated by ligating suitable fragments, using well known techniques.

Alternatively, amplification techniques, such as those described above, can be useful for obtaining a full length coding sequence from a partial cDNA sequence. One such amplification technique is inverse PCR (*see* Triglia et al., *Nucl. Acids Res.*

25   *16*:8186, 1988), which uses restriction enzymes to generate a fragment in the known region of the gene. The fragment is then circularized by intramolecular ligation and used as a template for PCR with divergent primers derived from the known region. Within an alternative approach, sequences adjacent to a partial sequence may be retrieved by amplification with a primer to a linker sequence and a primer specific to a

30   known region. The amplified sequences are typically subjected to a second round of

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amplification with the same linker primer and a second primer specific to the known region. A variation on this procedure, which employs two primers that initiate extension in opposite directions from the known sequence, is described in WO 96/38591. Another such technique is known as "rapid amplification of cDNA ends" or

5   RACE. This technique involves the use of an internal primer and an external primer, which hybridizes to a polyA region or vector sequence, to identify sequences that are 5' and 3' of a known sequence. Additional techniques include capture PCR (Lagerstrom et al., *PCR Methods Applic. 1*:111-19, 1991) and walking PCR (Parker et al., *Nucl. Acids. Res. 19*:3055-60, 1991). Other methods employing amplification may also be employed

10   to obtain a full length cDNA sequence.

In certain instances, it is possible to obtain a full length cDNA sequence by analysis of sequences provided in an expressed sequence tag (EST) database, such as that available from GenBank. Searches for overlapping ESTs may generally be performed using well known programs (*e.g.*, NCBI BLAST searches), and such ESTs

15   may be used to generate a contiguous full length sequence. Full length DNA sequences may also be obtained by analysis of genomic fragments.

In other embodiments of the invention, polynucleotide sequences or fragments thereof which encode polypeptides of the invention, or fusion proteins or functional equivalents thereof, may be used in recombinant DNA molecules to direct

20   expression of a polypeptide in appropriate host cells. Due to the inherent degeneracy of the genetic code, other DNA sequences that encode substantially the same or a functionally equivalent amino acid sequence may be produced and these sequences may be used to clone and express a given polypeptide.

As will be understood by those of skill in the art, it may be advantageous

25   in some instances to produce polypeptide-encoding nucleotide sequences possessing non-naturally occurring codons. For example, codons preferred by a particular prokaryotic or eukaryotic host can be selected to increase the rate of protein expression or to produce a recombinant RNA transcript having desirable properties, such as a half-life which is longer than that of a transcript generated from the naturally occurring

30   sequence.

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Moreover, the polynucleotide sequences of the present invention can be engineered using methods generally known in the art in order to alter polypeptide encoding sequences for a variety of reasons, including but not limited to, alterations which modify the cloning, processing, and/or expression of the gene product. For example, DNA shuffling by random fragmentation and PCR reassembly of gene fragments and synthetic oligonucleotides may be used to engineer the nucleotide sequences. In addition, site-directed mutagenesis may be used to insert new restriction sites, alter glycosylation patterns, change codon preference, produce splice variants, or introduce mutations, and so forth.

In another embodiment of the invention, natural, modified, or recombinant nucleic acid sequences may be ligated to a heterologous sequence to encode a fusion protein. For example, to screen peptide libraries for inhibitors of polypeptide activity, it may be useful to encode a chimeric protein that can be recognized by a commercially available antibody. A fusion protein may also be engineered to contain a cleavage site located between the polypeptide-encoding sequence and the heterologous protein sequence, so that the polypeptide may be cleaved and purified away from the heterologous moiety.

Sequences encoding a desired polypeptide may be synthesized, in whole or in part, using chemical methods well known in the art (see Caruthers, M. H. et al. (1980) *Nucl. Acids Res. Symp. Ser.* 215-223, Horn, T. et al. (1980) *Nucl. Acids Res. Symp. Ser.* 225-232). Alternatively, the protein itself may be produced using chemical methods to synthesize the amino acid sequence of a polypeptide, or a portion thereof. For example, peptide synthesis can be performed using various solid-phase techniques (Roberge, J. Y. et al. (1995) *Science 269*:202-204) and automated synthesis may be achieved, for example, using the ABI 431A Peptide Synthesizer (Perkin Elmer, Palo Alto, CA).

A newly synthesized peptide may be substantially purified by preparative high performance liquid chromatography (*e.g.*, Creighton, T. (1983) Proteins, Structures and Molecular Principles, WH Freeman and Co., New York, N.Y.) or other comparable techniques available in the art. The composition of the synthetic peptides may be

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confirmed by amino acid analysis or sequencing (*e.g.*, the Edman degradation procedure). Additionally, the amino acid sequence of a polypeptide, or any part thereof, may be altered during direct synthesis and/or combined using chemical methods with sequences from other proteins, or any part thereof, to produce a variant polypeptide.

5   In order to express a desired polypeptide, the nucleotide sequences encoding the polypeptide, or functional equivalents, may be inserted into appropriate expression vector, *i.e.*, a vector which contains the necessary elements for the transcription and translation of the inserted coding sequence. Methods which are well known to those skilled in the art may be used to construct expression vectors containing

10   sequences encoding a polypeptide of interest and appropriate transcriptional and translational control elements. These methods include *in vitro* recombinant DNA techniques, synthetic techniques, and *in vivo* genetic recombination. Such techniques are described, for example, in Sambrook, J. et al. (1989) Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Press, Plainview, N.Y., and Ausubel, F. M. et

15   al. (1989) Current Protocols in Molecular Biology, John Wiley & Sons, New York. N.Y.

          A variety of expression vector/host systems may be utilized to contain and express polynucleotide sequences. These include, but are not limited to, microorganisms such as bacteria transformed with recombinant bacteriophage, plasmid,

20   or cosmid DNA expression vectors; yeast transformed with yeast expression vectors; insect cell systems infected with virus expression vectors (*e.g.*, baculovirus); plant cell systems transformed with virus expression vectors (*e.g.*, cauliflower mosaic virus, CaMV; tobacco mosaic virus, TMV) or with bacterial expression vectors (*e.g.*, Ti or pBR322 plasmids); or animal cell systems.

25   The "control elements" or "regulatory sequences" present in an expression vector are those non-translated regions of the vector--enhancers, promoters, 5' and 3' untranslated regions--which interact with host cellular proteins to carry out transcription and translation. Such elements may vary in their strength and specificity. Depending on the vector system and host utilized, any number of suitable transcription

30   and translation elements, including constitutive and inducible promoters, may be used.

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For example, when cloning in bacterial systems, inducible promoters such as the hybrid lacZ promoter of the PBLUESCRIPT phagemid (Stratagene, La Jolla, Calif.) or PSPORT1 plasmid (Gibco BRL, Gaithersburg, MD) and the like may be used. In mammalian cell systems, promoters from mammalian genes or from mammalian viruses

5   are generally preferred. If it is necessary to generate a cell line that contains multiple copies of the sequence encoding a polypeptide, vectors based on SV40 or EBV may be advantageously used with an appropriate selectable marker.

In bacterial systems, any of a number of expression vectors may be selected depending upon the use intended for the expressed polypeptide. For example,

10   when large quantities are needed, for example for the induction of antibodies, vectors which direct high level expression of fusion proteins that are readily purified may be used. Such vectors include, but are not limited to, the multifunctional *E. coli* cloning and expression vectors such as BLUESCRIPT (Stratagene), in which the sequence encoding the polypeptide of interest may be ligated into the vector in frame with

15   sequences for the amino-terminal Met and the subsequent 7 residues of .beta.- galactosidase so that a hybrid protein is produced; pIN vectors (Van Heeke, G. and S. M. Schuster (1989) *J. Biol. Chem.* *264*:5503-5509); and the like. pGEX Vectors (Promega, Madison, Wis.) may also be used to express foreign polypeptides as fusion proteins with glutathione S-transferase (GST). In general, such fusion proteins are

20   soluble and can easily be purified from lysed cells by adsorption to glutathione-agarose beads followed by elution in the presence of free glutathione. Proteins made in such systems may be designed to include heparin, thrombin, or factor XA protease cleavage sites so that the cloned polypeptide of interest can be released from the GST moiety at will.

25   In the yeast, Saccharomyces cerevisiae, a number of vectors containing constitutive or inducible promoters such as alpha factor, alcohol oxidase, and PGH may be used. For reviews, see Ausubel et al. (supra) and Grant et al. (1987) *Methods Enzymol.* 153:516-544.

In cases where plant expression vectors are used, the expression of

30   sequences encoding polypeptides may be driven by any of a number of promoters. For

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example, viral promoters such as the 35S and 19S promoters of CaMV may be used
alone or in combination with the omega leader sequence from TMV (Takamatsu, N.
(1987) *EMBO J. 6*:307-311. Alternatively, plant promoters such as the small subunit of
RUBISCO or heat shock promoters may be used (Coruzzi, G. et al. (1984) *EMBO J.*

5   *3*:1671-1680; Broglie, R. et al. (1984) *Science 224*:838-843; and Winter, J. et al. (1991)
Results Probl. Cell Differ. 17:85-105). These constructs can be introduced into plant
cells by direct DNA transformation or pathogen-mediated transfection. Such techniques
are described in a number of generally available reviews (see, for example, Hobbs, S. or
Murry, L. E. in McGraw Hill Yearbook of Science and Technology (1992) McGraw

10   Hill, New York, N.Y.; pp. 191-196).

An insect system may also be used to express a polypeptide of interest.
For example, in one such system, Autographa californica nuclear polyhedrosis virus
(AcNPV) is used as a vector to express foreign genes in Spodoptera frugiperda cells or
in Trichoplusia larvae. The sequences encoding the polypeptide may be cloned into a

15   non-essential region of the virus, such as the polyhedrin gene, and placed under control
of the polyhedrin promoter. Successful insertion of the polypeptide-encoding sequence
will render the polyhedrin gene inactive and produce recombinant virus lacking coat
protein. The recombinant viruses may then be used to infect, for example, S. frugiperda
cells or Trichoplusia larvae in which the polypeptide of interest may be expressed

20   (Engelhard, E. K. et al. (1994) *Proc. Natl. Acad. Sci. 91* :3224-3227).

In mammalian host cells, a number of viral-based expression systems are
generally available. For example, in cases where an adenovirus is used as an expression
vector, sequences encoding a polypeptide of interest may be ligated into an adenovirus
transcription/translation complex consisting of the late promoter and tripartite leader

25   sequence. Insertion in a non-essential E1 or E3 region of the viral genome may be used
to obtain a viable virus which is capable of expressing the polypeptide in infected host
cells (Logan, J. and Shenk, T. (1984) *Proc. Natl. Acad. Sci. 81*:3655-3659). In addition,
transcription enhancers, such as the Rous sarcoma virus (RSV) enhancer, may be used
to increase expression in mammalian host cells.

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Specific initiation signals may also be used to achieve more efficient translation of sequences encoding a polypeptide of interest. Such signals include the ATG initiation codon and adjacent sequences. In cases where sequences encoding the polypeptide, its initiation codon, and upstream sequences are inserted into the appropriate expression vector, no additional transcriptional or translational control signals may be needed. However, in cases where only coding sequence, or a portion thereof, is inserted, exogenous translational control signals including the ATG initiation codon should be provided. Furthermore, the initiation codon should be in the correct reading frame to ensure translation of the entire insert. Exogenous translational elements and initiation codons may be of various origins, both natural and synthetic. The efficiency of expression may be enhanced by the inclusion of enhancers which are appropriate for the particular cell system which is used, such as those described in the literature (Scharf, D. et al. (1994) *Results Probl. Cell Differ.* 20:125-162).

In addition, a host cell strain may be chosen for its ability to modulate the expression of the inserted sequences or to process the expressed protein in the desired fashion. Such modifications of the polypeptide include, but are not limited to, acetylation, carboxylation. glycosylation, phosphorylation, lipidation, and acylation. Post-translational processing which cleaves a "prepro" form of the protein may also be used to facilitate correct insertion, folding and/or function. Different host cells such as CHO, COS, HeLa, MDCK, HEK293, and WI38, which have specific cellular machinery and characteristic mechanisms for such post-translational activities, may be chosen to ensure the correct modification and processing of the foreign protein.

For long-term, high-yield production of recombinant proteins, stable expression is generally preferred. For example, cell lines which stably express a polynucleotide of interest may be transformed using expression vectors which may contain viral origins of replication and/or endogenous expression elements and a selectable marker gene on the same or on a separate vector. Following the introduction of the vector, cells may be allowed to grow for 1-2 days in an enriched media before they are switched to selective media. The purpose of the selectable marker is to confer resistance to selection, and its presence allows growth and recovery of cells which

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successfully express the introduced sequences. Resistant clones of stably transformed cells may be proliferated using tissue culture techniques appropriate to the cell type.

Any number of selection systems may be used to recover transformed cell lines. These include, but are not limited to, the herpes simplex virus thymidine

5   kinase (Wigler, M. et al. (1977) *Cell 11*:223-32) and adenine phosphoribosyltransferase (Lowy, I. et al. (1990) *Cell 22*:817-23) genes which can be employed in tk.sup.- or aprt.sup.- cells, respectively. Also, antimetabolite, antibiotic or herbicide resistance can be used as the basis for selection; for example, dhfr which confers resistance to methotrexate (Wigler, M. et al. (1980) *Proc. Natl. Acad. Sci. 77*:3567-70); npt, which

10   confers resistance to the aminoglycosides, neomycin and G-418 (Colbere-Garapin, F. et al (1981) *J. Mol. Biol. 150*:1-14); and als or pat, which confer resistance to chlorsulfuron and phosphinotricin acetyltransferase, respectively (Murry, *supra*). Additional selectable genes have been described, for example, trpB, which allows cells to utilize indole in place of tryptophan, or hisD, which allows cells to utilize histinol in

15   place of histidine (Hartman, S. C. and R. C. Mulligan (1988) *Proc. Natl. Acad. Sci. 85*:8047-51). The use of visible markers has gained popularity with such markers as anthocyanins, beta-glucuronidase and its substrate GUS, and luciferase and its substrate luciferin, being widely used not only to identify transformants, but also to quantify the amount of transient or stable protein expression attributable to a specific vector system

20   (Rhodes, C. A. et al. (1995) *Methods Mol. Biol. 55*:121-131).

Although the presence/absence of marker gene expression suggests that the gene of interest is also present, its presence and expression may need to be confirmed. For example, if the sequence encoding a polypeptide is inserted within a marker gene sequence, recombinant cells containing sequences can be identified by the

25   absence of marker gene function. Alternatively, a marker gene can be placed in tandem with a polypeptide-encoding sequence under the control of a single promoter. Expression of the marker gene in response to induction or selection usually indicates expression of the tandem gene as well.

Alternatively, host cells that contain and express a desired

30   polynucleotide sequence may be identified by a variety of procedures known to those of

skill in the art. These procedures include, but are not limited to, DNA-DNA or DNA-RNA hybridizations and protein bioassay or immunoassay techniques which include, for example, membrane, solution, or chip based technologies for the detection and/or quantification of nucleic acid or protein.

5   A variety of protocols for detecting and measuring the expression of polynucleotide-encoded products, using either polyclonal or monoclonal antibodies specific for the product are known in the art. Examples include enzyme-linked immunosorbent assay (ELISA), radioimmunoassay (RIA), and fluorescence activated cell sorting (FACS). A two-site, monoclonal-based immunoassay utilizing monoclonal

10   antibodies reactive to two non-interfering epitopes on a given polypeptide may be preferred for some applications, but a competitive binding assay may also be employed. These and other assays are described, among other places, in Hampton, R. et al. (1990; Serological Methods, a Laboratory Manual, APS Press, St Paul. Minn.) and Maddox, D. E. et al. (1983; *J. Exp. Med. 158*:1211-1216).

15   A wide variety of labels and conjugation techniques are known by those skilled in the art and may be used in various nucleic acid and amino acid assays. Means for producing labeled hybridization or PCR probes for detecting sequences related to polynucleotides include oligolabeling, nick translation, end-labeling or PCR amplification using a labeled nucleotide. Alternatively, the sequences, or any portions

20   thereof may be cloned into a vector for the production of an mRNA probe. Such vectors are known in the art, are commercially available, and may be used to synthesize RNA probes in vitro by addition of an appropriate RNA polymerase such as T7, T3, or SP6 and labeled nucleotides. These procedures may be conducted using a variety of commercially available kits. Suitable reporter molecules or labels, which may be used

25   include radionuclides, enzymes, fluorescent, chemiluminescent, or chromogenic agents as well as substrates, cofactors, inhibitors, magnetic particles, and the like.

Host cells transformed with a polynucleotide sequence of interest may be cultured under conditions suitable for the expression and recovery of the protein from cell culture. The protein produced by a recombinant cell may be secreted or contained

30   intracellularly depending on the sequence and/or the vector used. As will be understood

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by those of skill in the art, expression vectors containing polynucleotides of the invention may be designed to contain signal sequences which direct secretion of the encoded polypeptide through a prokaryotic or eukaryotic cell membrane. Other recombinant constructions may be used to join sequences encoding a polypeptide of

5   interest to nucleotide sequence encoding a polypeptide domain which will facilitate purification of soluble proteins. Such purification facilitating domains include, but are not limited to, metal chelating peptides such as histidine-tryptophan modules that allow purification on immobilized metals, protein A domains that allow purification on immobilized immunoglobulin, and the domain utilized in the FLAGS extension/affinity

10   purification system (Immunex Corp., Seattle, Wash.). The inclusion of cleavable linker sequences such as those specific for Factor XA or enterokinase (Invitrogen. San Diego, Calif.) between the purification domain and the encoded polypeptide may be used to facilitate purification. One such expression vector provides for expression of a fusion protein containing a polypeptide of interest and a nucleic acid encoding 6 histidine

15   residues preceding a thioredoxin or an enterokinase cleavage site. The histidine residues facilitate purification on IMIAC (immobilized metal ion affinity chromatography) as described in Porath, J. et al. (1992, *Prot. Exp. Purif. 3*:263-281) while the enterokinase cleavage site provides a means for purifying the desired polypeptide from the fusion protein. A discussion of vectors which contain fusion proteins is provided in Kroll, D. J.

20   et al. (1993; *DNA Cell Biol. 12*:441-453).

In addition to recombinant production methods, polypeptides of the invention, and fragments thereof, may be produced by direct peptide synthesis using solid-phase techniques (Merrifield J. (1963) *J. Am. Chem. Soc. 85*:2149-2154). Protein synthesis may be performed using manual techniques or by automation. Automated

25   synthesis may be achieved, for example, using Applied Biosystems 431A Peptide Synthesizer (Perkin Elmer). Alternatively, various fragments may be chemically synthesized separately and combined using chemical methods to produce the full length molecule.

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Antibody Compositions, Fragments Thereof and Other Binding Agents

According to another aspect, the present invention further provides binding agents, such as antibodies and antigen-binding fragments thereof, that exhibit immunological binding to a tumor polypeptide disclosed herein, or to a portion, variant

5   or derivative thereof. An antibody, or antigen-binding fragment thereof, is said to "specifically bind," "immunogically bind," and/or is "immunologically reactive" to a polypeptide of the invention if it reacts at a detectable level (within, for example, an ELISA assay) with the polypeptide, and does not react detectably with unrelated polypeptides under similar conditions.

10   Immunological binding, as used in this context, generally refers to the non-covalent interactions of the type which occur between an immunoglobulin molecule and an antigen for which the immunoglobulin is specific. The strength, or affinity of immunological binding interactions can be expressed in terms of the dissociation constant (K_d) of the interaction, wherein a smaller K_d represents a greater

15   affinity. Immunological binding properties of selected polypeptides can be quantified using methods well known in the art. One such method entails measuring the rates of antigen-binding site/antigen complex formation and dissociation, wherein those rates depend on the concentrations of the complex partners, the affinity of the interaction, and on geometric parameters that equally influence the rate in both directions. Thus, both

20   the "on rate constant" (K_{on}) and the "off rate constant" (K_{off}) can be determined by calculation of the concentrations and the actual rates of association and dissociation. The ratio of K_{off}/K_{on} enables cancellation of all parameters not related to affinity, and is thus equal to the dissociation constant K_d. See, generally, Davies et al. (1990) Annual Rev. Biochem. 59:439-473.

25   An "antigen-binding site," or "binding portion" of an antibody refers to the part of the immunoglobulin molecule that participates in antigen binding. The antigen binding site is formed by amino acid residues of the N-terminal variable ("V") regions of the heavy ("H") and light ("L") chains. Three highly divergent stretches within the V regions of the heavy and light chains are referred to as "hypervariable

30   regions" which are interposed between more conserved flanking stretches known as

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"framework regions," or "FRs". Thus the term "FR" refers to amino acid sequences which are naturally found between and adjacent to hypervariable regions in immunoglobulins. In an antibody molecule, the three hypervariable regions of a light chain and the three hypervariable regions of a heavy chain are disposed relative to each

5   other in three dimensional space to form an antigen-binding surface. The antigen-binding surface is complementary to the three-dimensional surface of a bound antigen, and the three hypervariable regions of each of the heavy and light chains are referred to as "complementarity-determining regions," or "CDRs."

Binding agents may be further capable of differentiating between patients

10   with and without a cancer, such as prostate cancer, using the representative assays provided herein. For example, antibodies or other binding agents that bind to a tumor protein will preferably generate a signal indicating the presence of a cancer in at least about 20% of patients with the disease, more preferably at least about 30% of patients. Alternatively, or in addition, the antibody will generate a negative signal indicating the

15   absence of the disease in at least about 90% of individuals without the cancer. To determine whether a binding agent satisfies this requirement, biological samples (e.g., blood, sera, sputum, urine and/or tumor biopsies) from patients with and without a cancer (as determined using standard clinical tests) may be assayed as described herein for the presence of polypeptides that bind to the binding agent. Preferably, a statistically

20   significant number of samples with and without the disease will be assayed. Each binding agent should satisfy the above criteria; however, those of ordinary skill in the art will recognize that binding agents may be used in combination to improve sensitivity.

Any agent that satisfies the above requirements may be a binding agent.

25   For example, a binding agent may be a ribosome, with or without a peptide component, an RNA molecule or a polypeptide. In a preferred embodiment, a binding agent is an antibody or an antigen-binding fragment thereof. Antibodies may be prepared by any of a variety of techniques known to those of ordinary skill in the art. See, e.g., Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In

30   general, antibodies can be produced by cell culture techniques, including the generation

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of monoclonal antibodies as described herein, or via transfection of antibody genes into suitable bacterial or mammalian cell hosts, in order to allow for the production of recombinant antibodies. In one technique, an immunogen comprising the polypeptide is initially injected into any of a wide variety of mammals (*e.g.,* mice, rats, rabbits, sheep

5   or goats). In this step, the polypeptides of this invention may serve as the immunogen without modification. Alternatively, particularly for relatively short polypeptides, a superior immune response may be elicited if the polypeptide is joined to a carrier protein, such as bovine serum albumin or keyhole limpet hemocyanin. The immunogen is injected into the animal host, preferably according to a predetermined schedule

10   incorporating one or more booster immunizations, and the animals are bled periodically. Polyclonal antibodies specific for the polypeptide may then be purified from such antisera by, for example, affinity chromatography using the polypeptide coupled to a suitable solid support.

       Monoclonal antibodies specific for an antigenic polypeptide of interest

15   may be prepared, for example, using the technique of Kohler and Milstein, *Eur. J. Immunol. 6*:511-519, 1976, and improvements thereto. Briefly, these methods involve the preparation of immortal cell lines capable of producing antibodies having the desired specificity (*i.e.,* reactivity with the polypeptide of interest). Such cell lines may be produced, for example, from spleen cells obtained from an animal immunized as

20   described above. The spleen cells are then immortalized by, for example, fusion with a myeloma cell fusion partner, preferably one that is syngeneic with the immunized animal. A variety of fusion techniques may be employed. For example, the spleen cells and myeloma cells may be combined with a nonionic detergent for a few minutes and then plated at low density on a selective medium that supports the growth of hybrid

25   cells, but not myeloma cells. A preferred selection technique uses HAT (hypoxanthine, aminopterin, thymidine) selection. After a sufficient time, usually about 1 to 2 weeks, colonies of hybrids are observed. Single colonies are selected and their culture supernatants tested for binding activity against the polypeptide. Hybridomas having high reactivity and specificity are preferred.

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Monoclonal antibodies may be isolated from the supernatants of growing hybridoma colonies. In addition, various techniques may be employed to enhance the yield, such as injection of the hybridoma cell line into the peritoneal cavity of a suitable vertebrate host, such as a mouse. Monoclonal antibodies may then be harvested from

5   the ascites fluid or the blood. Contaminants may be removed from the antibodies by conventional techniques, such as chromatography, gel filtration, precipitation, and extraction. The polypeptides of this invention may be used in the purification process in, for example, an affinity chromatography step.

A number of therapeutically useful molecules are known in the art which

10   comprise antigen-binding sites that are capable of exhibiting immunological binding properties of an antibody molecule. The proteolytic enzyme papain preferentially cleaves IgG molecules to yield several fragments, two of which (the "F(ab)" fragments) each comprise a covalent heterodimer that includes an intact antigen-binding site. The enzyme pepsin is able to cleave IgG molecules to provide several fragments, including

15   the "F(ab')$_2$" fragment which comprises both antigen-binding sites. An "Fv" fragment can be produced by preferential proteolytic cleavage of an IgM, and on rare occasions IgG or IgA immunoglobulin molecule. Fv fragments are, however, more commonly derived using recombinant techniques known in the art. The Fv fragment includes a non-covalent $V_H::V_L$ heterodimer including an antigen-binding site which retains much

20   of the antigen recognition and binding capabilities of the native antibody molecule. Inbar et al. (1972) Proc. Nat. Acad. Sci. USA 69:2659-2662; Hochman et al. (1976) Biochem 15:2706-2710; and Ehrlich et al. (1980) Biochem 19:4091-4096.

A single chain Fv ("sFv") polypeptide is a covalently linked $V_H::V_L$ heterodimer which is expressed from a gene fusion including V_H- and V_L-encoding

25   genes linked by a peptide-encoding linker. Huston et al. (1988) Proc. Nat. Acad. Sci. USA 85(16):5879-5883. A number of methods have been described to discern chemical structures for converting the naturally aggregated--but chemically separated--light and heavy polypeptide chains from an antibody V region into an sFv molecule which will fold into a three dimensional structure substantially similar to the structure of an

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antigen-binding site. See, *e.g.*, U.S. Pat. Nos. 5,091,513 and 5,132,405, to Huston et al.; and U.S. Pat. No. 4,946,778, to Ladner et al.

Each of the above-described molecules includes a heavy chain and a light chain CDR set, respectively interposed between a heavy chain and a light chain FR set which provide support to the CDRS and define the spatial relationship of the CDRs relative to each other. As used herein, the term "CDR set" refers to the three hypervariable regions of a heavy or light chain V region. Proceeding from the N-terminus of a heavy or light chain, these regions are denoted as "CDR1," "CDR2," and "CDR3" respectively. An antigen-binding site, therefore, includes six CDRs, comprising the CDR set from each of a heavy and a light chain V region. A polypeptide comprising a single CDR, (*e.g.*, a CDR1, CDR2 or CDR3) is referred to herein as a "molecular recognition unit." Crystallographic analysis of a number of antigen-antibody complexes has demonstrated that the amino acid residues of CDRs form extensive contact with bound antigen, wherein the most extensive antigen contact is with the heavy chain CDR3. Thus, the molecular recognition units are primarily responsible for the specificity of an antigen-binding site.

As used herein, the term "FR set" refers to the four flanking amino acid sequences which frame the CDRs of a CDR set of a heavy or light chain V region. Some FR residues may contact bound antigen; however, FRs are primarily responsible for folding the V region into the antigen-binding site, particularly the FR residues directly adjacent to the CDRS. Within FRs, certain amino residues and certain structural features are very highly conserved. In this regard, all V region sequences contain an internal disulfide loop of around 90 amino acid residues. When the V regions fold into a binding-site, the CDRs are displayed as projecting loop motifs which form an antigen-binding surface. It is generally recognized that there are conserved structural regions of FRs which influence the folded shape of the CDR loops into certain "canonical" structures--regardless of the precise CDR amino acid sequence. Further, certain FR residues are known to participate in non-covalent interdomain contacts which stabilize the interaction of the antibody heavy and light chains.

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A number of "humanized" antibody molecules comprising an antigen-binding site derived from a non-human immunoglobulin have been described, including chimeric antibodies having rodent V regions and their associated CDRs fused to human constant domains (Winter et al. (1991) Nature 349:293-299; Lobuglio et al. (1989)

5   Proc. Nat. Acad. Sci. USA 86:4220-4224; Shaw et al. (1987) J Immunol. 138:4534-4538; and Brown et al. (1987) Cancer Res. 47:3577-3583), rodent CDRs grafted into a human supporting FR prior to fusion with an appropriate human antibody constant domain (Riechmann et al. (1988) Nature 332:323-327; Verhoeyen et al. (1988) Science 239:1534-1536; and Jones et al. (1986) Nature 321:522-525), and rodent CDRs

10 supported by recombinantly veneered rodent FRs (European Patent Publication No. 519,596, published Dec. 23, 1992). These "humanized" molecules are designed to minimize unwanted immunological response toward rodent antihuman antibody molecules which limits the duration and effectiveness of therapeutic applications of those moieties in human recipients.

15   As used herein, the terms "veneered FRs" and "recombinantly veneered FRs" refer to the selective replacement of FR residues from, e.g., a rodent heavy or light chain V region, with human FR residues in order to provide a xenogeneic molecule comprising an antigen-binding site which retains substantially all of the native FR polypeptide folding structure. Veneering techniques are based on the understanding that

20 the ligand binding characteristics of an antigen-binding site are determined primarily by the structure and relative disposition of the heavy and light chain CDR sets within the antigen-binding surface. Davies et al. (1990) Ann. Rev. Biochem. 59:439-473. Thus, antigen binding specificity can be preserved in a humanized antibody only wherein the CDR structures, their interaction with each other, and their interaction with the rest of

25 the V region domains are carefully maintained. By using veneering techniques, exterior (e.g., solvent-accessible) FR residues which are readily encountered by the immune system are selectively replaced with human residues to provide a hybrid molecule that comprises either a weakly immunogenic, or substantially non-immunogenic veneered surface.

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The process of veneering makes use of the available sequence data for human antibody variable domains compiled by Kabat et al., in Sequences of Proteins of Immunological Interest, 4th ed., (U.S. Dept. of Health and Human Services, U.S. Government Printing Office, 1987), updates to the Kabat database, and other accessible

5   U.S. and foreign databases (both nucleic acid and protein). Solvent accessibilities of V region amino acids can be deduced from the known three-dimensional structure for human and murine antibody fragments. There are two general steps in veneering a murine antigen-binding site. Initially, the FRs of the variable domains of an antibody molecule of interest are compared with corresponding FR sequences of human variable

10   domains obtained from the above-identified sources. The most homologous human V regions are then compared residue by residue to corresponding murine amino acids. The residues in the murine FR which differ from the human counterpart are replaced by the residues present in the human moiety using recombinant techniques well known in the art. Residue switching is only carried out with moieties which are at least partially

15   exposed (solvent accessible), and care is exercised in the replacement of amino acid residues which may have a significant effect on the tertiary structure of V region domains, such as proline, glycine and charged amino acids.

In this manner, the resultant "veneered" murine antigen-binding sites are thus designed to retain the murine CDR residues, the residues substantially adjacent to

20   the CDRs, the residues identified as buried or mostly buried (solvent inaccessible), the residues believed to participate in non-covalent (e.g., electrostatic and hydrophobic) contacts between heavy and light chain domains, and the residues from conserved structural regions of the FRs which are believed to influence the "canonical" tertiary structures of the CDR loops. These design criteria are then used to prepare recombinant

25   nucleotide sequences which combine the CDRs of both the heavy and light chain of a murine antigen-binding site into human-appearing FRs that can be used to transfect mammalian cells for the expression of recombinant human antibodies which exhibit the antigen specificity of the murine antibody molecule.

In another embodiment of the invention, monoclonal antibodies of the

30   present invention may be coupled to one or more therapeutic agents. Suitable agents in

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this regard include radionuclides, differentiation inducers, drugs, toxins, and derivatives thereof. Preferred radionuclides include ^{90}Y, ^{123}I, ^{125}I, ^{131}I, ^{186}Re, ^{188}Re, ^{211}At, and ^{212}Bi. Preferred drugs include methotrexate, and pyrimidine and purine analogs. Preferred differentiation inducers include phorbol esters and butyric acid. Preferred

5   toxins include ricin, abrin, diptheria toxin, cholera toxin, gelonin, Pseudomonas exotoxin, Shigella toxin, and pokeweed antiviral protein.

A therapeutic agent may be coupled (e.g., covalently bonded) to a suitable monoclonal antibody either directly or indirectly (e.g., via a linker group). A direct reaction between an agent and an antibody is possible when each possesses a

10   substituent capable of reacting with the other. For example, a nucleophilic group, such as an amino or sulfhydryl group, on one may be capable of reacting with a carbonyl-containing group, such as an anhydride or an acid halide, or with an alkyl group containing a good leaving group (e.g., a halide) on the other.

Alternatively, it may be desirable to couple a therapeutic agent and an

15   antibody via a linker group. A linker group can function as a spacer to distance an antibody from an agent in order to avoid interference with binding capabilities. A linker group can also serve to increase the chemical reactivity of a substituent on an agent or an antibody, and thus increase the coupling efficiency. An increase in chemical reactivity may also facilitate the use of agents, or functional groups on agents, which

20   otherwise would not be possible.

It will be evident to those skilled in the art that a variety of bifunctional or polyfunctional reagents, both homo- and hetero-functional (such as those described in the catalog of the Pierce Chemical Co., Rockford, IL), may be employed as the linker group. Coupling may be effected, for example, through amino groups, carboxyl groups,

25   sulfhydryl groups or oxidized carbohydrate residues. There are numerous references describing such methodology, e.g., U.S. Patent No. 4,671,958, to Rodwell et al.

Where a therapeutic agent is more potent when free from the antibody portion of the immunoconjugates of the present invention, it may be desirable to use a linker group which is cleavable during or upon internalization into a cell. A number of

30   different cleavable linker groups have been described. The mechanisms for the

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intracellular release of an agent from these linker groups include cleavage by reduction of a disulfide bond (*e.g.*, U.S. Patent No. 4,489,710, to Spitler), by irradiation of a photolabile bond (*e.g.*, U.S. Patent No. 4,625,014, to Senter et al.), by hydrolysis of derivatized amino acid side chains (*e.g.*, U.S. Patent No. 4,638,045, to Kohn et al.), by

5   serum complement-mediated hydrolysis (*e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.), and acid-catalyzed hydrolysis (*e.g.*, U.S. Patent No. 4,569,789, to Blattler et al.).

It may be desirable to couple more than one agent to an antibody. In one embodiment, multiple molecules of an agent are coupled to one antibody molecule. In another embodiment, more than one type of agent may be coupled to one antibody.

10   Regardless of the particular embodiment, immunoconjugates with more than one agent may be prepared in a variety of ways. For example, more than one agent may be coupled directly to an antibody molecule, or linkers that provide multiple sites for attachment can be used. Alternatively, a carrier can be used.

A carrier may bear the agents in a variety of ways, including covalent

15   bonding either directly or via a linker group. Suitable carriers include proteins such as albumins (*e.g.*, U.S. Patent No. 4,507,234, to Kato et al.), peptides and polysaccharides such as aminodextran (*e.g.*, U.S. Patent No. 4,699,784, to Shih et al.). A carrier may also bear an agent by noncovalent bonding or by encapsulation, such as within a liposome vesicle (*e.g.*, U.S. Patent Nos. 4,429,008 and 4,873,088). Carriers specific for

20   radionuclide agents include radiohalogenated small molecules and chelating compounds. For example, U.S. Patent No. 4,735,792 discloses representative radiohalogenated small molecules and their synthesis. A radionuclide chelate may be formed from chelating compounds that include those containing nitrogen and sulfur atoms as the donor atoms for binding the metal, or metal oxide, radionuclide. For

25   example, U.S. Patent No. 4,673,562, to Davison et al. discloses representative chelating compounds and their synthesis.

T Cell Compositions

The present invention, in another aspect, provides T cells specific for a tumor polypeptide disclosed herein, or for a variant or derivative thereof. Such cells

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may generally be prepared *in vitro* or *ex vivo*, using standard procedures. For example, T cells may be isolated from bone marrow, peripheral blood, or a fraction of bone marrow or peripheral blood of a patient, using a commercially available cell separation system, such as the Isolex™ System, available from Nexell Therapeutics, Inc. (Irvine,

5   CA; see also U.S. Patent No. 5,240,856; U.S. Patent No. 5,215,926; WO 89/06280; WO 91/16116 and WO 92/07243). Alternatively, T cells may be derived from related or unrelated humans, non-human mammals, cell lines or cultures.

T cells may be stimulated with a polypeptide, polynucleotide encoding a polypeptide and/or an antigen presenting cell (APC) that expresses such a polypeptide.

10   Such stimulation is performed under conditions and for a time sufficient to permit the generation of T cells that are specific for the polypeptide of interest. Preferably, a tumor polypeptide or polynucleotide of the invention is present within a delivery vehicle, such as a microsphere, to facilitate the generation of specific T cells.

T cells are considered to be specific for a polypeptide of the present

15   invention if the T cells specifically proliferate, secrete cytokines or kill target cells coated with the polypeptide or expressing a gene encoding the polypeptide. T cell specificity may be evaluated using any of a variety of standard techniques. For example, within a chromium release assay or proliferation assay, a stimulation index of more than two fold increase in lysis and/or proliferation, compared to negative controls,

20   indicates T cell specificity. Such assays may be performed, for example, as described in Chen et al., *Cancer Res.* *54*:1065-1070, 1994. Alternatively, detection of the proliferation of T cells may be accomplished by a variety of known techniques. For example, T cell proliferation can be detected by measuring an increased rate of DNA synthesis (*e.g.*, by pulse-labeling cultures of T cells with tritiated thymidine and

25   measuring the amount of tritiated thymidine incorporated into DNA). Contact with a tumor polypeptide (100 ng/ml - 100 µg/ml, preferably 200 ng/ml - 25 µg/ml) for 3 - 7 days will typically result in at least a two fold increase in proliferation of the T cells. Contact as described above for 2-3 hours should result in activation of the T cells, as measured using standard cytokine assays in which a two fold increase in the level of

30   cytokine release (*e.g.*, TNF or IFN-γ) is indicative of T cell activation (*see* Coligan et

al., Current Protocols in Immunology, vol. 1, Wiley Interscience (Greene 1998)). T cells that have been activated in response to a tumor polypeptide, polynucleotide or polypeptide-expressing APC may be CD4$^+$ and/or CD8$^+$. Tumor polypeptide-specific T cells may be expanded using standard techniques. Within preferred embodiments, the T

5   cells are derived from a patient, a related donor or an unrelated donor, and are administered to the patient following stimulation and expansion.

For therapeutic purposes, CD4$^+$ or CD8$^+$ T cells that proliferate in response to a tumor polypeptide, polynucleotide or APC can be expanded in number either *in vitro* or *in vivo*. Proliferation of such T cells *in vitro* may be accomplished in a

10   variety of ways. For example, the T cells can be re-exposed to a tumor polypeptide, or a short peptide corresponding to an immunogenic portion of such a polypeptide, with or without the addition of T cell growth factors, such as interleukin-2, and/or stimulator cells that synthesize a tumor polypeptide. Alternatively, one or more T cells that proliferate in the presence of the tumor polypeptide can be expanded in number by

15   cloning. Methods for cloning cells are well known in the art, and include limiting dilution.

Pharmaceutical Compositions

In additional embodiments, the present invention concerns formulation of one or more of the polynucleotide, polypeptide, T-cell and/or antibody compositions

20   disclosed herein in pharmaceutically-acceptable carriers for administration to a cell or an animal, either alone, or in combination with one or more other modalities of therapy.

It will be understood that, if desired, a composition as disclosed herein may be administered in combination with other agents as well, such as, *e.g.*, other proteins or polypeptides or various pharmaceutically-active agents. In fact, there is

25   virtually no limit to other components that may also be included, given that the additional agents do not cause a significant adverse effect upon contact with the target cells or host tissues. The compositions may thus be delivered along with various other agents as required in the particular instance. Such compositions may be purified from host cells or other biological sources, or alternatively may be chemically synthesized as

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described herein. Likewise, such compositions may further comprise substituted or derivatized RNA or DNA compositions.

Therefore, in another aspect of the present invention, pharmaceutical compositions are provided comprising one or more of the polynucleotide, polypeptide, antibody, and/or T-cell compositions described herein in combination with a physiologically acceptable carrier. In certain preferred embodiments, the pharmaceutical compositions of the invention comprise immunogenic polynucleotide and/or polypeptide compositions of the invention for use in prophylactic and theraputic vaccine applications. Vaccine preparation is generally described in, for example, M.F. Powell and M.J. Newman, eds., "Vaccine Design (the subunit and adjuvant approach)," Plenum Press (NY, 1995). Generally, such compositions will comprise one or more polynucleotide and/or polypeptide compositions of the present invention in combination with one or more immunostimulants.

It will be apparent that any of the pharmaceutical compositions described herein can contain pharmaceutically acceptable salts of the polynucleotides and polypeptides of the invention. Such salts can be prepared, for example, from pharmaceutically acceptable non-toxic bases, including organic bases (e.g., salts of primary, secondary and tertiary amines and basic amino acids) and inorganic bases (e.g., sodium, potassium, lithium, ammonium, calcium and magnesium salts).

In another embodiment, illustrative immunogenic compositions, e.g., vaccine compositions, of the present invention comprise DNA encoding one or more of the polypeptides as described above, such that the polypeptide is generated in situ. As noted above, the polynucleotide may be administered within any of a variety of delivery systems known to those of ordinary skill in the art. Indeed, numerous gene delivery techniques are well known in the art, such as those described by Rolland, Crit. Rev. Therap. Drug Carrier Systems 15:143-198, 1998, and references cited therein. Appropriate polynucleotide expression systems will, of course, contain the necessary regulatory DNA regulatory sequences for expression in a patient (such as a suitable promoter and terminating signal). Alternatively, bacterial delivery systems may involve

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the administration of a bacterium (such as *Bacillus-Calmette-Guerrin*) that expresses an immunogenic portion of the polypeptide on its cell surface or secretes such an epitope.

Therefore, in certain embodiments, polynucleotides encoding immunogenic polypeptides described herein are introduced into suitable mammalian host cells for expression using any of a number of known viral-based systems. In one illustrative embodiment, retroviruses provide a convenient and effective platform for gene delivery systems. A selected nucleotide sequence encoding a polypeptide of the present invention can be inserted into a vector and packaged in retroviral particles using techniques known in the art. The recombinant virus can then be isolated and delivered to a subject. A number of illustrative retroviral systems have been described (*e.g.*, U.S. Pat. No. 5,219,740; Miller and Rosman (1989) BioTechniques 7:980-990; Miller, A. D. (1990) Human Gene Therapy 1:5-14; Scarpa et al. (1991) Virology 180:849-852; Burns et al. (1993) Proc. Natl. Acad. Sci. USA 90:8033-8037; and Boris-Lawrie and Temin (1993) Cur. Opin. Genet. Develop. 3:102-109.

In addition, a number of illustrative adenovirus-based systems have also been described. Unlike retroviruses which integrate into the host genome, adenoviruses persist extrachromosomally thus minimizing the risks associated with insertional mutagenesis (Haj-Ahmad and Graham (1986) J. Virol. 57:267-274; Bett et al. (1993) J. Virol. 67:5911-5921; Mittereder et al. (1994) Human Gene Therapy 5:717-729; Seth et al. (1994) J. Virol. 68:933-940; Barr et al. (1994) Gene Therapy 1:51-58; Berkner, K. L. (1988) BioTechniques 6:616-629; and Rich et al. (1993) Human Gene Therapy 4:461-476).

Various adeno-associated virus (AAV) vector systems have also been developed for polynucleotide delivery. AAV vectors can be readily constructed using techniques well known in the art. See, *e.g.*, U.S. Pat. Nos. 5,173,414 and 5,139,941; International Publication Nos. WO 92/01070 and WO 93/03769; Lebkowski et al. (1988) Molec. Cell. Biol. 8:3988-3996; Vincent et al. (1990) Vaccines 90 (Cold Spring Harbor Laboratory Press); Carter, B. J. (1992) Current Opinion in Biotechnology 3:533-539; Muzyczka, N. (1992) Current Topics in Microbiol. and Immunol. 158:97-129;

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Kotin, R. M. (1994) Human Gene Therapy 5:793-801; Shelling and Smith (1994) Gene Therapy 1:165-169; and Zhou et al. (1994) J. Exp. Med. 179:1867-1875.

Additional viral vectors useful for delivering the polynucleotides encoding polypeptides of the present invention by gene transfer include those derived

5   from the pox family of viruses, such as vaccinia virus and avian poxvirus. By way of example, vaccinia virus recombinants expressing the novel molecules can be constructed as follows. The DNA encoding a polypeptide is first inserted into an appropriate vector so that it is adjacent to a vaccinia promoter and flanking vaccinia DNA sequences, such as the sequence encoding thymidine kinase (TK). This vector is

10 then used to transfect cells which are simultaneously infected with vaccinia. Homologous recombination serves to insert the vaccinia promoter plus the gene encoding the polypeptide of interest into the viral genome. The resulting TK.sup.(-) recombinant can be selected by culturing the cells in the presence of 5-bromodeoxyuridine and picking viral plaques resistant thereto.

15   A vaccinia-based infection/transfection system can be conveniently used to provide for inducible, transient expression or coexpression of one or more polypeptides described herein in host cells of an organism. In this particular system, cells are first infected in vitro with a vaccinia virus recombinant that encodes the bacteriophage T7 RNA polymerase. This polymerase displays exquisite specificity in

20 that it only transcribes templates bearing T7 promoters. Following infection, cells are transfected with the polynucleotide or polynucleotides of interest, driven by a T7 promoter. The polymerase expressed in the cytoplasm from the vaccinia virus recombinant transcribes the transfected DNA into RNA which is then translated into polypeptide by the host translational machinery. The method provides for high level,

25 transient, cytoplasmic production of large quantities of RNA and its translation products. See, e.g., Elroy-Stein and Moss, Proc. Natl. Acad. Sci. USA (1990) 87:6743-6747; Fuerst et al. Proc. Natl. Acad. Sci. USA (1986) 83:8122-8126.

Alternatively, avipoxviruses, such as the fowlpox and canarypox viruses, can also be used to deliver the coding sequences of interest. Recombinant avipox

30 viruses, expressing immunogens from mammalian pathogens, are known to confer

protective immunity when administered to non-avian species. The use of an Avipox vector is particularly desirable in human and other mammalian species since members of the Avipox genus can only productively replicate in susceptible avian species and therefore are not infective in mammalian cells. Methods for producing recombinant Avipoxviruses are known in the art and employ genetic recombination, as described above with respect to the production of vaccinia viruses. See, *e.g.*, WO 91/12882; WO 89/03429; and WO 92/03545.

Any of a number of alphavirus vectors can also be used for delivery of polynucleotide compositions of the present invention, such as those vectors described in U.S. Patent Nos. 5,843,723; 6,015,686; 6,008,035 and 6,015,694. Certain vectors based on Venezuelan Equine Encephalitis (VEE) can also be used, illustrative examples of which can be found in U.S. Patent Nos. 5,505,947 and 5,643,576.

Moreover, molecular conjugate vectors, such as the adenovirus chimeric vectors described in Michael et al. J. Biol. Chem. (1993) 268:6866-6869 and Wagner et al. Proc. Natl. Acad. Sci. USA (1992) 89:6099-6103, can also be used for gene delivery under the invention.

Additional illustrative information on these and other known viral-based delivery systems can be found, for example, in Fisher-Hoch et al., *Proc. Natl. Acad. Sci. USA 86*:317-321, 1989; Flexner et al., *Ann. N.Y. Acad. Sci. 569*:86-103, 1989; Flexner et al., *Vaccine 8*:17-21, 1990; U.S. Patent Nos. 4,603,112, 4,769,330, and 5,017,487; WO 89/01973; U.S. Patent No. 4,777,127; GB 2,200,651; EP 0,345,242; WO 91/02805; Berkner, *Biotechniques 6*:616-627, 1988; Rosenfeld et al., *Science 252*:431-434, 1991; Kolls et al., *Proc. Natl. Acad. Sci. USA 91*:215-219, 1994; Kass-Eisler et al., *Proc. Natl. Acad. Sci. USA 90*:11498-11502, 1993; Guzman et al., *Circulation 88*:2838-2848, 1993; and Guzman et al., *Cir. Res. 73*:1202-1207, 1993.

In certain embodiments, a polynucleotide may be integrated into the genome of a target cell. This integration may be in a specific location and orientation *via* homologous recombination (gene replacement) or it may be integrated in a random, non-specific location (gene augmentation). In yet further embodiments, the polynucleotide may be stably maintained in the cell as a separate, episomal segment of

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DNA. Such polynucleotide segments or "episomes" encode sequences sufficient to permit maintenance and replication independent of or in synchronization with the host cell cycle. The manner in which the expression construct is delivered to a cell and where in the cell the polynucleotide remains is dependent on the type of expression construct employed.

In another embodiment of the invention, a polynucleotide is administered/delivered as "naked" DNA, for example as described in Ulmer et al., *Science 259*:1745-1749, 1993 and reviewed by Cohen, *Science 259*:1691-1692, 1993. The uptake of naked DNA may be increased by coating the·DNA onto biodegradable beads, which are efficiently transported into the cells.

In still another embodiment, a composition of the present invention can be delivered via a particle bombardment approach, many of which have been described. In one illustrative example, gas-driven particle acceleration can be achieved with devices such as those manufactured by Powderject Pharmaceuticals PLC (Oxford, UK) and Powderject Vaccines Inc. (Madison, WI), some examples of which are described in U.S. Patent Nos. 5,846,796; 6,010,478; 5,865,796; 5,584,807; and EP Patent No. 0500 799. This approach offers a needle-free delivery approach wherein a dry powder formulation of microscopic particles, such as polynucleotide or polypeptide particles, are accelerated to high speed within a helium gas jet generated by a hand held device, propelling the particles into a target tissue of interest.

In a related embodiment, other devices and methods that may be useful for gas-driven needle-less injection of compositions of the present invention include those provided by Bioject, Inc. (Portland, OR), some examples of which are described in U.S. Patent Nos. 4,790,824; 5,064,413; 5,312,335; 5,383,851; 5,399,163; 5,520,639 and 5,993,412.

According to another embodiment, the pharmaceutical compositions described herein will comprise one or more immunostimulants in addition to the immunogenic polynucleotide, polypeptide, antibody, T-cell and/or APC compositions of this invention. An immunostimulant refers to essentially any substance that enhances or potentiates an immune response (antibody and/or cell-mediated) to an exogenous

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antigen. One preferred type of immunostimulant comprises an adjuvant. Many adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, *Bortadella pertussis* or *Mycobacterium tuberculosis* derived proteins.

5   Certain adjuvants are commercially available as, for example, Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); AS-2 (SmithKline Beecham, Philadelphia, PA); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron or zinc; an insoluble suspension of acylated tyrosine; acylated

10 sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes; biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF, interleukin-2, -7, -12, and other like growth factors, may also be used as adjuvants.

Within certain embodiments of the invention, the adjuvant composition
15 is preferably one that induces an immune response predominantly of the Th1 type. High levels of Th1-type cytokines (*e.g.*, IFN-γ, TNFα, IL-2 and IL-12) tend to favor the induction of cell mediated immune responses to an administered antigen. In contrast, high levels of Th2-type cytokines (*e.g.*, IL-4, IL-5, IL-6 and IL-10) tend to favor the induction of humoral immune responses. Following application of a vaccine as
20 provided herein, a patient will support an immune response that includes Th1- and Th2-type responses. Within a preferred embodiment, in which a response is predominantly Th1-type, the level of Th1-type cytokines will increase to a greater extent than the level of Th2-type cytokines. The levels of these cytokines may be readily assessed using standard assays. For a review of the families of cytokines, see Mosmann and Coffman,
25 *Ann. Rev. Immunol.* 7:145-173, 1989.

Certain preferred adjuvants for eliciting a predominantly Th1-type response include, for example, a combination of monophosphoryl lipid A, preferably 3-de-O-acylated monophosphoryl lipid A, together with an aluminum salt. MPL® adjuvants are available from Corixa Corporation (Seattle, WA; *see*, for example, US
30 Patent Nos. 4,436,727; 4,877,611; 4,866,034 and 4,912,094). CpG-containing

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oligonucleotides (in which the CpG dinucleotide is unmethylated) also induce a predominantly Th1 response. Such oligonucleotides are well known and are described, for example, in WO 96/02555, WO 99/33488 and U.S. Patent Nos. 6,008,200 and 5,856,462. Immunostimulatory DNA sequences are also described, for example, by

5 Sato et al., *Science* 273:352, 1996. Another preferred adjuvant comprises a saponin, such as Quil A, or derivatives thereof, including QS21 and QS7 (Aquila Biopharmaceuticals Inc., Framingham, MA); Escin; Digitonin; or *Gypsophila* or *Chenopodium quinoa* saponins . Other preferred formulations include more than one saponin in the adjuvant combinations of the present invention, for example

10 combinations of at least two of the following group comprising QS21, QS7, Quil A, β-escin, or digitonin.

Alternatively the saponin formulations may be combined with vaccine vehicles composed of chitosan or other polycationic polymers, polylactide and polylactide-co-glycolide particles, poly-N-acetyl glucosamine-based polymer matrix,

15 particles composed of polysaccharides or chemically modified polysaccharides, liposomes and lipid-based particles, particles composed of glycerol monoesters, etc. The saponins may also be formulated in the presence of cholesterol to form particulate structures such as liposomes or ISCOMs. Furthermore, the saponins may be formulated together with a polyoxyethylene ether or ester, in either a non-particulate solution or

20 suspension, or in a particulate structure such as a paucilamelar liposome or ISCOM. The saponins may also be formulated with excipients such as Carbopol^R to increase viscosity, or may be formulated in a dry powder form with a powder excipient such as lactose.

In one preferred embodiment, the adjuvant system includes the

25 combination of a monophosphoryl lipid A and a saponin derivative, such as the combination of QS21 and 3D-MPL$^®$ adjuvant, as described in WO 94/00153, or a less reactogenic composition where the QS21 is quenched with cholesterol, as described in WO 96/33739. Other preferred formulations comprise an oil-in-water emulsion and tocopherol. Another particularly preferred adjuvant formulation employing QS21, 3D-

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MPL® adjuvant and tocopherol in an oil-in-water emulsion is described in WO
95/17210.

Another enhanced adjuvant system involves the combination of a CpG-
containing oligonucleotide and a saponin derivative particularly the combination of
5   CpG and QS21 is disclosed in WO 00/09159. Preferably the formulation additionally
comprises an oil in water emulsion and tocopherol.

Additional illustrative adjuvants for use in the pharmaceutical
compositions of the invention include Montanide ISA 720 (Seppic, France), SAF
(Chiron, California, United States), ISCOMS (CSL), MF-59 (Chiron), the SBAS series
10   of adjuvants (e.g., SBAS-2 or SBAS-4, available from SmithKline Beecham, Rixensart,
Belgium), Detox (Enhanzyn®; Corixa, Hamilton, MT), RC-529 (Corixa, Hamilton, MT)
and other aminoalkyl glucosaminide 4-phosphates (AGPs), such as those described in
. pending U.S. Patent Application Serial Nos. 08/853,826 and 09/074,720, the disclosures
of which are incorporated herein by reference in their entireties, and polyoxyethylene
15   ether adjuvants such as those described in WO 99/52549A1.

Other preferred adjuvants include adjuvant molecules of the general
formula

(I): $HO(CH_2CH_2O)_n\text{-}A\text{-}R$,
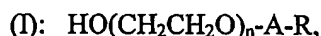
wherein, n is 1-50, A is a bond or $-C(O)-$, R is $C_{1\text{-}50}$ alkyl or Phenyl $C_{1\text{-}50}$ alkyl.

20   One embodiment of the present invention consists of a vaccine
formulation comprising a polyoxyethylene ether of general formula (I), wherein _n_ is
between 1 and 50, preferably 4-24, most preferably 9; the _R_ component is $C_{1\text{-}50}$,
preferably $C_4\text{-}C_{20}$ alkyl and most preferably C_{12} alkyl, and _A_ is a bond. The
concentration of the polyoxyethylene ethers should be in the range 0.1-20%, preferably
25   from 0.1-10%, and most preferably in the range 0.1-1%. Preferred polyoxyethylene
ethers are selected from the following group: polyoxyethylene-9-lauryl ether,
polyoxyethylene-9-steoryl ether, polyoxyethylene-8-steoryl ether, polyoxyethylene-4-
lauryl ether, polyoxyethylene-35-lauryl ether, and polyoxyethylene-23-lauryl ether.
Polyoxyethylene ethers such as polyoxyethylene lauryl ether are described in the Merck
30   index (12th edition: entry 7717). These adjuvant molecules are described in WO

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99/52549. The polyoxyethylene ether according to the general formula (I) above may, if desired, be combined with another adjuvant. For example, a preferred adjuvant combination is preferably with CpG as described in the pending UK patent application GB 9820956.2.

5   According to another embodiment of this invention, an immunogenic composition described herein is delivered to a host via antigen presenting cells (APCs), such as dendritic cells, macrophages, B cells, monocytes and other cells that may be engineered to be efficient APCs. Such cells may, but need not, be genetically modified to increase the capacity for presenting the antigen, to improve activation and/or

10   maintenance of the T cell response, to have anti-tumor effects *per se* and/or to be immunologically compatible with the receiver (*i.e.,* matched HLA haplotype). APCs may generally be isolated from any of a variety of biological fluids and organs, including tumor and peritumoral tissues, and may be autologous, allogeneic, syngeneic or xenogeneic cells.

15   Certain preferred embodiments of the present invention use dendritic cells or progenitors thereof as antigen-presenting cells. Dendritic cells are highly potent APCs (Banchereau and Steinman, *Nature 392*:245-251, 1998) and have been shown to be effective as a physiological adjuvant for eliciting prophylactic or therapeutic antitumor immunity (*see* Timmerman and Levy, *Ann. Rev. Med. 50*:507-529, 1999). In

20   general, dendritic cells may be identified based on their typical shape (stellate *in situ,* with marked cytoplasmic processes (dendrites) visible *in vitro*), their ability to take up, process and present antigens with high efficiency and their ability to activate naïve T cell responses. Dendritic cells may, of course, be engineered to express specific cell-surface receptors or ligands that are not commonly found on dendritic cells *in vivo* or *ex*

25   *vivo*, and such modified dendritic cells are contemplated by the present invention. As an alternative to dendritic cells, secreted vesicles antigen-loaded dendritic cells (called exosomes) may be used within a vaccine (*see* Zitvogel et al., *Nature Med. 4*:594-600, 1998).

         Dendritic cells and progenitors may be obtained from peripheral blood,

30   bone marrow, tumor-infiltrating cells, peritumoral tissues-infiltrating cells, lymph

nodes, spleen, skin, umbilical cord blood or any other suitable tissue or fluid. For example, dendritic cells may be differentiated *ex vivo* by adding a combination of cytokines such as GM-CSF, IL-4, IL-13 and/or TNFα to cultures of monocytes harvested from peripheral blood. Alternatively, CD34 positive cells harvested from

5   peripheral blood, umbilical cord blood or bone marrow may be differentiated into dendritic cells by adding to the culture medium combinations of GM-CSF, IL-3, TNFα, CD40 ligand, LPS, flt3 ligand and/or other compound(s) that induce differentiation, maturation and proliferation of dendritic cells.

Dendritic cells are conveniently categorized as "immature" and "mature"

10   cells, which allows a simple way to discriminate between two well characterized phenotypes. However, this nomenclature should not be construed to exclude all possible intermediate stages of differentiation. Immature dendritic cells are characterized as APC with a high capacity for antigen uptake and processing, which correlates with the high expression of Fcγ receptor and mannose receptor. The mature

15   phenotype is typically characterized by a lower expression of these markers, but a high expression of cell surface molecules responsible for T cell activation such as class I and class II MHC, adhesion molecules (*e.g.*, CD54 and CD11) and costimulatory molecules (*e.g.*, CD40, CD80, CD86 and 4-1BB).

APCs may generally be transfected with a polynucleotide of the

20   invention (or portion or other variant thereof) such that the encoded polypeptide, or an immunogenic portion thereof, is expressed on the cell surface. Such transfection may take place *ex vivo*, and a pharmaceutical composition comprising such transfected cells may then be used for therapeutic purposes, as described herein. Alternatively, a gene delivery vehicle that targets a dendritic or other antigen presenting cell may be

25   administered to a patient, resulting in transfection that occurs *in vivo*. *In vivo* and *ex vivo* transfection of dendritic cells, for example, may generally be performed using any methods known in the art, such as those described in WO 97/24447, or the gene gun approach described by Mahvi et al., *Immunology and cell Biology 75*:456-460, 1997. Antigen loading of dendritic cells may be achieved by incubating dendritic cells or

30   progenitor cells with the tumor polypeptide, DNA (naked or within a plasmid vector) or

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RNA; or with antigen-expressing recombinant bacterium or viruses (*e.g.*, vaccinia, fowlpox, adenovirus or lentivirus vectors). Prior to loading, the polypeptide may be covalently conjugated to an immunological partner that provides T cell help (*e.g.*, a carrier molecule). Alternatively, a dendritic cell may be pulsed with a non-conjugated

5   immunological partner, separately or in the presence of the polypeptide.

While any suitable carrier known to those of ordinary skill in the art may be employed in the pharmaceutical compositions of this invention, the type of carrier will typically vary depending on the mode of administration. Compositions of the present invention may be formulated for any appropriate manner of administration,

10 including for example, topical, oral, nasal, mucosal, intravenous, intracranial, intraperitoneal, subcutaneous and intramuscular administration.

Carriers for use within such pharmaceutical compositions are biocompatible, and may also be biodegradable. In certain embodiments, the formulation preferably provides a relatively constant level of active component release.

15 In other embodiments, however, a more rapid rate of release immediately upon administration may be desired. The formulation of such compositions is well within the level of ordinary skill in the art using known techniques. Illustrative carriers useful in this regard include microparticles of poly(lactide-co-glycolide), polyacrylate, latex, starch, cellulose, dextran and the like. Other illustrative delayed-release carriers

20 include supramolecular biovectors, which comprise a non-liquid hydrophilic core (*e.g.*, a cross-linked polysaccharide or oligosaccharide) and, optionally, an external layer comprising an amphiphilic compound, such as a phospholipid (*see e.g.*, U.S. Patent No. 5,151,254 and PCT applications WO 94/20078, WO/94/23701 and WO 96/06638). The amount of active compound contained within a sustained release formulation depends

25 upon the site of implantation, the rate and expected duration of release and the nature of the condition to be treated or prevented.

In another illustrative embodiment, biodegradable microspheres (*e.g.*, polylactate polyglycolate) are employed as carriers for the compositions of this invention. Suitable biodegradable microspheres are disclosed, for example, in U.S.

30 Patent Nos. 4,897,268; 5,075,109; 5,928,647; 5,811,128; 5,820,883; 5,853,763;

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5,814,344, 5,407,609 and 5,942,252. Modified hepatitis B core protein carrier systems,
such as described in WO/99 40934, and references cited therein, will also be useful for
many applications.   Another illustrative carrier/delivery system employs a carrier
comprising particulate-protein complexes, such as those described in U.S. Patent No.

5   5,928,647, which are capable of inducing a class I-restricted cytotoxic T lymphocyte
responses in a host.

The pharmaceutical compositions of the invention will often further
comprise one or more buffers (e.g., neutral buffered saline or phosphate buffered
saline), carbohydrates (e.g., glucose, mannose, sucrose or dextrans), mannitol, proteins,

10   polypeptides or amino acids such as glycine, antioxidants, bacteriostats, chelating
agents such as EDTA or glutathione, adjuvants (e.g., aluminum hydroxide), solutes that
render the formulation isotonic, hypotonic or weakly hypertonic with the blood of a
recipient, suspending agents, thickening agents and/or preservatives.   Alternatively,
compositions of the present invention may be formulated as a lyophilizate.

15   The pharmaceutical compositions described herein may be presented in
unit-dose or multi-dose containers, such as sealed ampoules or vials.   Such containers
are typically sealed in such a way to preserve the sterility and stability of the
formulation until use.   In general, formulations may be stored as suspensions, solutions
or emulsions in oily or aqueous vehicles.   Alternatively, a pharmaceutical composition

20   may be stored in a freeze-dried condition requiring only the addition of a sterile liquid
carrier immediately prior to use.

The development of suitable dosing and treatment regimens for using the
particular compositions described herein in a variety of treatment regimens, including
e.g., oral, parenteral, intravenous, intranasal, and intramuscular administration and

25   formulation, is well known in the art, some of which are briefly discussed below for
general purposes of illustration.

In certain applications, the pharmaceutical compositions disclosed herein
may be delivered via oral administration to an animal.   As such, these compositions
may be formulated with an inert diluent or with an assimilable edible carrier, or they

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may be enclosed in hard- or soft-shell gelatin capsule, or they may be compressed into tablets, or they may be incorporated directly with the food of the diet.

The active compounds may even be incorporated with excipients and used in the form of ingestible tablets, buccal tables, troches, capsules, elixirs,
5   suspensions, syrups, wafers, and the like (see, for example, Mathiowitz *et al.*, Nature 1997 Mar 27;386(6623):410-4; Hwang *et al.*, Crit Rev Ther Drug Carrier Syst 1998;15(3):243-84; U. S. Patent 5,641,515; U. S. Patent 5,580,579 and U. S. Patent 5,792,451). Tablets, troches, pills, capsules and the like may also contain any of a variety of additional components, for example, a binder, such as gum tragacanth, acacia,
10   cornstarch, or gelatin; excipients, such as dicalcium phosphate; a disintegrating agent, such as corn starch, potato starch, alginic acid and the like; a lubricant, such as magnesium stearate; and a sweetening agent, such as sucrose, lactose or saccharin may be added or a flavoring agent, such as peppermint, oil of wintergreen, or cherry flavoring. When the dosage unit form is a capsule, it may contain, in addition to
15   materials of the above type, a liquid carrier. Various other materials may be present as coatings or to otherwise modify the physical form of the dosage unit. For instance, tablets, pills, or capsules may be coated with shellac, sugar, or both. Of course, any material used in preparing any dosage unit form should be pharmaceutically pure and substantially non-toxic in the amounts employed. In addition, the active compounds
20   may be incorporated into sustained-release preparation and formulations.

Typically, these formulations will contain at least about 0.1% of the active compound or more, although the percentage of the active ingredient(s) may, of course, be varied and may conveniently be between about 1 or 2% and about 60% or 70% or more of the weight or volume of the total formulation. Naturally, the amount of
25   active compound(s) in each therapeutically useful composition may be prepared is such a way that a suitable dosage will be obtained in any given unit dose of the compound. Factors such as solubility, bioavailability, biological half-life, route of administration, product shelf life, as well as other pharmacological considerations will be contemplated by one skilled in the art of preparing such pharmaceutical formulations, and as such, a
30   variety of dosages and treatment regimens may be desirable.

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For oral administration, the compositions of the present invention may alternatively be incorporated with one or more excipients in the form of a mouthwash, dentifrice, buccal tablet, oral spray, or sublingual orally-administered formulation. Alternatively, the active ingredient may be incorporated into an oral solution such as one containing sodium borate, glycerin and potassium bicarbonate, or dispersed in a dentifrice, or added in a therapeutically-effective amount to a composition that may include water, binders, abrasives, flavoring agents, foaming agents, and humectants. Alternatively the compositions may be fashioned into a tablet or solution form that may be placed under the tongue or otherwise dissolved in the mouth.

In certain circumstances it will be desirable to deliver the pharmaceutical compositions disclosed herein parenterally, intravenously, intramuscularly, or even intraperitoneally. Such approaches are well known to the skilled artisan, some of which are further described, for example, in U. S. Patent 5,543,158; U. S. Patent 5,641,515 and U. S. Patent 5,399,363. In certain embodiments, solutions of the active compounds as free base or pharmacologically acceptable salts may be prepared in water suitably mixed with a surfactant, such as hydroxypropylcellulose. Dispersions may also be prepared in glycerol, liquid polyethylene glycols, and mixtures thereof and in oils. Under ordinary conditions of storage and use, these preparations generally will contain a preservative to prevent the growth of microorganisms.

Illustrative pharmaceutical forms suitable for injectable use include sterile aqueous solutions or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersions (for example, see U. S. Patent 5,466,468). In all cases the form must be sterile and must be fluid to the extent that easy syringability exists. It must be stable under the conditions of manufacture and storage and must be preserved against the contaminating action of microorganisms, such as bacteria and fungi. The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (*e.g.*, glycerol, propylene glycol, and liquid polyethylene glycol, and the like), suitable mixtures thereof, and/or vegetable oils. Proper fluidity may be maintained, for example, by the use of a coating, such as lecithin, by the maintenance of the required particle size in the case of dispersion and/or

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by the use of surfactants. The prevention of the action of microorganisms can be facilitated by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, sorbic acid, thimerosal, and the like. In many cases, it will be preferable to include isotonic agents, for example, sugars or sodium chloride. Prolonged absorption of the injectable compositions can be brought about by the use in the compositions of agents delaying absorption, for example, aluminum monostearate and gelatin.

In one embodiment, for parenteral administration in an aqueous solution, the solution should be suitably buffered if necessary and the liquid diluent first rendered isotonic with sufficient saline or glucose. These particular aqueous solutions are especially suitable for intravenous, intramuscular, subcutaneous and intraperitoneal administration. In this connection, a sterile aqueous medium that can be employed will be known to those of skill in the art in light of the present disclosure. For example, one dosage may be dissolved in 1 ml of isotonic NaCl solution and either added to 1000 ml of hypodermoclysis fluid or injected at the proposed site of infusion, (see for example, "Remington's Pharmaceutical Sciences" 15th Edition, pages 1035-1038 and 1570-1580). Some variation in dosage will necessarily occur depending on the condition of the subject being treated. Moreover, for human administration, preparations will of course preferably meet sterility, pyrogenicity, and the general safety and purity standards as required by FDA Office of Biologics standards.

In another embodiment of the invention, the compositions disclosed herein may be formulated in a neutral or salt form. Illustrative pharmaceutically-acceptable salts include the acid addition salts (formed with the free amino groups of the protein) and which are formed with inorganic acids such as, for example, hydrochloric or phosphoric acids, or such organic acids as acetic, oxalic, tartaric, mandelic, and the like. Salts formed with the free carboxyl groups can also be derived from inorganic bases such as, for example, sodium, potassium, ammonium, calcium, or ferric hydroxides, and such organic bases as isopropylamine, trimethylamine, histidine, procaine and the like. Upon formulation, solutions will be

administered in a manner compatible with the dosage formulation and in such amount as is therapeutically effective.

The carriers can further comprise any and all solvents, dispersion media, vehicles, coatings, diluents, antibacterial and antifungal agents, isotonic and absorption delaying agents, buffers, carrier solutions, suspensions, colloids, and the like. The use of such media and agents for pharmaceutical active substances is well known in the art. Except insofar as any conventional media or agent is incompatible with the active ingredient, its use in the therapeutic compositions is contemplated. Supplementary active ingredients can also be incorporated into the compositions. The phrase "pharmaceutically-acceptable" refers to molecular entities and compositions that do not produce an allergic or similar untoward reaction when administered to a human.

In certain embodiments, the pharmaceutical compositions may be delivered by intranasal sprays, inhalation, and/or other aerosol delivery vehicles. Methods for delivering genes, nucleic acids, and peptide compositions directly to the lungs *via* nasal aerosol sprays has been described, *e.g.,* in U. S. Patent 5,756,353 and U. S. Patent 5,804,212. Likewise, the delivery of drugs using intranasal microparticle resins (Takenaga *et al.,* J Controlled Release 1998 Mar 2;52(1-2):81-7) and lysophosphatidyl-glycerol compounds (U. S. Patent 5,725,871) are also well-known in the pharmaceutical arts. Likewise, illustrative transmucosal drug delivery in the form of a polytetrafluoroetheylene support matrix is described in U. S. Patent 5,780,045.

In certain embodiments, liposomes, nanocapsules, microparticles, lipid particles, vesicles, and the like, are used for the introduction of the compositions of the present invention into suitable host cells/organisms. In particular, the compositions of the present invention may be formulated for delivery either encapsulated in a lipid particle, a liposome, a vesicle, a nanosphere, or a nanoparticle or the like. Alternatively, compositions of the present invention can be bound, either covalently or non-covalently, to the surface of such carrier vehicles.

The formation and use of liposome and liposome-like preparations as potential drug carriers is generally known to those of skill in the art (see for example, Lasic, Trends Biotechnol 1998 Jul;16(7):307-21; Takakura, Nippon Rinsho 1998

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Mar;56(3):691-5; Chandran *et al.*, Indian J Exp Biol. 1997 Aug;35(8):801-9; Margalit, Crit Rev Ther Drug Carrier Syst. 1995;12(2-3):233-61; U.S. Patent 5,567,434; U.S. Patent 5,552,157; U.S. Patent 5,565,213; U.S. Patent 5,738,868 and U.S. Patent 5,795,587, each specifically incorporated herein by reference in its entirety).

5   Liposomes have been used successfully with a number of cell types that are normally difficult to transfect by other procedures, including T cell suspensions, primary hepatocyte cultures and PC 12 cells (Renneisen *et al.*, J Biol Chem. 1990 Sep 25;265(27):16337-42; Muller *et al.*, DNA Cell Biol. 1990 Apr;9(3):221-9). In addition, liposomes are free of the DNA length constraints that are typical of viral-based delivery
10   systems. Liposomes have been used effectively to introduce genes, various drugs, radiotherapeutic agents, enzymes, viruses, transcription factors, allosteric effectors and the like, into a variety of cultured cell lines and animals. Furthermore, he use of liposomes does not appear to be associated with autoimmune responses or unacceptable toxicity after systemic delivery.

15   In certain embodiments, liposomes are formed from phospholipids that are dispersed in an aqueous medium and spontaneously form multilamellar concentric bilayer vesicles (also termed multilamellar vesicles (MLVs).

          Alternatively, in other embodiments, the invention provides for pharmaceutically-acceptable nanocapsule formulations of the compositions of the
20   present invention. Nanocapsules can generally entrap compounds in a stable and reproducible way (see, for example, Quintanar-Guerrero *et al.*, Drug Dev Ind Pharm. 1998 Dec;24(12):1113-28). To avoid side effects due to intracellular polymeric overloading, such ultrafine particles (sized around 0.1 μm) may be designed using polymers able to be degraded *in vivo*. Such particles can be made as described, for
25   example, by Couvreur *et al.*, Crit Rev Ther Drug Carrier Syst. 1988;5(1):1-20; zur Muhlen *et al.*, Eur J Pharm Biopharm. 1998 Mar;45(2):149-55; Zambaux *et al.* J Controlled Release. 1998 Jan 2;50(1-3):31-40; and U. S. Patent 5,145,684.

Cancer Therapeutic Methods

In further aspects of the present invention, the pharmaceutical compositions described herein may be used for the treatment of cancer, particularly for the immunotherapy of prostate cancer. Within such methods, the pharmaceutical compositions described herein are administered to a patient, typically a warm-blooded animal, preferably a human. A patient may or may not be afflicted with cancer. Accordingly, the above pharmaceutical compositions may be used to prevent the development of a cancer or to treat a patient afflicted with a cancer. Pharmaceutical compositions and vaccines may be administered either prior to or following surgical removal of primary tumors and/or treatment such as administration of radiotherapy or conventional chemotherapeutic drugs. As discussed above, administration of the pharmaceutical compositions may be by any suitable method, including administration by intravenous, intraperitoneal, intramuscular, subcutaneous, intranasal, intradermal, anal, vaginal, topical and oral routes.

Within certain embodiments, immunotherapy may be active immunotherapy, in which treatment relies on the *in vivo* stimulation of the endogenous host immune system to react against tumors with the administration of immune response-modifying agents (such as polypeptides and polynucleotides as provided herein).

Within other embodiments, immunotherapy may be passive immunotherapy, in which treatment involves the delivery of agents with established tumor-immune reactivity (such as effector cells or antibodies) that can directly or indirectly mediate antitumor effects and does not necessarily depend on an intact host immune system. Examples of effector cells include T cells as discussed above, T lymphocytes (such as CD8$^+$ cytotoxic T lymphocytes and CD4$^+$ T-helper tumor-infiltrating lymphocytes), killer cells (such as Natural Killer cells and lymphokine-activated killer cells), B cells and antigen-presenting cells (such as dendritic cells and macrophages) expressing a polypeptide provided herein. T cell receptors and antibody receptors specific for the polypeptides recited herein may be cloned, expressed and transferred into other vectors or effector cells for adoptive immunotherapy. The

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polypeptides provided herein may also be used to generate antibodies or anti-idiotypic antibodies (as described above and in U.S. Patent No. 4,918,164) for passive immunotherapy.

Effector cells may generally be obtained in sufficient quantities for adoptive immunotherapy by growth *in vitro*, as described herein. Culture conditions for expanding single antigen-specific effector cells to several billion in number with retention of antigen recognition *in vivo* are well known in the art. Such *in vitro* culture conditions typically use intermittent stimulation with antigen, often in the presence of cytokines (such as IL-2) and non-dividing feeder cells. As noted above, immunoreactive polypeptides as provided herein may be used to rapidly expand antigen-specific T cell cultures in order to generate a sufficient number of cells for immunotherapy. In particular, antigen-presenting cells, such as dendritic, macrophage, monocyte, fibroblast and/or B cells, may be pulsed with immunoreactive polypeptides or transfected with one or more polynucleotides using standard techniques well known in the art. For example, antigen-presenting cells can be transfected with a polynucleotide having a promoter appropriate for increasing expression in a recombinant virus or other expression system. Cultured effector cells for use in therapy must be able to grow and distribute widely, and to survive long term *in vivo*. Studies have shown that cultured effector cells can be induced to grow in vivo and to survive long term in substantial numbers by repeated stimulation with antigen supplemented with IL-2 (*see*, for example, Cheever et al., *Immunological Reviews 157*:177, 1997).

Alternatively, a vector expressing a polypeptide recited herein may be introduced into antigen presenting cells taken from a patient and clonally propagated *ex vivo* for transplant back into the same patient. Transfected cells may be reintroduced into the patient using any means known in the art, preferably in sterile form by intravenous, intracavitary, intraperitoneal or intratumor administration.

Routes and frequency of administration of the therapeutic compositions described herein, as well as dosage, will vary from individual to individual, and may be readily established using standard techniques. In general, the pharmaceutical compositions and vaccines may be administered by injection (*e.g.*, intracutaneous,

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intramuscular, intravenous or subcutaneous), intranasally (*e.g.*, by aspiration) or orally. Preferably, between 1 and 10 doses may be administered over a 52 week period. Preferably, 6 doses are administered, at intervals of 1 month, and booster vaccinations may be given periodically thereafter. Alternate protocols may be appropriate for

5   individual patients. A suitable dose is an amount of a compound that, when administered as described above, is capable of promoting an anti-tumor immune response, and is at least 10-50% above the basal (*i.e.*, untreated) level. Such response can be monitored by measuring the anti-tumor antibodies in a patient or by vaccine-dependent generation of cytolytic effector cells capable of killing the patient's tumor

10 cells *in vitro*. Such vaccines should also be capable of causing an immune response that leads to an improved clinical outcome (*e.g.*, more frequent remissions, complete or partial or longer disease-free survival) in vaccinated patients as compared to non-vaccinated patients. In general, for pharmaceutical compositions and vaccines comprising one or more polypeptides, the amount of each polypeptide present in a dose

15 ranges from about 25 µg to 5 mg per kg of host. Suitable dose sizes will vary with the size of the patient, but will typically range from about 0.1 mL to about 5 mL.

In general, an appropriate dosage and treatment regimen provides the active compound(s) in an amount sufficient to provide therapeutic and/or prophylactic benefit. Such a response can be monitored by establishing an improved clinical

20 outcome (*e.g.*, more frequent remissions, complete or partial, or longer disease-free survival) in treated patients as compared to non-treated patients. Increases in preexisting immune responses to a tumor protein generally correlate with an improved clinical outcome. Such immune responses may generally be evaluated using standard proliferation, cytotoxicity or cytokine assays, which may be performed using samples

25 obtained from a patient before and after treatment.

Cancer Detection and Diagnostic Compositions, Methods and Kits

In general, a cancer may be detected in a patient based on the presence of one or more prostate tumor proteins and/or polynucleotides encoding such proteins in a biological sample (for example, blood, sera, sputum urine and/or tumor biopsies)

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obtained from the patient. In other words, such proteins may be used as markers to indicate the presence or absence of a cancer such as prostate cancer. In addition, such proteins may be useful for the detection of other cancers. The binding agents provided herein generally permit detection of the level of antigen that binds to the agent in the

5   biological sample. Polynucleotide primers and probes may be used to detect the level of mRNA encoding a tumor protein, which is also indicative of the presence or absence of a cancer. In general, a prostate tumor sequence should be present at a level that is at least three fold higher in tumor tissue than in normal tissue

There are a variety of assay formats known to those of ordinary skill in

10   the art for using a binding agent to detect polypeptide markers in a sample. *See, e.g.,* Harlow and Lane, *Antibodies: A Laboratory Manual,* Cold Spring Harbor Laboratory, 1988. In general, the presence or absence of a cancer in a patient may be determined by (a) contacting a biological sample obtained from a patient with a binding agent; (b) detecting in the sample a level of polypeptide that binds to the binding agent; and (c)

15   comparing the level of polypeptide with a predetermined cut-off value.

In a preferred embodiment, the assay involves the use of binding agent immobilized on a solid support to bind to and remove the polypeptide from the remainder of the sample. The bound polypeptide may then be detected using a detection reagent that contains a reporter group and specifically binds to the binding

20   agent/polypeptide complex. Such detection reagents may comprise, for example, a binding agent that specifically binds to the polypeptide or an antibody or other agent that specifically binds to the binding agent, such as an anti-immunoglobulin, protein G, protein A or a lectin. Alternatively, a competitive assay may be utilized, in which a polypeptide is labeled with a reporter group and allowed to bind to the immobilized

25   binding agent after incubation of the binding agent with the sample. The extent to which components of the sample inhibit the binding of the labeled polypeptide to the binding agent is indicative of the reactivity of the sample with the immobilized binding agent. Suitable polypeptides for use within such assays include full length prostate tumor proteins and polypeptide portions thereof to which the binding agent binds, as

30   described above.

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The solid support may be any material known to those of ordinary skill in the art to which the tumor protein may be attached. For example, the solid support may be a test well in a microtiter plate or a nitrocellulose or other suitable membrane. Alternatively, the support may be a bead or disc, such as glass, fiberglass, latex or a

5   plastic material such as polystyrene or polyvinylchloride. The support may also be a magnetic particle or a fiber optic sensor, such as those disclosed, for example, in U.S. Patent No. 5,359,681. The binding agent may be immobilized on the solid support using a variety of techniques known to those of skill in the art, which are amply described in the patent and scientific literature. In the context of the present invention,

10   the term "immobilization" refers to both noncovalent association, such as adsorption, and covalent attachment (which may be a direct linkage between the agent and functional groups on the support or may be a linkage by way of a cross-linking agent). Immobilization by adsorption to a well in a microtiter plate or to a membrane is preferred. In such cases, adsorption may be achieved by contacting the binding agent, in

15   a suitable buffer, with the solid support for a suitable amount of time. The contact time varies with temperature, but is typically between about 1 hour and about 1 day. In general, contacting a well of a plastic microtiter plate (such as polystyrene or polyvinylchloride) with an amount of binding agent ranging from about 10 ng to about 10 μg, and preferably about 100 ng to about 1 μg, is sufficient to immobilize an

20   adequate amount of binding agent.

Covalent attachment of binding agent to a solid support may generally be achieved by first reacting the support with a bifunctional reagent that will react with both the support and a functional group, such as a hydroxyl or amino group, on the binding agent. For example, the binding agent may be covalently attached to supports

25   having an appropriate polymer coating using benzoquinone or by condensation of an aldehyde group on the support with an amine and an active hydrogen on the binding partner (see, e.g., Pierce Immunotechnology Catalog and Handbook, 1991, at A12-A13).

In certain embodiments, the assay is a two-antibody sandwich assay.

30   This assay may be performed by first contacting an antibody that has been immobilized

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on a solid support, commonly the well of a microtiter plate, with the sample, such that polypeptides within the sample are allowed to bind to the immobilized antibody. Unbound sample is then removed from the immobilized polypeptide-antibody complexes and a detection reagent (preferably a second antibody capable of binding to a

5   different site on the polypeptide) containing a reporter group is added. The amount of detection reagent that remains bound to the solid support is then determined using a method appropriate for the specific reporter group.

More specifically, once the antibody is immobilized on the support as described above, the remaining protein binding sites on the support are typically

10   blocked. Any suitable blocking agent known to those of ordinary skill in the art, such as bovine serum albumin or Tween 20™ (Sigma Chemical Co., St. Louis, MO). The immobilized antibody is then incubated with the sample, and polypeptide is allowed to bind to the antibody. The sample may be diluted with a suitable diluent, such as phosphate-buffered saline (PBS) prior to incubation. In general, an appropriate contact

15   time (i.e., incubation time) is a period of time that is sufficient to detect the presence of polypeptide within a sample obtained from an individual with prostate cancer. Preferably, the contact time is sufficient to achieve a level of binding that is at least about 95% of that achieved at equilibrium between bound and unbound polypeptide. Those of ordinary skill in the art will recognize that the time necessary to achieve

20   equilibrium may be readily determined by assaying the level of binding that occurs over a period of time. At room temperature, an incubation time of about 30 minutes is generally sufficient.

Unbound sample may then be removed by washing the solid support with an appropriate buffer, such as PBS containing 0.1% Tween 20™. The second

25   antibody, which contains a reporter group, may then be added to the solid support. Preferred reporter groups include those groups recited above.

The detection reagent is then incubated with the immobilized antibody-polypeptide complex for an amount of time sufficient to detect the bound polypeptide. An appropriate amount of time may generally be determined by assaying the level of

30   binding that occurs over a period of time. Unbound detection reagent is then removed

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and bound detection reagent is detected using the reporter group. The method employed for detecting the reporter group depends upon the nature of the reporter group. For radioactive groups, scintillation counting or autoradiographic methods are generally appropriate. Spectroscopic methods may be used to detect dyes, luminescent groups 5 and fluorescent groups. Biotin may be detected using avidin, coupled to a different reporter group (commonly a radioactive or fluorescent group or an enzyme). Enzyme reporter groups may generally be detected by the addition of substrate (generally for a specific period of time), followed by spectroscopic or other analysis of the reaction products.

10   To determine the presence or absence of a cancer, such as prostate cancer, the signal detected from the reporter group that remains bound to the solid support is generally compared to a signal that corresponds to a predetermined cut-off value. In one preferred embodiment, the cut-off value for the detection of a cancer is the average mean signal obtained when the immobilized antibody is incubated with 15 samples from patients without the cancer. In general, a sample generating a signal that is three standard deviations above the predetermined cut-off value is considered positive for the cancer. In an alternate preferred embodiment, the cut-off value is determined using a Receiver Operator Curve, according to the method of Sackett et al., *Clinical Epidemiology: A Basic Science for Clinical Medicine*, Little Brown and Co., 1985, 20 p. 106-7. Briefly, in this embodiment, the cut-off value may be determined from a plot of pairs of true positive rates (*i.e.*, sensitivity) and false positive rates (100%-specificity) that correspond to each possible cut-off value for the diagnostic test result. The cut-off value on the plot that is the closest to the upper left-hand corner (*i.e.*, the value that encloses the largest area) is the most accurate cut-off value, and a sample generating a 25 signal that is higher than the cut-off value determined by this method may be considered positive. Alternatively, the cut-off value may be shifted to the left along the plot, to minimize the false positive rate, or to the right, to minimize the false negative rate. In general, a sample generating a signal that is higher than the cut-off value determined by this method is considered positive for a cancer.

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In a related embodiment, the assay is performed in a flow-through or strip test format, wherein the binding agent is immobilized on a membrane, such as nitrocellulose. In the flow-through test, polypeptides within the sample bind to the immobilized binding agent as the sample passes through the membrane. A second,

5 labeled binding agent then binds to the binding agent-polypeptide complex as a solution containing the second binding agent flows through the membrane. The detection of bound second binding agent may then be performed as described above. In the strip test format, one end of the membrane to which binding agent is bound is immersed in a solution containing the sample. The sample migrates along the membrane through a

10 region containing second binding agent and to the area of immobilized binding agent. Concentration of second binding agent at the area of immobilized antibody indicates the presence of a cancer. Typically, the concentration of second binding agent at that site generates a pattern, such as a line, that can be read visually. The absence of such a pattern indicates a negative result. In general, the amount of binding agent immobilized

15 on the membrane is selected to generate a visually discernible pattern when the biological sample contains a level of polypeptide that would be sufficient to generate a positive signal in the two-antibody sandwich assay, in the format discussed above. Preferred binding agents for use in such assays are antibodies and antigen-binding fragments thereof. Preferably, the amount of antibody immobilized on the membrane

20 ranges from about 25 ng to about 1μg, and more preferably from about 50 ng to about 500 ng. Such tests can typically be performed with a very small amount of biological sample.

Of course, numerous other assay protocols exist that are suitable for use with the tumor proteins or binding agents of the present invention. The above

25 descriptions are intended to be exemplary only. For example, it will be apparent to those of ordinary skill in the art that the above protocols may be readily modified to use tumor polypeptides to detect antibodies that bind to such polypeptides in a biological sample. The detection of such tumor protein specific antibodies may correlate with the presence of a cancer.

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A cancer may also, or alternatively, be detected based on the presence of T cells that specifically react with a tumor protein in a biological sample. Within certain methods, a biological sample comprising CD4$^+$ and/or CD8$^+$ T cells isolated from a patient is incubated with a tumor polypeptide, a polynucleotide encoding such a

5   polypeptide and/or an APC that expresses at least an immunogenic portion of such a polypeptide, and the presence or absence of specific activation of the T cells is detected. Suitable biological samples include, but are not limited to, isolated T cells. For example, T cells may be isolated from a patient by routine techniques (such as by Ficoll/Hypaque density gradient centrifugation of peripheral blood lymphocytes). T

10   cells may be incubated *in vitro* for 2-9 days (typically 4 days) at 37°C with polypeptide (*e.g.*, 5 - 25 μg/ml). It may be desirable to incubate another aliquot of a T cell sample in the absence of tumor polypeptide to serve as a control. For CD4$^+$ T cells, activation is preferably detected by evaluating proliferation of the T cells. For CD8$^+$ T cells, activation is preferably detected by evaluating cytolytic activity. A level of proliferation

15   that is at least two fold greater and/or a level of cytolytic activity that is at least 20% greater than in disease-free patients indicates the presence of a cancer in the patient.

As noted above, a cancer may also, or alternatively, be detected based on the level of mRNA encoding a tumor protein in a biological sample. For example, at least two oligonucleotide primers may be employed in a polymerase chain reaction

20   (PCR) based assay to amplify a portion of a tumor cDNA derived from a biological sample, wherein at least one of the oligonucleotide primers is specific for (*i.e.*, hybridizes to) a polynucleotide encoding the tumor protein. The amplified cDNA is then separated and detected using techniques well known in the art, such as gel electrophoresis. Similarly, oligonucleotide probes that specifically hybridize to a

25   polynucleotide encoding a tumor protein may be used in a hybridization assay to detect the presence of polynucleotide encoding the tumor protein in a biological sample.

To permit hybridization under assay conditions, oligonucleotide primers and probes should comprise an oligonucleotide sequence that has at least about 60%, preferably at least about 75% and more preferably at least about 90%, identity to a

30   portion of a polynucleotide encoding a tumor protein of the invention that is at least 10

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nucleotides, and preferably at least 20 nucleotides, in length.   Preferably, oligonucleotide primers and/or probes hybridize to a polynucleotide encoding a polypeptide described herein under moderately stringent conditions, as defined above. Oligonucleotide primers and/or probes which may be usefully employed in the

5   diagnostic methods described herein preferably are at least 10-40 nucleotides in length. In a preferred embodiment, the oligonucleotide primers comprise at least 10 contiguous nucleotides, more preferably at least 15 contiguous nucleotides, of a DNA molecule having a sequence as disclosed herein.   Techniques for both PCR based assays and hybridization assays are well known in the art (*see,* for example, Mullis et al., *Cold*

10   *Spring Harbor Symp. Quant. Biol., 51:263,* 1987; Erlich ed., *PCR Technology,* Stockton Press, NY, 1989).

One preferred assay employs RT-PCR, in which PCR is applied in conjunction with reverse transcription.   Typically, RNA is extracted from a biological sample, such as biopsy tissue, and is reverse transcribed to produce cDNA molecules.

15   PCR amplification using at least one specific primer generates a cDNA molecule, which may be separated and visualized using, for example, gel electrophoresis. Amplification may be performed on biological samples taken from a test patient and from an individual who is not afflicted with a cancer. The amplification reaction may be performed on several dilutions of cDNA spanning two orders of magnitude. A two-fold

20   or greater increase in expression in several dilutions of the test patient sample as compared to the same dilutions of the non-cancerous sample is typically considered positive.

In another embodiment, the compositions described herein may be used as markers for the progression of cancer. In this embodiment, assays as described above

25   for the diagnosis of a cancer may be performed over time, and the change in the level of reactive polypeptide(s) or polynucleotide(s) evaluated. For example, the assays may be performed every 24-72 hours for a period of 6 months to 1 year, and thereafter performed as needed. In general, a cancer is progressing in those patients in whom the level of polypeptide or polynucleotide detected increases over time. In contrast, the

cancer is not progressing when the level of reactive polypeptide or polynucleotide either remains constant or decreases with time.

Certain *in vivo* diagnostic assays may be performed directly on a tumor. One such assay involves contacting tumor cells with a binding agent. The bound

5   binding agent may then be detected directly or indirectly via a reporter group. Such binding agents may also be used in histological applications. Alternatively, polynucleotide probes may be used within such applications.

As noted above, to improve sensitivity, multiple tumor protein markers may be assayed within a given sample. It will be apparent that binding agents specific

10   for different proteins provided herein may be combined within a single assay. Further, multiple primers or probes may be used concurrently. The selection of tumor protein markers may be based on routine experiments to determine combinations that results in optimal sensitivity. In addition, or alternatively, assays for tumor proteins provided herein may be combined with assays for other known tumor antigens.

15   The present invention further provides kits for use within any of the above diagnostic methods. Such kits typically comprise two or more components necessary for performing a diagnostic assay. Components may be compounds, reagents, containers and/or equipment. For example, one container within a kit may contain a monoclonal antibody or fragment thereof that specifically binds to a tumor protein.

20   Such antibodies or fragments may be provided attached to a support material, as described above. One or more additional containers may enclose elements, such as reagents or buffers, to be used in the assay. Such kits may also, or alternatively, contain a detection reagent as described above that contains a reporter group suitable for direct or indirect detection of antibody binding.

25   Alternatively, a kit may be designed to detect the level of mRNA encoding a tumor protein in a biological sample. Such kits generally comprise at least one oligonucleotide probe or primer, as described above, that hybridizes to a polynucleotide encoding a tumor protein. Such an oligonucleotide may be used, for example, within a PCR or hybridization assay. Additional components that may be

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present within such kits include a second oligonucleotide and/or a diagnostic reagent or container to facilitate the detection of a polynucleotide encoding a tumor protein.

The following Examples are offered by way of illustration and not by way of limitation.

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EXAMPLES

EXAMPLE 1

5   ISOLATION AND CHARACTERIZATION OF PROSTATE-SPECIFIC POLYPEPTIDES

This Example describes the isolation of certain prostate-specific polypeptides from a prostate tumor cDNA library.

A human prostate tumor cDNA expression library was constructed from
10 prostate tumor poly A^+ RNA using a Superscript Plasmid System for cDNA Synthesis and Plasmid Cloning kit (BRL Life Technologies, Gaithersburg, MD 20897) following the manufacturer's protocol. Specifically, prostate tumor tissues were homogenized with polytron (Kinematica, Switzerland) and total RNA was extracted using Trizol reagent (BRL Life Technologies) as directed by the manufacturer. The poly A^+ RNA
15 was then purified using a Qiagen oligotex spin column mRNA purification kit (Qiagen, Santa Clarita, CA 91355) according to the manufacturer's protocol. First-strand cDNA was synthesized using the NotI/Oligo-dT18 primer. Double-stranded cDNA was synthesized, ligated with EcoRI/BAXI adaptors (Invitrogen, San Diego, CA) and digested with NotI. Following size fractionation with Chroma Spin-1000 columns
20 (Clontech, Palo Alto, CA), the cDNA was ligated into the EcoRI/NotI site of pCDNA3.1 (Invitrogen) and transformed into ElectroMax *E. coli* DH10B cells (BRL Life Technologies) by electroporation.

Using the same procedure, a normal human pancreas cDNA expression library was prepared from a pool of six tissue specimens (Clontech). The cDNA
25 libraries were characterized by determining the number of independent colonies, the percentage of clones that carried insert, the average insert size and by sequence analysis. The prostate tumor library contained 1.64×10^7 independent colonies, with 70% of clones having an insert and the average insert size being 1745 base pairs. The normal pancreas cDNA library contained 3.3×10^6 independent colonies, with 69% of clones
30 having inserts and the average insert size being 1120 base pairs. For both libraries,

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sequence analysis showed that the majority of clones had a full length cDNA sequence and were synthesized from mRNA, with minimal rRNA and mitochondrial DNA contamination.

cDNA library subtraction was performed using the above prostate tumor

5   and normal pancreas cDNA libraries, as described by Hara *et al.* (*Blood*, *84*:189-199, 1994) with some modifications. Specifically, a prostate tumor-specific subtracted cDNA library was generated as follows. Normal pancreas cDNA library (70 µg) was digested with EcoRI, NotI, and SfuI, followed by a filling-in reaction with DNA polymerase Klenow fragment. After phenol-chloroform extraction and ethanol

10   precipitation, the DNA was dissolved in 100 µl of H_2O, heat-denatured and mixed with 100 µl (100 µg) of Photoprobe biotin (Vector Laboratories, Burlingame, CA). As recommended by the manufacturer, the resulting mixture was irradiated with a 270 W sunlamp on ice for 20 minutes. Additional Photoprobe biotin (50 µl) was added and the biotinylation reaction was repeated. After extraction with butanol five times, the

15   DNA was ethanol-precipitated and dissolved in 23 µl H_2O to form the driver DNA.

To form the tracer DNA, 10 µg prostate tumor cDNA library was digested with BamHI and XhoI, phenol chloroform extracted and passed through Chroma spin-400 columns (Clontech). Following ethanol precipitation, the tracer DNA was dissolved in 5 µl H_2O. Tracer DNA was mixed with 15 µl driver DNA and 20 µl of

20   2 x hybridization buffer (1.5 M NaCl/10 mM EDTA/50 mM HEPES pH 7.5/0.2% sodium dodecyl sulfate), overlaid with mineral oil, and heat-denatured completely. The sample was immediately transferred into a 68 °C water bath and incubated for 20 hours (long hybridization [LH]). The reaction mixture was then subjected to a streptavidin treatment followed by phenol/chloroform extraction. This process was repeated three

25   more times. Subtracted DNA was precipitated, dissolved in 12 µl H_2O, mixed with 8 µl driver DNA and 20 µl of 2 x hybridization buffer, and subjected to a hybridization at 68 °C for 2 hours (short hybridization [SH]). After removal of biotinylated double-stranded DNA, subtracted cDNA was ligated into BamHI/XhoI site of chloramphenicol resistant pBCSK$^+$ (Stratagene, La Jolla, CA 92037) and transformed into ElectroMax *E.*

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coli DH10B cells by electroporation to generate a prostate tumor specific subtracted cDNA library (referred to as "prostate subtraction 1").

To analyze the subtracted cDNA library, plasmid DNA was prepared from 100 independent clones, randomly picked from the subtracted prostate tumor specific library and grouped based on insert size. Representative cDNA clones were further characterized by DNA sequencing with a Perkin Elmer/Applied Biosystems Division Automated Sequencer Model 373A (Foster City, CA). Six cDNA clones, hereinafter referred to as F1-13, F1-12, F1-16, H1-1, H1-9 and H1-4, were shown to be abundant in the subtracted prostate-specific cDNA library. The determined 3' and 5' cDNA sequences for F1-12 are provided in SEQ ID NO: 2 and 3, respectively, with determined 3' cDNA sequences for F1-13, F1-16, H1-1, H1-9 and H1-4 being provided in SEQ ID NO: 1 and 4-7, respectively.

The cDNA sequences for the isolated clones were compared to known sequences in the gene bank using the EMBL and GenBank databases (release 96). Four of the prostate tumor cDNA clones, F1-13, F1-16, H1-1, and H1-4, were determined to encode the following previously identified proteins: prostate specific antigen (PSA), human glandular kallikrein, human tumor expression enhanced gene, and mitochondria cytochrome C oxidase subunit II. H1-9 was found to be identical to a previously identified human autonomously replicating sequence. No significant homologies to the cDNA sequence for F1-12 were found.

Subsequent studies led to the isolation of a full-length cDNA sequence for F1-12 (also referred to as P504S). This sequence is provided in SEQ ID NO: 107, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 108. cDNA splice variants of P504S are provided in SEQ ID NO: 600-605.

To clone less abundant prostate tumor specific genes, cDNA library subtraction was performed by subtracting the prostate tumor cDNA library described above with the normal pancreas cDNA library and with the three most abundant genes in the previously subtracted prostate tumor specific cDNA library: human glandular kallikrein, prostate specific antigen (PSA), and mitochondria cytochrome C oxidase subunit II. Specifically, 1 μg each of human glandular kallikrein, PSA and

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mitochondria cytochrome C oxidase subunit II cDNAs in pCDNA3.1 were added to the driver DNA and subtraction was performed as described above to provide a second subtracted cDNA library hereinafter referred to as the "subtracted prostate tumor specific cDNA library with spike".

5   Twenty-two cDNA clones were isolated from the subtracted prostate tumor specific cDNA library with spike. The determined 3' and 5' cDNA sequences for the clones referred to as J1-17, L1-12, N1-1862, J1-13, J1-19, J1-25, J1-24, K1-58, K1-63, L1-4 and L1-14 are provided in SEQ ID NOS: 8-9, 10-11, 12-13, 14-15, 16-17, 18-19, 20-21, 22-23, 24-25, 26-27 and 28-29, respectively. The determined 3' cDNA

10   sequences for the clones referred to as J1-12, J1-16, J1-21, K1-48, K1-55, L1-2, L1-6, N1-1858, N1-1860, N1-1861, N1-1864 are provided in SEQ ID NOS: 30-40, respectively. Comparison of these sequences with those in the gene bank as described above, revealed no significant homologies to three of the five most abundant DNA species, (J1-17, L1-12 and N1-1862; SEQ ID NOS: 8-9, 10-11 and 12-13, respectively).

15   Of the remaining two most abundant species, one (J1-12; SEQ ID NO:30) was found to be identical to the previously identified human pulmonary surfactant-associated protein, and the other (K1-48; SEQ ID NO:33) was determined to have some homology to *R. norvegicus* mRNA for 2-arylpropionyl-CoA epimerase. Of the 17 less abundant cDNA clones isolated from the subtracted prostate tumor specific cDNA library with spike,

20   four (J1-16, K1-55, L1-6 and N1-1864; SEQ ID NOS:31, 34, 36 and 40, respectively) were found to be identical to previously identified sequences, two (J1-21 and N1-1860; SEQ ID NOS: 32 and 38, respectively) were found to show some homology to non-human sequences, and two (L1-2 and N1-1861; SEQ ID NOS: 35 and 39, respectively) were found to show some homology to known human sequences. No significant

25   homologies were found to the polypeptides J1-13, J1-19, J1-24, J1-25, K1-58, K1-63, L1-4, L1-14 (SEQ ID NOS: 14-15, 16-17, 20-21, 18-19, 22-23, 24-25, 26-27, 28-29, respectively).

Subsequent studies led to the isolation of full length cDNA sequences for J1-17, L1-12 and N1-1862 (SEQ ID NOS: 109-111, respectively). The corresponding

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predicted amino acid sequences are provided in SEQ ID NOS: 112-114. L1-12 is also referred to as P501S. A cDNA splice variant of P501S is provided in SEQ ID NO: 606.

In a further experiment, four additional clones were identified by subtracting a prostate tumor cDNA library with normal prostate cDNA prepared from a
5   pool of three normal prostate poly A+ RNA (referred to as "prostate subtraction 2"). The determined cDNA sequences for these clones, hereinafter referred to as U1-3064, U1-3065, V1-3692 and 1A-3905, are provided in SEQ ID NO: 69-72, respectively. Comparison of the determined sequences with those in the gene bank revealed no significant homologies to U1-3065.

10   A second subtraction with spike (referred to as "prostate subtraction spike 2") was performed by subtracting a prostate tumor specific cDNA library with spike with normal pancreas cDNA library and further spiked with PSA, J1-17, pulmonary surfactant-associated protein, mitochondrial DNA, cytochrome c oxidase subunit II, N1-1862, autonomously replicating sequence, L1-12 and tumor expression
15   enhanced gene. Four additional clones, hereinafter referred to as V1-3686, R1-2330, 1B-3976 and V1-3679, were isolated. The determined cDNA sequences for these clones are provided in SEQ ID NO:73-76, respectively. Comparison of these sequences with those in the gene bank revealed no significant homologies to V1-3686 and R1-2330.

20   Further analysis of the three prostate subtractions described above (prostate subtraction 2, subtracted prostate tumor specific cDNA library with spike, and prostate subtraction spike 2) resulted in the identification of sixteen additional clones, referred to as 1G-4736, 1G-4738, 1G-4741, 1G-4744, 1G-4734, 1H-4774, 1H-4781, 1H-4785, 1H-4787, 1H-4796, 1I-4810, 1I-4811, 1J-4876, 1K-4884 and 1K-4896. The
25   determined cDNA sequences for these clones are provided in SEQ ID NOS: 77-92, respectively. Comparison of these sequences with those in the gene bank as described above, revealed no significant homologies to 1G-4741, 1G-4734, 1I-4807, 1J-4876 and 1K-4896 (SEQ ID NOS: 79, 81, 87, 90 and 92, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1G-4736, 1G-
30   4738, 1G-4741, 1G-4744, 1H-4774, 1H-4781, 1H-4785, 1H-4787, 1H-4796, 1I-4807,

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1J-4876, 1K-4884 and 1K-4896, provided in SEQ ID NOS: 179-188 and 191-193, respectively, and to the determination of additional partial cDNA sequences for 1I-4810 and 1I-4811, provided in SEQ ID NOS: 189 and 190, respectively.

Additional studies with prostate subtraction spike 2 resulted in the
5   isolation of three more clones. Their sequences were determined as described above and compared to the most recent GenBank. All three clones were found to have homology to known genes, which are Cysteine-rich protein, KIAA0242, and KIAA0280 (SEQ ID NO: 317, 319, and 320, respectively). Further analysis of these clones by Synteni microarray (Synteni, Palo Alto, CA) demonstrated that all three clones were
10 over-expressed in most prostate tumors and prostate BPH, as well as in the majority of normal prostate tissues tested, but low expression in all other normal tissues.

An additional subtraction was performed by subtracting a normal prostate cDNA library with normal pancreas cDNA (referred to as "prostate subtraction 3"). This led to the identification of six additional clones referred to as 1G-4761, 1G-
15 4762, 1H-4766, 1H-4770, 1H-4771 and 1H-4772 (SEQ ID NOS: 93-98). Comparison of these sequences with those in the gene bank revealed no significant homologies to 1G-4761 and 1H-4771 (SEQ ID NOS: 93 and 97, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1G-4761, 1G-4762, 1H-4766 and 1H-4772 provided in SEQ ID NOS: 194-196 and 199, respectively,
20 and to the determination of additional partial cDNA sequences for 1H-4770 and 1H-4771, provided in SEQ ID NOS: 197 and 198, respectively.

Subtraction of a prostate tumor cDNA library, prepared from a pool of polyA+ RNA from three prostate cancer patients, with a normal pancreas cDNA library (prostate subtraction 4) led to the identification of eight clones, referred to as 1D-4297,
25 1D-4309, 1D.1-4278, 1D-4288, 1D-4283, 1D-4304, 1D-4296 and 1D-4280 (SEQ ID NOS: 99-107). These sequences were compared to those in the gene bank as described above. No significant homologies were found to 1D-4283 and 1D-4304 (SEQ ID NOS: 103 and 104, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1D-4309, 1D.1-4278, 1D-4288, 1D-

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4283, 1D-4304, 1D-4296 and 1D-4280, provided in SEQ ID NOS: 200-206, respectively.

cDNA clones isolated in prostate subtraction 1 and prostate subtraction 2, described above, were colony PCR amplified and their mRNA expression levels in prostate tumor, normal prostate and in various other normal tissues were determined using microarray technology (Synteni, Palo Alto, CA). Briefly, the PCR amplification products were dotted onto slides in an array format, with each product occupying a unique location in the array. mRNA was extracted from the tissue sample to be tested, reverse transcribed, and fluorescent-labeled cDNA probes were generated. The microarrays were probed with the labeled cDNA probes, the slides scanned and fluorescence intensity was measured. This intensity correlates with the hybridization intensity. Two clones (referred to as P509S and P510S) were found to be over-expressed in prostate tumor and normal prostate and expressed at low levels in all other normal tissues tested (liver, pancreas, skin, bone marrow, brain, breast, adrenal gland, bladder, testes, salivary gland, large intestine, kidney, ovary, lung, spinal cord, skeletal muscle and colon). The determined cDNA sequences for P509S and P510S are provided in SEQ ID NO: 223 and 224, respectively. Comparison of these sequences with those in the gene bank as described above, revealed some homology to previously identified ESTs.

Additional, studies led to the isolation of the full-length cDNA sequence for P509S. This sequence is provided in SEQ ID NO: 332, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 339. Two variant full-length cDNA sequences for P510S are provided in SEQ ID NO: 535 and 536, with the corresponding predicted amino acid sequences being provided in SEQ ID NO: 537 and 538, respectively. Additional splice variants of P510S are provided in SEQ ID NO: 598 and 599.

The determined cDNA sequences for additional prostate-specific clones isolated during characterization of prostate specific cDNA libraries are provided in SEQ ID NO: 618-689, 691-697 and 709-772. Comparison of these sequences with those in the public databases revealed no significant homologies to any of these sequences.

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EXAMPLE 2

DETERMINATION OF TISSUE SPECIFICITY OF PROSTATE-SPECIFIC POLYPEPTIDES

5   Using gene specific primers, mRNA expression levels for the representative prostate-specific polypeptides F1-16, H1-1, J1-17 (also referred to as P502S), L1-12 (also referred to as P501S), F1-12 (also referred to as P504S) and N1-1862 (also referred to as P503S) were examined in a variety of normal and tumor tissues using RT-PCR.

10   Briefly, total RNA was extracted from a variety of normal and tumor tissues using Trizol reagent as described above. First strand synthesis was carried out using 1-2 µg of total RNA with SuperScript II reverse transcriptase (BRL Life Technologies) at 42 ^{o}C for one hour. The cDNA was then amplified by PCR with gene-specific primers. To ensure the semi-quantitative nature of the RT-PCR, β-actin was

15   used as an internal control for each of the tissues examined. First, serial dilutions of the first strand cDNAs were prepared and RT-PCR assays were performed using β-actin specific primers. A dilution was then chosen that enabled the linear range amplification of the β-actin template and which was sensitive enough to reflect the differences in the initial copy numbers. Using these conditions, the β-actin levels were determined for

20   each reverse transcription reaction from each tissue. DNA contamination was minimized by DNase treatment and by assuring a negative PCR result when using first strand cDNA that was prepared without adding reverse transcriptase.

           mRNA Expression levels were examined in four different types of tumor tissue (prostate tumor from 2 patients, breast tumor from 3 patients, colon tumor, lung

25   tumor), and sixteen different normal tissues, including prostate, colon, kidney, liver, lung, ovary, pancreas, skeletal muscle, skin, stomach, testes, bone marrow and brain. F1-16 was found to be expressed at high levels in prostate tumor tissue, colon tumor and normal prostate, and at lower levels in normal liver, skin and testes, with expression being undetectable in the other tissues examined. H1-1 was found to be expressed at

30   high levels in prostate tumor, lung tumor, breast tumor, normal prostate, normal colon

and normal brain, at much lower levels in normal lung, pancreas, skeletal muscle, skin, small intestine, bone marrow, and was not detected in the other tissues tested. J1-17 (P502S) and L1-12 (P501S) appear to be specifically over-expressed in prostate, with both genes being expressed at high levels in prostate tumor and normal prostate but at

5   low to undetectable levels in all the other tissues examined. N1-1862 (P503S) was found to be over-expressed in 60% of prostate tumors and detectable in normal colon and kidney. The RT-PCR results thus indicate that F1-16, H1-1, J1-17 (P502S), N1-1862 (P503S) and L1-12 (P501S) are either prostate specific or are expressed at significantly elevated levels in prostate.

10   Further RT-PCR studies showed that F1-12 (P504S) is over-expressed in 60% of prostate tumors, detectable in normal kidney but not detectable in all other tissues tested. Similarly, R1-2330 was shown to be over-expressed in 40% of prostate tumors, detectable in normal kidney and liver, but not detectable in all other tissues tested. U1-3064 was found to be over-expressed in 60% of prostate tumors, and also

15   expressed in breast and colon tumors, but was not detectable in normal tissues.

               RT-PCR characterization of R1-2330, U1-3064 and 1D-4279 showed that these three antigens are over-expressed in prostate and/or prostate tumors.

               Northern analysis with four prostate tumors, two normal prostate samples, two BPH prostates, and normal colon, kidney, liver, lung, pancrease, skeletal

20 · muscle, brain, stomach, testes, small intestine and bone marrow, showed that L1-12 (P501S) is over-expressed in prostate tumors and normal prostate, while being undetectable in other normal tissues tested. J1-17 (P502S) was detected in two prostate tumors and not in the other tissues tested. N1-1862 (P503S) was found to be over-expressed in three prostate tumors and to be expressed in normal prostate, colon and

25   kidney, but not in other tissues tested. F1-12 (P504S) was found to be highly expressed in two prostate tumors and to be undetectable in all other tissues tested.

               The microarray technology described above was used to determine the expression levels of representative antigens described herein in prostate tumor, breast tumor and the following normal tissues: prostate, liver, pancreas, skin, bone marrow,

30   brain, breast, adrenal gland, bladder, testes, salivary gland, large intestine, kidney,

ovary, lung, spinal cord, skeletal muscle and colon. L1-12 (P501S) was found to be over-expressed in normal prostate and prostate tumor, with some expression being detected in normal skeletal muscle. Both J1-12 and F1-12 (P504S) were found to be over-expressed in prostate tumor, with expression being lower or undetectable in all

5   other tissues tested. N1-1862 (P503S) was found to be expressed at high levels in prostate tumor and normal prostate, and at low levels in normal large intestine and normal colon, with expression being undetectable in all other tissues tested. R1-2330 was found to be over-expressed in prostate tumor and normal prostate, and to be expressed at lower levels in all other tissues tested. 1D-4279 was found to be over-

10   expressed in prostate tumor and normal prostate, expressed at lower levels in normal spinal cord, and to be undetectable in all other tissues tested.

Further microarray analysis to specifically address the extent to which P501S (SEQ ID NO: 110) was expressed in breast tumor revealed moderate over-expression not only in breast tumor, but also in metastatic breast tumor (2/31), with

15   negligible to low expression in normal tissues. This data suggests that P501S may be over-expressed in various breast tumors as well as in prostate tumors.

The expression levels of 32 ESTs (expressed sequence tags) described by Vasmatzis *et al.* (*Proc. Natl. Acad. Sci. USA* 95:300-304, 1998) in a variety of tumor and normal tissues were examined by microarray technology as described above. Two

20   of these clones (referred to as P1000C and P1001C) were found to be over-expressed in prostate tumor and normal prostate, and expressed at low to undetectable levels in all other tissues tested (normal aorta, thymus, resting and activated PBMC, epithelial cells, spinal cord, adrenal gland, fetal tissues, skin, salivary gland, large intestine, bone marrow, liver, lung, dendritic cells, stomach, lymph nodes, brain, heart, small intestine,

25   skeletal muscle, colon and kidney. The determined cDNA sequences for P1000C and P1001C are provided in SEQ ID NO: 384 and 472, respectively. The sequence of P1001C was found to show some homology to the previously isolated Human mRNA for JM27 protein. Subsequent comparison of the sequence of SEQ ID NO: 384 with sequences in the public databases, led to the identification of a full-length cDNA

30   sequence of P1000C (SEQ ID NO: 929), which encodes a 492 amino acid sequence.

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Analysis of the amino acid sequence using the PSORT II program led to the identification of a putative transmembrane domain from amino acids 84-100. The cDNA sequence of the open reading frame of P1000C, including the stop codon, is provided in SEQ ID NO: 930, with the open reading frame without the stop codon being
5   provided in SEQ ID NO: 931. The full-length amino acid sequence of P1000C is provided in SEQ ID NO: 932. SEQ ID NO: 933 and 934 represent amino acids 1-100 and 100-492 of P1000C, respectively.

The expression of the polypeptide encoded by the full length cDNA sequence for F1-12 (also referred to as P504S; SEQ ID NO: 108) was investigated by
10   immunohistochemical analysis. Rabbit-anti-P504S polyclonal antibodies were generated against the full length P504S protein by standard techniques. Subsequent isolation and characterization of the polyclonal antibodies were also performed by techniques well known in the art. Immunohistochemical analysis showed that the P504S polypeptide was expressed in 100% of prostate carcinoma samples tested (n=5).
15   The rabbit-anti-P504S polyclonal antibody did not appear to label benign prostate cells with the same cytoplasmic granular staining, but rather with light nuclear staining. Analysis of normal tissues revealed that the encoded polypeptide was found to be expressed in some, but not all normal human tissues. Positive cytoplasmic staining with rabbit-anti-P504S polyclonal antibody was found in normal human kidney, liver,
20   brain, colon and lung-associated macrophages, whereas heart and bone marrow were negative.

This data indicates that the P504S polypeptide is present in prostate cancer tissues, and that there are qualitative and quantitative differences in the staining between benign prostatic hyperplasia tissues and prostate cancer tissues, suggesting that
25   this polypeptide may be detected selectively in prostate tumors and therefore be useful in the diagnosis of prostate cancer.

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EXAMPLE 3

ISOLATION AND CHARACTERIZATION OF PROSTATE-SPECIFIC

POLYPEPTIDES BY PCR-BASED SUBTRACTION

5   A cDNA subtraction library, containing cDNA from normal prostate
subtracted with ten other normal tissue cDNAs (brain, heart, kidney, liver, lung, ovary,
placenta, skeletal muscle, spleen and thymus) and then submitted to a first round of
PCR amplification, was purchased from Clontech. This library was subjected to a
second round of PCR amplification, following the manufacturer's protocol. The
10   resulting cDNA fragments were subcloned into the vector pT7 Blue T-vector (Novagen,
Madison, WI) and transformed into XL-1 Blue MRF' *E. coli* (Stratagene). DNA was
isolated from independent clones and sequenced using a Perkin Elmer/Applied
Biosystems Division Automated Sequencer Model 373A.

          Fifty-nine positive clones were sequenced. Comparison of the DNA
15   sequences of these clones with those in the gene bank, as described above, revealed no
significant homologies to 25 of these clones, hereinafter referred to as P5, P8, P9, P18,
P20, P30, P34, P36, P38, P39, P42, P49, P50, P53, P55, P60, P64, P65, P73, P75, P76,
P79 and P84. The determined cDNA sequences for these clones are provided in SEQ
ID NO: 41-45, 47-52 and 54-65, respectively. P29, P47, P68, P80 and P82 (SEQ ID
20   NO: 46, 53 and 66-68, respectively) were found to show some degree of homology to
previously identified DNA sequences. To the best of the inventors' knowledge, none of
these sequences have been previously shown to be present in prostate.

          Further studies employing the sequence of SEQ ID NO: 67 as a probe in
standard full-length cloning methods, resulted in the isolation of three cDNA sequences
25   which appear to be splice variants of P80 (also known as P704P). These sequences are
provided in SEQ ID NO: 699-701.

          Further studies using the PCR-based methodology described above
resulted in the isolation of more than 180 additional clones, of which 23 clones were
found to show no significant homologies to known sequences. The determined cDNA
30   sequences for these clones are provided in SEQ ID NO: 115-123, 127, 131, 137, 145,

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147-151, 153, 156-158 and 160. Twenty-three clones (SEQ ID NO: 124-126, 128-130, 132-136, 138-144, 146, 152, 154, 155 and 159) were found to show some homology to previously identified ESTs. An additional ten clones (SEQ ID NO: 161-170) were found to have some degree of homology to known genes. Larger cDNA clones

5 containing the P20 sequence represent splice variants of a gene referred to as P703P. The determined DNA sequence for the variants referred to as DE1, DE13 and DE14 are provided in SEQ ID NOS: 171, 175 and 177, respectively, with the corresponding predicted amino acid sequences being provided in SEQ ID NO: 172, 176 and 178, respectively. The determined cDNA sequence for an extended spliced form of P703 is

10 provided in SEQ ID NO: 225. The DNA sequences for the splice variants referred to as DE2 and DE6 are provided in SEQ ID NOS: 173 and 174, respectively.

mRNA Expression levels for representative clones in tumor tissues (prostate (n=5), breast (n=2), colon and lung) normal tissues (prostate (n=5), colon, kidney, liver, lung (n=2), ovary (n=2), skeletal muscle, skin, stomach, small intestine

15 and brain), and activated and non-activated PBMC was determined by RT-PCR as described above. Expression was examined in one sample of each tissue type unless otherwise indicated.

P9 was found to be highly expressed in normal prostate and prostate tumor compared to all normal tissues tested except for normal colon which showed

20 comparable expression. P20, a portion of the P703P gene, was found to be highly expressed in normal prostate and prostate tumor, compared to all twelve normal tissues tested. A modest increase in expression of P20 in breast tumor (n=2), colon tumor and lung tumor was seen compared to all normal tissues except lung (1 of 2). Increased expression of P18 was found in normal prostate, prostate tumor and breast tumor

25 compared to other normal tissues except lung and stomach. A modest increase in expression of P5 was observed in normal prostate compared to most other normal tissues. However, some elevated expression was seen in normal lung and PBMC. Elevated expression of P5 was also observed in prostate tumors (2 of 5), breast tumor and one lung tumor sample. For P30, similar expression levels were seen in normal

30 prostate and prostate tumor, compared to six of twelve other normal tissues tested.

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Increased expression was seen in breast tumors, one lung tumor sample and one colon
tumor sample, and also in normal PBMC. P29 was found to be over-expressed in
prostate tumor (5 of 5) and normal prostate (5 of 5) compared to the majority of normal
tissues. However, substantial expression of P29 was observed in normal colon and
5   normal lung (2 of 2). P80 was found to be over-expressed in prostate tumor (5 of 5) and
normal prostate (5 of 5) compared to all other normal tissues tested, with increased
expression also being seen in colon tumor.

Further studies resulted in the isolation of twelve additional clones,
hereinafter referred to as 10-d8, 10-h10, 11-c8, 7-g6, 8-b5, 8-b6, 8-d4, 8-d9, 8-g3, 8-
10   h11, 9-f12 and 9-f3. The determined DNA sequences for 10-d8, 10-h10, 11-c8, 8-d4, 8-
d9, 8-h11, 9-f12 and 9-f3 are provided in SEQ ID NO: 207, 208, 209, 216, 217, 220,
221 and 222, respectively. The determined forward and reverse DNA sequences for 7-
g6, 8-b5, 8-b6 and 8-g3 are provided in SEQ ID NO: 210 and 211; 212 and 213; 214
and 215; and 218 and 219, respectively. Comparison of these sequences with those in
15   the gene bank revealed no significant homologies to the sequence of 9-f3. The clones
10-d8, 11-c8 and 8-h11 were found to show some homology to previously isolated
ESTs, while 10-h10, 8-b5, 8-b6, 8-d4, 8-d9, 8-g3 and 9-f12 were found to show some
homology to previously identified genes. Further characterization of 7-G6 and 8-G3
showed identity to the known genes PAP and PSA, respectively.

20   mRNA expression levels for these clones were determined using the
micro-array technology described above. The clones 7-G6, 8-G3, 8-B5, 8-B6, 8-D4, 8-
D9, 9-F3, 9-F12, 9-H3, 10-A2, 10-A4, 11-C9 and 11-F2 were found to be over-
expressed in prostate tumor and normal prostate, with expression in other tissues tested
being low or undetectable. Increased expression of 8-F11 was seen in prostate tumor
25   and normal prostate, bladder, skeletal muscle and colon. Increased expression of 10-
H10 was seen in prostate tumor and normal prostate, bladder, lung, colon, brain and
large intestine. Increased expression of 9-B1 was seen in prostate tumor, breast tumor,
and normal prostate, salivary gland, large intestine and skin, with increased expression
of 11-C8 being seen in prostate tumor, and normal prostate and large intestine.

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An additional cDNA fragment derived from the PCR-based normal prostate subtraction, described above, was found to be prostate specific by both micro-array technology and RT-PCR. The determined cDNA sequence of this clone (referred to as 9-A11) is provided in SEQ ID NO: 226. Comparison of this sequence with those in the public databases revealed 99% identity to the known gene HOXB13.

Further studies led to the isolation of the clones 8-C6 and 8-H7. The determined cDNA sequences for these clones are provided in SEQ ID NO: 227 and 228, respectively. These sequences were found to show some homology to previously isolated ESTs.

PCR and hybridization-based methodologies were employed to obtain longer cDNA sequences for clone P20 (also referred to as P703P), yielding three additional cDNA fragments that progressively extend the 5' end of the gene. These fragments, referred to as P703PDE5, P703P6.26, and P703PX-23 (SEQ ID NO: 326, 328 and 330, with the predicted corresponding amino acid sequences being provided in SEQ ID NO: 327, 329 and 331, respectively) contain additional 5' sequence. P703PDE5 was recovered by screening of a cDNA library (#141-26) with a portion of P703P as a probe. P703P6.26 was recovered from a mixture of three prostate tumor cDNAs and P703PX_23 was recovered from cDNA library (#438-48). Together, the additional sequences include all of the putative mature serine protease along with part of the putative signal sequence. The full-length cDNA sequence for P703P is provided in SEQ ID NO: 524, with the corresponding amino acid sequence being provided in SEQ ID NO: 525.

Using computer algorithms, the following regions of P703P were predicted to represent potential HLA A2-binding CTL epitopes: amino acids 164-172 of SEQ ID NO: 525 (SEQ ID NO: 866); amino acids 160-168 of SEQ ID NO: 525 (SEQ ID NO: 867); amino acids 239-247 of SEQ ID NO: 525 (SEQ ID NO: 868); amino acids 118-126 of SEQ ID NO: 525 (SEQ ID NO: 869); amino acids 112-120 of SEQ ID NO: 525 (SEQ ID NO: 870); amino acids 155-164 of SEQ ID NO: 525 (SEQ ID NO: 871); amino acids 117-126 of SEQ ID NO: 525 (SEQ ID NO: 872); amino acids 164-173 of SEQ ID NO: 525 (SEQ ID NO: 873); amino acids 154-163 of SEQ ID NO:

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525 (SEQ ID NO: 874); amino acids 163-172 of SEQ ID NO: 525 (SEQ ID NO: 875); amino acids 58-66 of SEQ ID NO: 525 (SEQ ID NO: 876); and amino acids 59-67 of SEQ ID NO: 525 (SEQ ID NO: 877).

P703P was found to show some homology to previously identified proteases, such as thrombin. The thrombin receptor has been shown to be preferentially expressed in highly metastatic breast carcinoma cells and breast carcinoma biopsy samples. Introduction of thrombin receptor antisense cDNA has been shown to inhibit the invasion of metastatic breast carcinoma cells in culture. Antibodies against thrombin receptor inhibit thrombin receptor activation and thrombin-induced platelet activation. Furthermore, peptides that resemble the receptor's tethered ligand domain inhibit platelet aggregation by thrombin. P703P may play a role in prostate cancer through a protease-activated receptor on the cancer cell or on stromal cells. The potential trypsin-like protease activity of P703P may either activate a protease-activated receptor on the cancer cell membrane to promote tumorgenesis or activate a protease-activated receptor on the adjacent cells (such as stromal cells) to secrete growth factors and/or proteases (such as matrix metalloproteinases) that could promote tumor angiogenesis, invasion and metastasis. P703P may thus promote tumor progression and/or metastasis through the activation of protease-activated receptor. Polypeptides and antibodies that block the P703P-receptor interaction may therefore be usefully employed in the treatment of prostate cancer.

To determine whether P703P expression increases with increased severity of Gleason grade, an indicator of tumor stage, quantitative PCR analysis was performed on prostate tumor samples with a range of Gleason scores from 5 to > 8. The mean level of P703P expression increased with increasing Gleason score, indicating that P703P expression may correlate with increased disease severity.

Further studies using a PCR-based subtraction library of a prostate tumor pool subtracted against a pool of normal tissues (referred to as JP: PCR subtraction) resulted in the isolation of thirteen additional clones, seven of which did not share any significant homology to known GenBank sequences. The determined cDNA sequences for these seven clones (P711P, P712P, novel 23, P774P, P775P, P710P and P768P) are

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provided in SEQ ID NO: 307-311, 313 and 315, respectively. The remaining six clones (SEQ ID NO: 316 and 321-325) were shown to share some homology to known genes. By microarray analysis, all thirteen clones showed three or more fold over-expression in prostate tissues, including prostate tumors, BPH and normal prostate as compared to normal non-prostate tissues. Clones P711P, P712P, novel 23 and P768P showed over-expression in most prostate tumors and BPH tissues tested (n=29), and in the majority of normal prostate tissues (n=4), but background to low expression levels in all normal tissues. Clones P774P, P775P and P710P showed comparatively lower expression and expression in fewer prostate tumors and BPH samples, with negative to low expression in normal prostate.

Further studies led to the isolation of an extended cDNA sequence for P712P (SEQ ID NO: 552). The amino acid sequences encoded by 16 predicted open reading frames present within the sequence of SEQ ID NO: 552 are provided in SEQ ID NO: 553-568.

The full-length cDNA for P711P was obtained by employing the partial sequence of SEQ ID NO: 307 to screen a prostate cDNA library. Specifically, a directionally cloned prostate cDNA library was prepared using standard techniques. One million colonies of this library were plated onto LB/Amp plates. Nylon membrane filters were used to lift these colonies, and the cDNAs which were picked up by these filters were denatured and cross-linked to the filters by UV light. The P711P cDNA fragment of SEQ ID NO: 307 was radio-labeled and used to hybridize with these filters. Positive clones were selected, and cDNAs were prepared and sequenced using an automatic Perkin Elmer/Applied Biosystems sequencer. The determined full-length sequence of P711P is provided in SEQ ID NO: 382, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 383.

Using PCR and hybridization-based methodologies, additional cDNA sequence information was derived for two clones described above, 11-C9 and 9-F3, herein after referred to as P707P and P714P, respectively (SEQ ID NO: 333 and 334). After comparison with the most recent GenBank, P707P was found to be a splice variant of the known gene HoxB13. In contrast, no significant homologies to P714P

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were found. Further studies employing the sequence of SEQ ID NO: 334 as a probe in standard full-length cloning methods, resulted in an extended cDNA sequence for P714P. This sequence is provided in SEQ ID NO: 698. This sequence was found to show some homology to the gene that encodes human ribosomal L23A protein.

5   Clones 8-B3, P89, P98, P130 and P201 (as disclosed in U.S. Patent Application No. 09/020,956, filed February 9, 1998) were found to be contained within one contiguous sequence, referred to as P705P (SEQ ID NO: 335, with the predicted amino acid sequence provided in SEQ ID NO: 336), which was determined to be a splice variant of the known gene NKX 3.1.

10   Further studies on P775P resulted in the isolation of four additional sequences (SEQ ID NO: 473-476) which are all splice variants of the P775P gene. The sequence of SEQ ID NO: 474 was found to contain two open reading frames (ORFs). The predicted amino acid sequences encoded by these ORFs are provided in SEQ ID NO: 477 and 478. The cDNA sequence of SEQ ID NO: 475 was found to contain an

15 ORF which encodes the amino acid sequence of SEQ ID NO: 479. The cDNA sequence of SEQ ID NO: 473 was found to contain four ORFs. The predicted amino acid sequences encoded by these ORFs are provided in SEQ ID NO: 480-483. Additional splice variants of P775P are provided in SEQ ID NO: 593-597.

Subsequent studies led to the identification of a genomic region on

20 chromosome 22q11.2, known as the Cat Eye Syndrome region, that contains the five prostate genes P704P, P712P, P774P, P775P and B305D. The relative location of each of these five genes within the genomic region is shown in Fig. 10. This region may therefore be associated with malignant tumors, and other potential tumor genes may be contained within this region. These studies also led to the identification of a potential

25 open reading frame (ORF) for P775P (provided in SEQ ID NO: 533), which encodes the amino acid sequence of SEQ ID NO: 534.

Comparison of the clone of SEQ ID NO: 325 (referred to as P558S) with sequences in the GenBank and GeneSeq DNA databases showed that P558S is identical to the prostate-specific transglutaminase gene, which is known to have two forms. The

30 full-length sequences for the two forms are provided in SEQ ID NO: 773 and 774, with

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the corresponding amino acid sequences being provided in SEQ ID NO: 775 and 776, respectively. The cDNA sequence of SEQ ID NO: 774 has a 15 pair base insert, resulting in a 5˙amino acid insert in the corresponding amino acid sequence (SEQ ID NO: 776). This insert is not present in the sequence of SEQ ID NO: 773.

5   Further studies on P768P (SEQ ID NO: 315) led to the identification of the putative full-length open reading frame (ORF). The cDNA sequence of the ORF with stop codon is provided in SEQ ID NO: 907. The cDNA sequence of the ORF without stop codon is provided in SEQ ID NO: 908, with the corresponding amino acid sequence being provided in SEQ ID NO: 909. This sequence was found to show 86%
10   identity to a rat calcium transporter protein, indicating that P768P may represent a human calcium transporter protein. The locations of transmembrane domains within P768P were predicted using the PSORT II computer algorithm. Six transmembrane domains were predicted at amino acid positions 118-134, 172-188, 211-227, 230-246, 282-298 and 348-364. The amino acid sequences of SEQ ID NO: 910-915 represent
15   amino acids 1-134, 135-188, 189-227, 228-246, 247-298 and 299-511 of P768P, respectively.

EXAMPLE 4

SYNTHESIS OF POLYPEPTIDES

20

Polypeptides may be synthesized on a Perkin Elmer/Applied Biosystems 430A peptide synthesizer using FMOC chemistry with HPTU (O-Benzotriazole-N,N,N',N'-tetramethyluronium hexafluorophosphate) activation. A Gly-Cys-Gly sequence may be attached to the amino terminus of the peptide to provide a method of
25   conjugation, binding to an immobilized surface, or labeling of the peptide. Cleavage of the peptides from the solid support may be carried out using the following cleavage mixture: trifluoroacetic acid:ethanedithiol:thioanisole:water:phenol (40:1:2:2:3). After cleaving for 2 hours, the peptides may be precipitated in cold methyl-t-butyl-ether. The peptide pellets may then be dissolved in water containing 0.1% trifluoroacetic acid
30   (TFA) and lyophilized prior to purification by C18 reverse phase HPLC. A gradient of

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0%-60% acetonitrile (containing 0.1% TFA) in water (containing 0.1% TFA) may be used to elute the peptides. Following lyophilization of the pure fractions, the peptides may be characterized using electrospray or other types of mass spectrometry and by amino acid analysis.

EXAMPLE 5

FURTHER ISOLATION AND CHARACTERIZATION OF
PROSTATE-SPECIFIC POLYPEPTIDES BY PCR-BASED SUBTRACTION

A cDNA library generated from prostate primary tumor mRNA as described above was subtracted with cDNA from normal prostate. The subtraction was performed using a PCR-based protocol (Clontech), which was modified to generate larger fragments. Within this protocol, tester and driver double stranded cDNA were separately digested with five restriction enzymes that recognize six-nucleotide restriction sites (MluI, MscI, PvuII, SalI and StuI). This digestion resulted in an average cDNA size of 600 bp, rather than the average size of 300 bp that results from digestion with RsaI according to the Clontech protocol. This modification did not affect the subtraction efficiency. Two tester populations were then created with different adapters, and the driver library remained without adapters.

The tester and driver libraries were then hybridized using excess driver cDNA. In the first hybridization step, driver was separately hybridized with each of the two tester cDNA populations. This resulted in populations of (a) unhybridized tester cDNAs, (b) tester cDNAs hybridized to other tester cDNAs, (c) tester cDNAs hybridized to driver cDNAs and (d) unhybridized driver cDNAs. The two separate hybridization reactions were then combined, and rehybridized in the presence of additional denatured driver cDNA. Following this second hybridization, in addition to populations (a) through (d), a fifth population (e) was generated in which tester cDNA with one adapter hybridized to tester cDNA with the second adapter. Accordingly, the second hybridization step resulted in enrichment of differentially expressed sequences which could be used as templates for PCR amplification with adaptor-specific primers.

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The ends were then filled in, and PCR amplification was performed using adaptor-specific primers. Only population (e), which contained tester cDNA that did not hybridize to driver cDNA, was amplified exponentially. A second PCR amplification step was then performed, to reduce background and further enrich
5 differentially expressed sequences.

This PCR-based subtraction technique normalizes differentially expressed cDNAs so that rare transcripts that are overexpressed in prostate tumor tissue may be recoverable. Such transcripts would be difficult to recover by traditional subtraction methods.
10 In addition to genes known to be overexpressed in prostate tumor, seventy-seven further clones were identified. Sequences of these partial cDNAs are provided in SEQ ID NO: 29 to 305. Most of these clones had no significant homology to database sequences. Exceptions were JPTPN23 (SEQ ID NO: 231; similarity to pig valosin-containing protein), JPTPN30 (SEQ ID NO: 234; similarity to rat mRNA for
15 proteasome subunit), JPTPN45 (SEQ ID NO: 243; similarity to rat *norvegicus* cytosolic NADP-dependent isocitrate dehydrogenase), JPTPN46 (SEQ ID NO: 244; similarity to human subclone H8 4 d4 DNA sequence), JP1D6 (SEQ ID NO: 265; similarity to *G. gallus* dynein light chain-A), JP8D6 (SEQ ID NO: 288; similarity to human BAC clone RG016J04), JP8F5 (SEQ ID NO: 289; similarity to human subclone H8 3 b5 DNA
20 sequence), and JP8E9 (SEQ ID NO: 299; similarity to human Alu sequence).

Additional studies using the PCR-based subtraction library consisting of a prostate tumor pool subtracted against a normal prostate pool (referred to as PT-PN PCR subtraction) yielded three additional clones. Comparison of the cDNA sequences of these clones with the most recent release of GenBank revealed no significant
25 homologies to the two clones referred to as P715P and P767P (SEQ ID NO: 312 and 314). The remaining clone was found to show some homology to the known gene KIAA0056 (SEQ ID NO: 318). Using microarray analysis to measure mRNA expression levels in various tissues, all three clones were found to be over-expressed in prostate tumors and BPH tissues. Specifically, clone P715P was over-expressed in most
30 prostate tumors and BPH tissues by a factor of three or greater, with elevated expression

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seen in the majority of normal prostate samples and in fetal tissue, but negative to low expression in all other normal tissues. Clone P767P was over-expressed in several prostate tumors and BPH tissues, with moderate expression levels in half of the normal prostate samples, and background to low expression in all other normal tissues tested.

5   Further analysis, by microarray as described above, of the PT-PN PCR subtraction library and of a DNA subtraction library containing cDNA from prostate tumor subtracted with a pool of normal tissue cDNAs, led to the isolation of 27 additional clones (SEQ ID NO: 340-365 and 381) which were determined to be over-expressed in prostate tumor. The clones of SEQ ID NO: 341, 342, 345, 347, 348, 349,

10   351, 355-359, 361, 362 and 364 were also found to be expressed in normal prostate. Expression of all 26 clones in a variety of normal tissues was found to be low or undetectable, with the exception of P544S (SEQ ID NO: 356) which was found to be expressed in small intestine. Of the 26 clones, 11 (SEQ ID NO: 340-349 and 362) were found to show some homology to previously identified sequences. No significant

15   homologies were found to the clones of SEQ ID NO: 350, 351, 353-361, and 363-365.

            Comparison of the sequence of SEQ ID NO: 362 with sequences in the GenBank and GeneSeq DNA databases showed that this clone (referred to as P788P) is identical to GeneSeq Accession No. X27262, which encodes a protein found in the GeneSeq protein Accession No. Y00931. The full length cDNA sequence of P788P is

20   shown in Figure 12A (SEQ ID NO: 777), with the corresponding predicted amino acid being shown in Figure 12B (SEQ ID NO: 778). Subsequently, a full-length cDNA sequence for P788P that contains polymorphisms not found in the sequence of SEQ ID NO: 779, was cloned multiple times by PCR amplification from cDNA prepared from several RNA templates from three individuals. This determined cDNA sequence of this

25   polymorphic variant of P788P is provided in SEQ ID NO: 779, with the corresponding amino acid sequence being provided in SEQ ID NO: 780. The sequence of SEQ ID NO: 780 differs from that of SEQ ID NO: 778 by six amino acid residues. The P788P protein has 7 potential transmembrane domains at the C-terminal portion and is predicted to be a plasma membrane protein with an extracellular N-terminal region.

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Further studies on the clone of SEQ ID NO: 352 (referred to as P790P) led to the isolation of the full-length cDNA sequence of SEQ ID NO: 526. The corresponding predicted amino acid is provided in SEQ ID NO: 527. Data from two quantitative PCR experiments indicated that P790P is over-expressed in 11/15 tested prostate tumor samples and is expressed at low levels in spinal cord, with no expression being seen in all other normal samples tested. Data from further PCR experiments and microarray experiments showed over-expression in normal prostate and prostate tumor with little or no expression in other tissues tested. P790P was subsequently found to show significant homology to a previously identified G-protein coupled prostate tissue receptor.

Additional studies on the clone of SEQ ID NO: 354 (referred to as P776P) led to the isolation of an extended cDNA sequence, provided in SEQ ID NO: 569. The determined cDNA sequences of three additional splice variants of P776P are provided in SEQ ID NO: 570-572. The amino acid sequences encoded by two predicted open reading frames (ORFs) contained within SEQ ID NO: 570, one predicted ORF contained within SEQ ID NO: 571, and 11 predicted ORFs contained within SEQ ID NO: 569, are provided in SEQ ID NO: 573-586, respectively. Further studies led to the isolation of the full-length sequence for the clone of SEQ ID NO: 570 (provided in SEQ ID NO: 880). Full-length cloning efforts on the clone of SEQ ID NO: 571 led to the isolation of two sequences (provided in SEQ ID NO: 881 and 882), representing a single clone, that are identical with the exception of a polymorphic insertion/deletion at position 1293. Specifically, the clone of SEQ ID NO: 882 (referred to as clone F1) has a C at position 1293. The clone of SEQ ID NO: 881 (referred to as clone F2) has a single base pair deletion at position 1293. The predicted amino acid sequences encoded by 5 open reading frames located within SEQ ID NO: 880 are provided in SEQ ID NO: 883-887, with the predicted amino acid sequences encoded by the clone of SEQ ID NO: 881 and 882 being provided in SEQ ID NO: 888-893.

Comparison of the cDNA sequences for the clones P767P (SEQ ID NO: 314) and P777P (SEQ ID NO: 350) with sequences in the GenBank human EST database showed that the two clones matched many EST sequences in common,

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suggesting that P767P and P777P may represent the same gene. A DNA consensus sequence derived from a DNA sequence alignment of P767P, P777P and multiple EST clones is provided in SEQ ID NO: 587. The amino acid sequences encoded by three putative ORFs located within SEQ ID NO: 587 are provided in SEQ ID NO: 588-590.

5   The clone of SEQ ID NO: 342 (referred to as P789P) was found to show homology to a previously identified gene. The full length cDNA sequence for P789P and the corresponding amino acid sequence are provided in SEQ ID NO: 878 and 879, respectively.

10   EXAMPLE 6

PEPTIDE PRIMING OF MICE AND PROPAGATION OF CTL LINES

        6.1. This Example illustrates the preparation of a CTL cell line specific for cells expressing the P502S gene.

15   Mice expressing the transgene for human HLA A2Kb (provided by Dr L. Sherman, The Scripps Research Institute, La Jolla, CA) were immunized with P2S#12 peptide (VLGWVAEL; SEQ ID NO: 306), which is derived from the P502S gene (also referred to herein as J1-17, SEQ ID NO: 8), as described by Theobald et al., *Proc. Natl. Acad. Sci. USA* 92:11993-11997, 1995 with the following modifications. Mice were

20 immunized with 100μg of P2S#12 and 120μg of an I-A^b binding peptide derived from hepatitis B Virus protein emulsified in incomplete Freund's adjuvant. Three weeks later these mice were sacrificed and using a nylon mesh single cell suspensions prepared. Cells were then resuspended at 6 x 10^6 cells/ml in complete media (RPMI-1640; Gibco BRL, Gaithersburg, MD) containing 10% FCS, 2mM Glutamine (Gibco BRL), sodium

25 pyruvate (Gibco BRL), non-essential amino acids (Gibco BRL), 2 x 10^{-5} M 2-mercaptoethanol, 50U/ml penicillin and streptomycin, and cultured in the presence of irradiated (3000 rads) P2S#12-pulsed (5mg/ml P2S#12 and 10mg/ml β2-microglobulin) LPS blasts (A2 transgenic spleens cells cultured in the presence of 7μg/ml dextran sulfate and 25μg/ml LPS for 3 days). Six days later, cells (5 x 10^5/ml) were

30 restimulated with 2.5 x 10^6/ml peptide pulsed irradiated (20,000 rads) EL4A2Kb cells

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(Sherman et al, *Science 258*:815-818, 1992) and 3 x 10^6/ml A2 transgenic spleen feeder cells. Cells were cultured in the presence of 20U/ml IL-2. Cells continued to be restimulated on a weekly basis as described, in preparation for cloning the line.

P2S#12 line was cloned by limiting dilution analysis with peptide pulsed EL4 A2Kb tumor cells (1 x 10^4 cells/ well) as stimulators and A2 transgenic spleen cells as feeders (5 x 10^5 cells/ well) grown in the presence of 30U/ml IL-2. On day 14, cells were restimulated as before. On day 21, clones that were growing were isolated and maintained in culture. Several of these clones demonstrated significantly higher reactivity (lysis) against human fibroblasts (HLA A2Kb expressing) transduced with P502S than against control fibroblasts. An example is presented in Figure 1.

This data indicates that P2S #12 represents a naturally processed epitope of the P502S protein that is expressed in the context of the human HLA A2Kb molecule.

6.2. This Example illustrates the preparation of murine CTL lines and CTL clones specific for cells expressing the P501S gene.

This series of experiments were performed similarly to that described above. Mice were immunized with the P1S#10 peptide (SEQ ID NO: 337), which is derived from the P501S gene (also referred to herein as L1-12, SEQ ID NO: 110). The P1S#10 peptide was derived by analysis of the predicted polypeptide sequence for P501S for potential HLA-A2 binding sequences as defined by published HLA-A2 binding motifs (Parker, KC, et al, *J. Immunol.*, 152:163, 1994). P1S#10 peptide was synthesized as described in Example 4, and empirically tested for HLA-A2 binding using a T cell based competition assay. Predicted A2 binding peptides were tested for their ability to compete HLA-A2 specific peptide presentation to an HLA-A2 restricted CTL clone (D150M58), which is specific for the HLA-A2 binding influenza matrix peptide fluM58. D150M58 CTL secretes TNF in response to self-presentation of peptide fluM58. In the competition assay, test peptides at 100-200 μg/ml were added to cultures of D150M58 CTL in order to bind HLA-A2 on the CTL. After thirty minutes,

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CTL cultured with test peptides, or control peptides, were tested for their antigen dose response to the fluM58 peptide in a standard TNF bioassay. As shown in Figure 3, peptide P1S#10 competes HLA-A2 restricted presentation of fluM58, demonstrating that peptide P1S#10 binds HLA-A2.

5   Mice expressing the transgene for human HLA A2Kb were immunized as described by Theobald et al. (*Proc. Natl. Acad. Sci. USA 92*:11993-11997, 1995) with the following modifications. Mice were immunized with 62.5µg of P1S #10 and 120µg of an I-A^b binding peptide derived from Hepatitis B Virus protein emulsified in incomplete Freund's adjuvant. Three weeks later these mice were sacrificed and single
10   cell suspensions prepared using a nylon mesh. Cells were then resuspended at 6 x 10^6 cells/ml in complete media (as described above) and cultured in the presence of irradiated (3000 rads) P1S#10-pulsed (2µg/ml P1S#10 and 10mg/ml β2-microglobulin) LPS blasts (A2 transgenic spleens cells cultured in the presence of 7µg/ml dextran sulfate and 25µg/ml LPS for 3 days). Six days later cells (5 x 10^5/ml) were restimulated
15   with 2.5 x 10^6/ml peptide-pulsed irradiated (20,000 rads) EL4A2Kb cells, as described above, and 3 x 10^6/ml A2 transgenic spleen feeder cells. Cells were cultured in the presence of 20 U/ml IL-2. Cells were restimulated on a weekly basis in preparation for cloning. After three rounds of *in vitro* stimulations, one line was generated that recognized P1S#10-pulsed Jurkat A2Kb targets and P501S-transduced Jurkat targets as
20   shown in Figure 4.

A P1S#10-specific CTL line was cloned by limiting dilution analysis with peptide pulsed EL4 A2Kb tumor cells (1 x 10^4 cells/ well) as stimulators and A2 transgenic spleen cells as feeders (5 x 10^5 cells/ well) grown in the presence of 30U/ml IL-2. On day 14, cells were restimulated as before. On day 21, viable clones were
25   isolated and maintained in culture. As shown in Figure 5, five of these clones demonstrated specific cytolytic reactivity against P501S-transduced Jurkat A2Kb targets. This data indicates that P1S#10 represents a naturally processed epitope of the P501S protein that is expressed in the context of the human HLA-A2.1 molecule.

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EXAMPLE 7

PRIMING OF CTL *IN VIVO* USING NAKED DNA IMMUNIZATION

WITH A PROSTATE ANTIGEN

The prostate-specific antigen L1-12, as described above, is also referred

5   to as P501S. HLA A2Kb Tg mice (provided by Dr L. Sherman, The Scripps Research

Institute, La Jolla, CA) were immunized with 100 µg P501S in the vector VR1012

either intramuscularly or intradermally. The mice were immunized three times, with a

two week interval between immunizations. Two weeks after the last immunization,

immune spleen cells were cultured with Jurkat A2Kb-P501S transduced stimulator

10   cells. CTL lines were stimulated weekly. After two weeks of *in vitro* stimulation, CTL

activity was assessed against P501S transduced targets. Two out of 8 mice developed

strong anti-P501S CTL responses. These results demonstrate that P501S contains at

least one naturally processed HLA-A2-restricted CTL epitope.

15   EXAMPLE 8

ABILITY OF HUMAN T CELLS TO RECOGNIZE PROSTATE-SPECIFIC POLYPEPTIDES

This Example illustrates the ability of T cells specific for a prostate

tumor polypeptide to recognize human tumor.

20   Human CD8^{+} T cells were primed *in vitro* to the P2S-12 peptide (SEQ

ID NO: 306) derived from P502S (also referred to as J1-17) using dendritic cells

according to the protocol of Van Tsai et al. (*Critical Reviews in Immunology 18:65-75,*

1998). The resulting CD8^{+} T cell microcultures were tested for their ability to

recognize the P2S-12 peptide presented by autologous fibroblasts or fibroblasts which

25   were transduced to express the P502S gene in a γ-interferon ELISPOT assay (*see*

Lalvani et al., *J. Exp. Med. 186*:859-865, 1997). Briefly, titrating numbers of T cells

were assayed in duplicate on 10^4 fibroblasts in the presence of 3 µg/ml human β2-

microglobulin and 1 µg/ml P2S-12 peptide or control E75 peptide. In addition, T cells

were simultaneously assayed on autologous fibroblasts transduced with the P502S gene

30   or as a control, fibroblasts transduced with HER-2/*neu*. Prior to the assay, the

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fibroblasts were treated with 10 ng/ml γ-interferon for 48 hours to upregulate class I
MHC expression. One of the microcultures (#5) demonstrated strong recognition of
both peptide pulsed fibroblasts as well as transduced fibroblasts in a γ-interferon
ELISPOT assay. Figure 2A demonstrates that there was a strong increase in the number

5   of γ-interferon spots with increasing numbers of T cells on fibroblasts pulsed with the
P2S-12 peptide (solid bars) but not with the control E75 peptide (open bars). This
shows the ability of these T cells to specifically recognize the P2S-12 peptide. As
shown in Figure 2B, this microculture also demonstrated an increase in the number of γ-
interferon spots with increasing numbers of T cells on fibroblasts transduced to express

10 the P502S gene but not the HER-2/*neu* gene. These results provide additional
confirmatory evidence that the P2S-12 peptide is a naturally processed epitope of the
P502S protein. Furthermore, this also demonstrates that there exists in the human T cell
repertoire, high affinity T cells which are capable of recognizing this epitope. These T
cells should also be capable of recognizing human tumors which express the P502S

15 gene.

EXAMPLE 9

ELICITATION OF PROSTATE ANTIGEN-SPECIFIC CTL RESPONSES
IN HUMAN BLOOD

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This Example illustrates the ability of a prostate-specific antigen to elicit
a CTL response in blood of normal humans.

Autologous dendritic cells (DC) were differentiated from monocyte
cultures derived from PBMC of normal donors by growth for five days in RPMI

25 medium containing 10% human serum, 50 ng/ml GMCSF and 30 ng/ml IL-4.
Following culture, DC were infected overnight with recombinant P501S-expressing
vaccinia virus at an M.O.I. of 5 and matured for 8 hours by the addition of 2
micrograms/ml CD40 ligand. Virus was inactivated by UV irradiation, CD8$^+$ cells were
isolated by positive selection using magnetic beads, and priming cultures were initiated

30 in 24-well plates. Following five stimulation cycles using autologous fibroblasts

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retrovirally transduced to express P501S and CD80, CD8+ lines were identified that specifically produced interferon-gamma when stimulated with autologous P501S-transduced fibroblasts.   The P501S-specific activity of cell line 3A-1 could be maintained following additional stimulation cycles on autologous B-LCL transduced

5   with P501S.   Line 3A-1 was shown to specifically recognize autologous B-LCL transduced to express P501S, but not EGFP-transduced autologous B-LCL, as measured by cytotoxicity assays (^{51}Cr release) and interferon-gamma production (Interferon-gamma Elispot; *see* above and Lalvani et al., *J. Exp. Med. 186*:859-865, 1997). The results of these assays are presented in Figures 6A and 6B.

10

EXAMPLE 10

IDENTIFICATION OF A NATURALLY PROCESSED CTL EPITOPE CONTAINED WITHIN THE PROSTATE-SPECIFIC ANTIGEN P703P

15   The 9-mer peptide p5 (SEQ ID NO: 338) was derived from the P703P antigen (also referred to as P20). The p5 peptide is immunogenic in human HLA-A2 donors and is a naturally processed epitope. Antigen specific human CD8+ T cells can be primed following repeated *in vitro* stimulations with monocytes pulsed with p5 peptide. These CTL specifically recognize p5-pulsed and P703P-transduced target cells

20   in both ELISPOT (as described above) and chromium release assays.   Additionally, immunization of HLA-A2Kb transgenic mice with p5 leads to the generation of CTL lines which recognize a variety of HLA-A2Kb or HLA-A2 transduced target cells expressing P703P.

          Initial studies demonstrating that p5 is a naturally processed epitope were

25   done using HLA-A2Kb transgenic mice. HLA-A2Kb transgenic mice were immunized subcutaneously in the footpad with 100 μg of p5 peptide together with 140 μg of hepatitis B virus core peptide (a Th peptide) in Freund's incomplete adjuvant. Three weeks post immunization, spleen cells from immunized mice were stimulated *in vitro* with peptide-pulsed LPS blasts. CTL activity was assessed by chromium release assay

30   five days after primary *in vitro* stimulation. Retrovirally transduced cells expressing the

control antigen P703P and HLA-A2Kb were used as targets. CTL lines that specifically recognized both p5-pulsed targets as well as P703P-expressing targets were identified.

Human *in vitro* priming experiments demonstrated that the p5 peptide is immunogenic in humans. Dendritic cells (DC) were differentiated from monocyte

5   cultures derived from PBMC of normal human donors by culturing for five days in RPMI medium containing 10% human serum, 50 ng/ml human GM-CSF and 30 ng/ml human IL-4. Following culture, the DC were pulsed with 1 ug/ml p5 peptide and cultured with CD8+ T cell enriched PBMC. CTL lines were restimulated on a weekly basis with p5-pulsed monocytes. Five to six weeks after initiation of the CTL cultures,

10 CTL recognition of p5-pulsed target cells was demonstrated. CTL were additionally shown to recognize human cells transduced to express P703P, demonstrating that p5 is a naturally processed epitope.

Studies identifying a further peptide epitope (referred to as peptide 4) derived from the prostate tumor-specific antigen P703P that is capable of being

15 recognized by CD4 T cells on the surface of cells in the context of HLA class II molecules were carried out as follows. The amino acid sequence for peptide 4 is provided in SEQ ID NO: 781, with the corresponding cDNA sequence being provided in SEQ ID NO: 782.

Twenty 15-mer peptides overlapping by 10 amino acids and derived

20 from the carboxy-terminal fragment of P703P were generated using standard procedures. Dendritic cells (DC) were derived from PBMC of a normal female donor using GM-CSF and IL-4 by standard protocols. CD4 T cells were generated from the same donor as the DC using MACS beads and negative selection. DC were pulsed overnight with pools of the 15-mer peptides, with each peptide at a final concentration

25 of 0.25 microgram/ml. Pulsed DC were washed and plated at 1 x 10^4 cells/well of 96-well V-bottom plates and purified CD4 T cells were added at 1 x 10^5/well. Cultures were supplemented with 60 ng/ml IL-6 and 10 ng/ml IL-12 and incubated at 37 °C. Cultures were restimulated as above on a weekly basis using DC generated and pulsed as above as antigen presenting cells, supplemented with 5 ng/ml IL-7 and 10 u/ml IL-2.

30 Following 4 *in vitro* stimulation cycles, 96 lines (each line corresponding to one well) were tested for specific proliferation and cytokine production in response to the

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stimulating pools with an irrelevant pool of peptides derived from mammaglobin being used as a control.

One line (referred to as 1-F9) was identified from pool #1 that demonstrated specific proliferation (measured by 3H proliferation assays) and cytokine
5   production (measured by interferon-gamma ELISA assays) in response to pool #1 of P703P peptides. This line was further tested for specific recognition of the peptide pool, specific recognition of individual peptides in the pool, and in HLA mismatch analyses to identify the relevant restricting allele. Line 1-F9 was found to specifically proliferate and produce interferon-gamma in response to peptide pool #1, and also to
10 peptide 4 (SEQ ID NO: 781). Peptide 4 corresponds to amino acids 126-140 of SEQ ID NO: 327. Peptide titration experiments were conducted to assess the sensitivity of line 1-F9 for the specific peptide. The line was found to specifically respond to peptide 4 at concentrations as low as 0.25 ng/ml, indicating that the T cells are very sensitive and therefore likely to have high affinity for the epitope.

15   To determine the HLA restriction of the P703P response, a panel of antigen presenting cells (APC) was generated that was partially matched with the donor used to generate the T cells. The APC were pulsed with the peptide and used in proliferation and cytokine assays together with line 1-F9. APC matched with the donor at HLA-DRB0701 and HLA-DQB02 alleles were able to present the peptide to the T
20 cells, indicating that the P703P-specific response is restricted to one of these alleles.

Antibody blocking assays were utilized to determine if the restricting allele was HLA-DR0701 or HLA-DQ02. The anti-HLA-DR blocking antibody L243 or an irrelevant isotype matched IgG2a were added to T cells and APC cultures pulsed with the peptide RMPTVLQCVNVSVVS (SEQ ID NO: 781) at 250 ng/ml.
25 Standard interferon-gamma and proliferation assays were performed. Whereas the control antibody had no effect on the ability of the T cells to recognize peptide-pulsed APC, in both assays the anti-HLA-DR antibody completely blocked the ability of the T cells to specifically recognize peptide-pulsed APC.

To determine if the peptide epitope RMPTVLQCVNVSVVS (SEQ ID
30 NO: 781) was naturally processed, the ability of line 1-F9 to recognize APC pulsed with recombinant P703P protein was examined. For these experiments a number of

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recombinant P703P sources were utilized; *E. coli*-derived P703P, Pichia-derived P703P and baculovirus-derived P703P. Irrelevant protein controls used were *E. coli*-derived L3E a lung-specific antigen) and baculovirus-derived mammaglobin. In interferon-gamma ELISA assays, line 1-F9 was able to efficiently recognize both *E. coli* forms of
5   P703P as well as Pichia-derived recombinant P703P, while baculovirus-derived P703P was recognized less efficiently. Subsequent Western blot analysis revealed that the *E. coli* and Pichia P703P protein preparations were intact while the baculovirus P703P preparation was approximately 75% degraded. Thus, peptide RMPTVLQCVNVSVVS (SEQ ID NO: 781) from P703P is a naturally processed peptide epitope derived from
10   P703P and presented to T cells in the context of HLA-DRB-0701

In further studies, twenty-four 15-mer peptides overlapping by 10 amino acids and derived from the N-terminal fragment of P703P (corresponding to amino acids 27-154 of SEQ ID NO: 525) were generated by standard procedures and their ability to be recognized by CD4 cells was determined essentially as described above.
15   DC were pulsed overnight with pools of the peptides with each peptide at a final concentration of 10 microgram/ml. A large number of individual CD4 T cell lines (65/480) demonstrated significant proliferation and cytokine release (IFN-gamma) in response to the P703P peptide pools but not to a control peptide pool. The CD4 T cell lines which demonstrated specific activity were restimulated on the appropriate pool of
20   P703P peptides and reassayed on the individual peptides of each pool as well as a peptide dose titration of the pool of peptides in a IFN-gamma release assay and in a proliferation assay.

Sixteen immunogenic peptides were recognized by the T cells from the entire set of peptide antigens tested. The amino acid sequences of these peptides are
25   provided in SEQ ID NO: 799-814, with the corresponding cDNA sequences being provided in SEQ ID NO: 783-798, respectively. In some cases the peptide reactivity of the T cell line could be mapped to a single peptide, however some could be mapped to more than one peptide in each pool. Those CD4 T cell lines that displayed a representative pattern of recognition from each peptide pool with a reasonable affinity
30   for peptide were chosen for further analysis (I-1A, -6A; II-4C, -5E; III-6E, IV-4B, -3F, -9B, -10F, V-5B, -4D, and -10F). These CD4 T cells lines were restimulated on the

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appropriate individual peptide and reassayed on autologous DC pulsed with a truncated form of recombinant P703P protein made in *E. coli* (a.a. 96 - 254 of SEQ ID NO: 525), full-length P703P made in the baculovirus expression system, and a fusion between influenza virus NS1 and P703P made in *E. coli*. Of the T cell lines tested, line I-1A
5   recognized specifically the truncated form of P703P (*E. coli*) but no other recombinant form of P703P. This line also recognized the peptide used to elicit the T cells. Line 2-4C recognized the truncated form of P703P (*E. coli*) and the full length form of P703P made in baculovirus, as well as peptide. The remaining T cell lines tested were either peptide-specific only (II-5E, II-6F, IV-4B, IV-3F, IV-9B, IV-10F, V-5B and V-4D) or
10 were non-responsive to any antigen tested (V-10F). These results demonstrate that the peptide sequence RPLLANDLMLIKLDE (SEQ ID NO: 814; corresponding to a.a. 110-124 of SEQ ID NO: 525) recognized by the T cell line I-1A, and the peptide sequences SVSESDTIRSISIAS (SEQ ID NO: 811; corresponding to a.a. 125-139 of SEQ ID NO: 525) and ISIASQCPTAGNSCL (SEQ ID NO: 810; corresponding to a.a. 135-149 of
15 SEQ ID NO: 525) recognized by the T cell line II-4C may be naturally processed epitopes of the P703P protein.

In further studies, forty 15-mer peptides overlapping by 10 amino acids and derived spanning amino acids 47 to 254 of P703P (SEQ ID NO: 525) were generated by standard procedures and their ability to be recognized by CD4 cells was
20 determined essentially as described above. DC were prepared from PBMC of a donor having distinct HLA DR and DQ alleles from that used in previous experiments. DC were pulsed overnight with pools of the peptides with each peptide at a final concentration of 0.25 microgram/ml, and each pool containing 10 peptides. Twelve lines were identified that demonstrated specific proliferation and cytokine production
25 (measured in gamma-interferon ELISA assays) in response to the stimulating peptide pool. These lines were further tested for specific recognition of the peptide pool, specific recognition of individual peptides in the pool, and specific recognition of recombinant P703P protein. Lines 3A5H and 3A9H specifically proliferated and produced gamma-interferon in response to recombinant protein and one individual
30 peptide as well as the peptide pool. Following re-stimulation on targets loaded with the specific peptide, only 3A9H responded specifically to targets exposed to lysates of

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fibroblasts infected adenovirus expressing full-length P703P. These results indicates that the line 3A9H can respond to antigenic peptide derived from protein synthesized in mammalian cells. The peptide to which the specific CD4 line responded correspond to amino acids 155-170 of P703P (SEQ ID NO: 943). The DNA sequence for this peptide

5   is provided in SEQ ID NO: 942.

EXAMPLE 11

EXPRESSION OF A BREAST TUMOR-DERIVED ANTIGEN

IN PROSTATE

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Isolation of the antigen B305D from breast tumor by differential display is described in US Patent Application No. 08/700,014, filed August 20, 1996. Several different splice forms of this antigen were isolated. The determined cDNA sequences for these splice forms are provided in SEQ ID NO: 366-375, with the predicted amino

15   acid sequences corresponding to the sequences of SEQ ID NO: 292, 298 and 301-303 being provided in SEQ ID NO: 299-306, respectively. In further studies, a splice variant of the cDNA sequence of SEQ ID NO: 366 was isolated which was found to contain an additional guanine residue at position 884 (SEQ ID NO: 530), leading to a frameshift in the open reading frame. The determined DNA sequence of this ORF is

20   provided in SEQ ID NO: 531. This frameshift generates a protein sequence (provided in SEQ ID NO: 532) of 293 amino acids that contains the C-terminal domain common to the other isoforms of B305D but that differs in the N-terminal region.

The expression levels of B305D in a variety of tumor and normal tissues were examined by real time PCR and by Northern analysis. The results indicated that

25   B305D is highly expressed in breast tumor, prostate tumor, normal prostate and normal testes, with expression being low or undetectable in all other tissues examined (colon tumor, lung tumor, ovary tumor, and normal bone marrow, colon, kidney, liver, lung, ovary, skin, small intestine, stomach). Using real-time PCR on a panel of prostate tumors, expression of B305D in prostate tumors was shown to increase with increasing

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Gleason grade, demonstrating that expression of B305D increases as prostate cancer progresses.

EXAMPLE 12

5   GENERATION OF HUMAN CTL *In Vitro* USING WHOLE GENE PRIMING AND STIMULATION
TECHNIQUES WITH THE PROSTATE-SPECIFIC ANTIGEN P501S

Using *in vitro* whole-gene priming with P501S-vaccinia infected DC (see, for example, Yee et al, *The Journal of Immunology*, 157(9):4079-86, 1996),

10   human CTL lines were derived that specifically recognize autologous fibroblasts transduced with P501S (also known as L1-12), as determined by interferon-γ ELISPOT analysis as described above.   Using a panel of HLA-mismatched B-LCL lines transduced with P501S, these CTL lines were shown to be likely restricted to HLAB class I allele.   Specifically, dendritic cells (DC) were differentiated from monocyte

15   cultures derived from PBMC of normal human donors by growing for five days in RPMI medium containing 10% human serum, 50 ng/ml human GM-CSF and 30 ng/ml human IL-4.   Following culture, DC were infected overnight with recombinant P501S vaccinia virus at a multiplicity of infection (M.O.I) of five, and matured overnight by the addition of 3 μg/ml CD40 ligand.   Virus was inactivated by UV irradiation.   CD8+

20   T cells were isolated using a magnetic bead system, and priming cultures were initiated using standard culture techniques.   Cultures were restimulated every 7-10 days using autologous primary fibroblasts retrovirally transduced with P501S and CD80. Following four stimulation cycles, CD8+ T cell lines were identified that specifically produced interferon-γ when stimulated with P501S and CD80-transduced autologous

25   fibroblasts.   A panel of HLA-mismatched B-LCL lines transduced with P501S were generated to define the restriction allele of the response.   By measuring interferon-γ in an ELISPOT assay, the P501S specific response was shown to be likely restricted by HLA B alleles.   These results demonstrate that a CD8+ CTL response to P501S can be elicited.

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To identify the epitope(s) recognized, cDNA encoding P501S was fragmented by various restriction digests, and sub-cloned into the retroviral expression vector pBIB-KS. Retroviral supernatants were generated by transfection of the helper packaging line Phoenix-Ampho. Supernatants were then used to transduce

5   Jurkat/A2Kb cells for CTL screening. CTL were screened in IFN-gamma ELISPOT assays against these A2Kb targets transduced with the "library" of P501S fragments. Initial positive fragments P501S/H3 and P501S/F2 were sequenced and found to encode amino acids 106-553 and amino acids 136-547, respectively, of SEQ ID NO: 113. A truncation of H3 was made to encode amino acid residues 106-351 of SEQ ID NO: 113,

10   which was unable to stimulate the CTL, thus localizing the epitope to amino acid residues 351-547. Additional fragments encoding amino acids 1-472 (Fragment A) and amino acids 1-351 (Fragment B) were also constructed. Fragment A but not Fragment B stimulated the CTL thus localizing the epitope to amino acid residues 351-472. Overlapping 20-mer and 18-mer peptides representing this region were tested by pulsing

15   Jurkat/A2Kb cells versus CTL in an IFN-gamma assay. Only peptides P501S-369(20) and P501S-369(18) stimulated the CTL. Nine-mer and 10-mer peptides representing this region were synthesized and similarly tested. Peptide P501S-370 (SEQ ID NO: 539) was the minimal 9-mer giving a strong response. Peptide P501S-376 (SEQ ID NO: 540) also gave a weak response, suggesting that it might represent a cross-reactive

20   epitope.

In subsequent studies, the ability of primary human B cells transduced with P501S to prime MHC class I-restricted, P501S-specific, autologous CD8 T cells was examined. Primary B cells were derived from PBMC of a homozygous HLA-A2 donor by culture in CD40 ligand and IL-4, transduced at high frequency with

25   recombinant P501S in the vector pBIB, and selected with blastocidin-S. For *in vitro* priming, purified CD8+ T cells were cultured with autologous CD40 ligand + IL-4 derived, P501S-transduced B cells in a 96-well microculture format. These CTL microcultures were re-stimulated with P501S-transduced B cells and then assayed for specificity. Following this initial screen, microcultures with significant signal above

30   background were cloned on autologous EBV-transformed B cells (BLCL), also

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transduced with P501S. Using IFN-gamma ELISPOT for detection, several of these CD8 T cell clones were found to be specific for P501S, as demonstrated by reactivity to BLCL/P501S but not BLCL transduced with control antigen. It was further demonstrated that the anti-P501S CD8 T cell specificity is HLA-A2-restricted. First,

5   antibody blocking experiments with anti-HLA-A,B,C monoclonal antibody (W6.32), anti-HLA-B,C monoclonal antibody (B1.23.2) and a control monoclonal antibody showed that only the anti-HLA-A,B,C antibody blocked recognition of P501S-expressing autologous BLCL. Secondly, the anti-P501S CTL also recognized an HLA-A2 matched, heterologous BLCL transduced with P501S, but not the corresponding

10 EGFP transduced control BLCL.

A naturally processed, CD8, class I-restricted peptide epitope of P501S was identified as follows. Dendritic Cells (DC) were isolated by Percol gradient followed by differential adherence, and cultured for 5 days in the presence of RPMI medium containing 1% human serum, 50ng/ml GM-CSF and 30ng/ml IL-4. Following

15 culture, DC were infected for 24 hours with P501S-expressing adenovirus at an MOI of 10 and matured for an additional 24 hours by the addition of 2ug/ml CD40 ligand. CD8 cells were enriched for by the subtraction of CD4+, CD14+ and CD16+ populations from PBMC with magnetic beads. Priming cultures containing 10,000 P501S-expressing DC and 100,000 CD8+ T cells per well were set up in 96-well V-bottom

20 plates with RPMI containing 10% human serum, 5ng/ml IL-12 and 10ng/ml IL-6. Cultures were stimulated every 7 days using autologous fibroblasts retrovirally transduced to express P501S and CD80, and were treated with IFN-gamma for 48-72 hours to upregulate MHC Class I expression. 10u/ml IL-2 was added at the time of stimulation and on days 2 and 5 following stimulation. Following 4 stimulation cycles,

25 one P501S-specific CD8+ T cell line (referred to as 2A2) was identified that produced IFN-gamma in response to IFN-gamma-treated P501S/CD80 expressing autologous fibroblasts, but not in response to IFN-gamma-treated P703P/CD80 expressing autologous fibroblasts in a γ-IFN Elispot assay. Line 2A2 was cloned in 96-well plates with 0.5 cell/well or 2 cells/well in the presence of 75,000 PBMC/well, 10,000 B-

30 LCL/well, 30ng/ml OKT3 and 50u/ml IL-2. Twelve clones were isolated that showed strong P501S specificity in response to transduced fibroblasts.

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Fluorescence activated cell sorting (FACS) analysis was performed on P501S-specific clones using CD3-, CD4- and CD8-specific antibodies conjugated to PercP, FITC and PE respectively. Consistent with the use of CD8 enriched T cells in the priming cultures, P5401S-specific clones were determined to be CD3+, CD8+ and
5   CD4-.

To identify the relevant P501S epitope recognized by P501S specific CTL, pools of 18-20 mer or 30-mer peptides that spanned the majority of the amino acid sequence of P501S were loaded onto autologous B-LCL and tested in γ-IFN Elispot assays for the ability to stimulate two P501S-specific CTL clones, referred to as 4E5
10   and 4E7. One pool, composed of five 18-20 mer peptides that spanned amino acids 411-486 of P501S (SEQ ID NO: 113), was found to be recognized by both P501S-specific clones. To identify the specific 18-20 mer peptide recognized by the clones, each of the 18-20 mer peptides that comprised the positive pool were tested individually in γ-IFN Elispot assays for the ability to stimulate the two P501S-specific CTL clones, 4E5 and
15   4E7. Both 4E5 and 4E7 specifically recognized one 20-mer peptide (SEQ ID NO: 853; cDNA sequence provided in SEQ ID NO: 854) that spanned amino acids 453-472 of P501S. Since the minimal epitope recognized by CD8+ T cells is almost always either a 9 or 10-mer peptide sequence, 10-mer peptides that spanned the entire sequence of SEQ ID NO: 853 were synthesized that differed by 1 amino acid. Each of these 10-mer
20   peptides was tested for the ability to stimulate two P501S-specific clones, (referred to as 1D5 and 1E12). One 10-mer peptide (SEQ ID NO: 855; cDNA sequence provided in SEQ ID NO: 856) was identified that specifically stimulated the P501S-specific clones. This epitope spans amino acids 463-472 of P501S. This sequence defines a minimal 10-mer epitope from P501S that can be naturally processed and to which CTL responses
25   can be identified in normal PBMC. Thus, this epitope is a candidate for use as a vaccine moiety, and as a therapeutic and/or diagnostic reagent for prostate cancer.

To identify the class I restriction element for the P501S-derived sequence of SEQ ID NO: 855, HLA blocking and mismatch analyses were performed. In γ-IFN Elispot assays, the specific response of clones 4A7 and 4E5 to P501S-transduced
30   autologous fibroblasts was blocked by pre-incubation with 25ug/ml W6/32 (pan-Class I blocking antibody) and B1.23.2 (HLA-B/C blocking antibody). These results

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demonstrate that the SEQ ID NO: 855-specific response is restricted to an HLA-B or HLA-C allele.

     For the HLA mismatch analysis, autologous B-LCL (HLA-A1,A2,B8,B51, Cw1, Cw7) and heterologous B-LCL (HLA-

5   A2,A3,B18,B51,Cw5,Cw14) that share the HLAB51 allele were pulsed for one hour with 20ug/ml of peptide of SEQ ID NO: 855, washed, and tested in γ-IFN Elispot assays for the ability to stimulate clones 4A7 and 4E5. Antibody blocking assays with the B1.23.2 (HLA-B/C blocking antibody) were also performed. SEQ ID NO: 855-specific response was detected using both the autologous (D326) and heterologous (D107) B-

10 LCL, and furthermore the responses were blocked by pre-incubation with 25ug/ml of B1.23.2 HLA-B/C blocking antibody. Together these results demonstrate that the P501S-specific response to the peptide of SEQ ID NO: 855 is restricted to the HLA-B51 class I allele. Molecular cloning and sequence analysis of the HLA-B51 allele from D3326 revealed that the HLA-B51 subtype of D326 is HLA-B51011.

15   Based on the 10-mer P501S-derived epitope of SEQ ID NO: 855, two 9-mers with the sequences of SEQ ID NO: 857 and 858 were synthesized and tested in Elispot assays for the ability to stimulate two P501S-specific CTL clones derived from line 2A2. The 10-mer peptide of SEQ ID NO: 855, as well as the 9-mer peptide of SEQ ID NO: 858, but not the 9-mer peptide of SEQ ID NO: 857, were capable of stimulating

20 the P501S-specific CTL to produce IFN-gamma. These results demonstrate that the peptide of SEQ ID NO: 858 is a 9-mer P501S-derived epitope recognized by P501S-specific CTL. The DNA sequence encoding the epitope of SEQ ID NO: 858 is provided in SEQ ID NO: 859.

     To identify the class I restricting allele for the P501S-derived peptide of

25 SEQ ID NO: 855 and 858 specific response, each of the HLA B and C alleles were cloned from the donor used in the *in vitro* priming experiment. Sequence analysis indicated that the relevant alleles were HLA-B8, HLA-B51, HLA-Cw01 and HLA-Cw07. Each of these alleles were subcloned into an expression vector and co-transfected together with the P501S gene into VA-13 cells. Transfected VA-13 cells

30 were then tested for the ability to specifically stimulate the P501S-specific CTL in ELISPOT assays. VA-13 cells transfected with P501S and HLA-B51 were capable of

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stimulating the P501S-specific CTL to secrete gamma-IFN. VA-13 cells transfected
with HLA-B51 alone or P501S + the other HLA-alleles were not capable of stimulating
the P501S-specific CTL. These results demonstrate that the restricting allele for the
P501S-specific response is the HLAB51 allele. Sequence analysis revealed that the
5   subtype of the relevant restricting allele is HLA-B51011.

        To determine if the P501S-specific CTL could recognize prostate tumor
cells that express P501S, the P501S-positive lines LnCAP and CRL2422 (both
· expressing "moderate" amounts of P501S mRNA and protein), and PC-3 (expressing
low amounts of P501S mRNA and protein), plus the P501S-negative cell line DU-145
10   were retrovirally transduced with the HLA-B51011 allele that was cloned from the
donor used to generate the P501S-specific CTL. HLA-B51011- or EGFP-transduced
and selected tumor cells were treated with gamma-interferon and androgen (to
upregulate stimulatory functions and P501S, respectively) and used in gamma-
interferon Elispot assays with the P501S-specific CTL clones 4E5 and 4E7. Untreated
15   cells were used as a control.

        Both 4E5 and 4E7 efficiently and specifically recognized LnCAP and
CRL2422 cells that were transduced with the HLA-B51011 allele, but not the same cell
lines transduced with EGFP. Additionally, both CTL clones specifically recognized
PC-3 cells transduced with HLA-B51011, but not the P501S-negative tumor cell line
20   DU-145. Treatment with gamma-interferon or androgen did not enhance the ability of
CTL to recognize tumor cells. These results demonstrate that P501S-specific CTL,
generated by *in vitro* whole gene priming, specifically and efficiently recognize prostate
tumor cell lines that express P501S.

        A naturally processed CD4 epitope of P501S was identified as follows.
25   CD4 cells specific for P501S were prepared as described above. A series
of 16 overlapping peptides were synthesized that spanned approximately 50% of the
amino terminal portion of the P501S gene (amino acids 1- 325 of SEQ ID NO: 113).
For priming, peptides were combined into pools of 4 peptides, pulsed at 4 µg/ml onto
dendritic cells (DC) for 24 hours, with TNF-alpha. DC were then washed and mixed
30   with negatively selected CD4+ T cells in 96 well U-bottom plates. Cultures were re-
stimulated weekly on fresh DC loaded with peptide pools. Following a total of 4

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stimulation cycles, cells were rested for an additional week and tested for specificity to APC pulsed with peptide pools using γ-IFN ELISA and proliferation assays. For these assays, adherent monocytes loaded with either the relevant peptide pool at 4ug/ml or an irrelevant peptide at μg/ml were used as APC. T cell lines that demonstrated either

5   specific cytokine secretion or proliferation were then tested for recognition of individual peptides that were present in the pool. T cell lines could be identified from pools A and B that recognized individual peptides from these pools.

From pool A, lines AD9 and AE10 specifically recognized peptide 1 (SEQ ID NO: 862), and line AF5 recognized peptide 39 (SEQ ID NO: 861). From pool

10   B, line BC6 could be identified that recognized peptide 58 (SEQ ID NO: 860). Each of these lines were stimulated on the specific peptide and tested for specific recognition of the peptide in a titration assay as well as cell lysates generated by infection of HEK 293 cells with adenovirus expressing either P501S or an irrelevant antigen. For these assays, APC-adherent monocytes were pulsed with either 10, 1, or 0.1 μg/ml individual P501S

15   peptides, and DC were pulsed overnight with a 1:5 dilution of adenovirally infected cell lysates. Lines AD9, AE10 and AF5 retained significant recognition of the relevant P501S-derived peptides even at 0.1 mg/ml. Furthermore, line AD9 demonstrated significant (8.1 fold stimulation index) specific activity for lysates from adenovirus-P501S infected cells. These results demonstrate that high affinity CD4 T cell lines can

20   be generated toward P501S-derived epitopes, and that at least a subset of these T cells specific for the P501S derived sequence of SEQ ID NO: 862 are specific for an epitope that is naturally processed by human cells. The DNA sequences encoding the amino acid sequences of SEQ ID NO: 860-862 are provided in SEQ ID NO: 863-865, respectively.

25   To further characterize the P501S-specific activity of AD9, the line was cloned using anti-CD3. Three clones, referred to as 1A1, 1A9 and 1F5, were identified that were specific for the P501S-1 peptide (SEQ ID NO: 862). To determine the HLA restriction allele for the P501S-specific response, each of these clones was tested in class II antibody blocking and HLA mismatch assays using proliferation and gamma-

30   interferon assays. In antibody blocking assays and measuring gamma-interferon production using ELISA assays, the ability of all three clones to recognize peptide

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pulsed APC was specifically blocked by co-incubation with either a pan-class II
blocking antibody or a HLA-DR blocking antibody, but not with a HLA-DQ or an
irrelevant antibody. Proliferation assays performed simultaneously with the same cells
confirmed these results. These data indicate that the P501S-specific response of the
5   clones is restricted by an HLA-DR allele. Further studies demonstrated that the
restricting allele for the P501S-specific response is HLA-DRB1501.

EXAMPLE 13

IDENTIFICATION OF PROSTATE-SPECIFIC ANTIGENS
10   BY MICROARRAY ANALYSIS

This Example describes the isolation of certain prostate-specific
polypeptides from a prostate tumor cDNA library.

A human prostate tumor cDNA expression library as described above
15   was screened using microarray analysis to identify clones that display at least a three
fold over-expression in prostate tumor and/or normal prostate tissue, as compared to
non-prostate normal tissues (not including testis). 372 clones were identified, and 319
were successfully sequenced. Table I presents a summary of these clones, which are
shown in SEQ ID NOs:385-400. Of these sequences SEQ ID NOs:386, 389, 390 and
20   392 correspond to novel genes, and SEQ ID NOs: 393 and 396 correspond to previously
identified sequences. The others (SEQ ID NOs:385, 387, 388, 391, 394, 395 and 397-
400) correspond to known sequences, as shown in Table I.

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Table I

Summary of Prostate Tumor Antigens

Known Genes	Previously Identified Genes	Novel Genes
T-cell gamma chain	P504S	23379 (SEQ ID NO:389)
Kallikrein	P1000C	23399 (SEQ ID NO:392)
Vector	P501S	23320 (SEQ ID NO:386)
CGI-82 protein mRNA (23319; SEQ ID NO:385)	P503S	23381 (SEQ ID NO:390)
PSA	P510S	
Ald. 6 Dehyd.	P784P	
L-iditol-2 dehydrogenase (23376; SEQ ID NO:388)	P502S	
Ets transcription factor PDEF (22672; SEQ ID NO:398)	P706P	
hTGR (22678; SEQ ID NO:399)	19142.2, bangur.seq (22621; SEQ ID NO:396)	
KIAA0295(22685; SEQ ID NO:400)	5566.1 Wang (23404; SEQ ID NO:393)	
Prostatic Acid Phosphatase(22655; SEQ ID NO:397)	P712P	
transglutaminase (22611; SEQ ID NO:395)	P778P	
HDLBP (23508; SEQ ID NO:394)		
CGI-69 Protein(23367; SEQ ID NO:387)		
KIAA0122(23383; SEQ ID NO:391)		
TEEG		

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CGI-82 showed 4.06 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 43% of prostate tumors, 25% normal prostate, not detected in other normal tissues tested. L-iditol-2 dehydrogenase showed 4.94 fold over-expression in prostate tissues as compared to

5 other normal tissues tested. It was over-expressed in 90% of prostate tumors, 100% of normal prostate, and not detected in other normal tissues tested. Ets transcription factor PDEF showed 5.55 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 47% prostate tumors, 25% normal prostate and not detected in other normal tissues tested. hTGR1 showed 9.11 fold over-expression in

10 prostate tissues as compared to other normal tissues tested. It was over-expressed in 63% of prostate tumors and is not detected in normal tissues tested including normal prostate. KIAA0295 showed 5.59 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 47% of prostate tumors, low to undetectable in normal tissues tested including normal prostate tissues. Prostatic acid

15 phosphatase showed 9.14 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 67% of prostate tumors, 50% of normal prostate, and not detected in other normal tissues tested. Transglutaminase showed 14.84 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 30% of prostate tumors, 50% of normal prostate, and is

20 not detected in other normal tissues tested. High density lipoprotein binding protein. (HDLBP) showed 28.06 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 97% of prostate tumors, 75% of normal prostate, and is undetectable in all other normal tissues tested. CGI-69 showed 3.56 fold over-expression in prostate tissues as compared to other normal tissues tested. It is

25 a low abundant gene, detected in more than 90% of prostate tumors, and in 75% normal prostate tissues. The expression of this gene in normal tissues was very low. KIAA0122 showed 4.24 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 57% of prostate tumors, it was undetectable in all normal tissues tested including normal prostate tissues. 19142.2

30 bangur showed 23.25 fold over-expression in prostate tissues as compared to other

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normal tissues tested. It was over-expressed in 97% of prostate tumors and 100% of normal prostate. It was undetectable in other normal tissues tested. 5566.1 Wang showed 3.31 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 97% of prostate tumors, 75% normal prostate

5   and was also over-expressed in normal bone marrow, pancreas, and activated PBMC. Novel clone 23379 (also referred to as P553S) showed 4.86 fold over-expression in prostate tissues as compared to other normal tissues tested. It was detectable in 97% of prostate tumors and 75% normal prostate and is undetectable in all other normal tissues tested. Novel clone 23399 showed 4.09 fold over-expression in prostate tissues as

10   compared to other normal tissues tested. It was over-expressed in 27% of prostate tumors and was undetectable in all normal tissues tested including normal prostate tissues. Novel clone 23320 showed 3.15 fold over-expression in prostate tissues as compared to other normal tissues tested. It was detectable in all prostate tumors and 50% of normal prostate tissues. It was also expressed in normal colon and trachea.

15   Other normal tissues do not express this gene at high level.

Subsequent full-length cloning studies on P553S, using standard techniques, revealed that this clone is an incomplete spliced form of P501S. The determined cDNA sequences for four splice variants of P553S are provided in SEQ ID NO: 702-705. An amino acid sequence encoded by SEQ ID NO: 705 is provided in

20   SEQ ID NO: 706. The cDNA sequence of SEQ ID NO: 702 was found to contain two open reading frames (ORFs). The amino acid sequences encoded by these two ORFs are provided in SEQ ID NO: 707 and 708.

EXAMPLE 14

25   IDENTIFICATION OF PROSTATE-SPECIFIC ANTIGENS
BY ELECTRONIC SUBTRACTION

This Example describes the use of an electronic subtraction technique to identify prostate-specific antigens.

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Potential prostate-specific genes present in the GenBank human EST database were identified by electronic subtraction (similar to that described by Vasmatizis et al., *Proc. Natl. Acad. Sci. USA 95*:300-304, 1998). The sequences of EST clones (43,482) derived from various prostate libraries were obtained from the GenBank

5   public human EST database. Each prostate EST sequence was used as a query sequence in a BLASTN (National Center for Biotechnology Information) search against the human EST database. All matches considered identical (length of matching sequence >100 base pairs, density of identical matches over this region > 70%) were grouped (aligned) together in a cluster. Clusters containing more than 200 ESTs were discarded

10   since they probably represented repetitive elements or highly expressed genes such as those for ribosomal proteins. If two or more clusters shared common ESTs, those clusters were grouped together into a "supercluster," resulting in 4,345 prostate superclusters.

Records for the 479 human cDNA libraries represented in the GenBank

15   release were downloaded to create a database of these cDNA library records. These 479 cDNA libraries were grouped into three groups: Plus (normal prostate and prostate tumor libraries, and breast cell line libraries, in which expression was desired), Minus (libraries from other normal adult tissues, in which expression was not desirable), and Other (libraries from fetal tissue, infant tissue, tissues found only in women, non-

20   prostate tumors and cell lines other than prostate cell lines, in which expression was considered to be irrelevant). A summary of these library groups is presented in Table II.

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Table II

Prostate cDNA Libraries and ESTs

Library	# of Libraries	# of ESTs
Plus	25	43,482
Normal	11	18,875
Tumor	11	21,769
Cell lines	3	2,838
Minus	166	
Other	287	

5   Each supercluster was analyzed in terms of the ESTs within the supercluster. The tissue source of each EST clone was noted and used to classify the superclusters into four groups: Type 1- EST clones found in the Plus group libraries only; no expression detected in Minus or Other group libraries; Type 2- EST clones derived from the Plus and Other group libraries only; no expression detected in the

10   Minus group; Type 3- EST clones derived from the Plus, Minus and Other group libraries, but the number of ESTs derived from the Plus group is higher than in either the Minus or Other groups; and Type 4- EST clones derived from Plus, Minus and Other group libraries, but the number derived from the Plus group is higher than the number derived from the Minus group. This analysis identified 4,345 breast clusters

15   (see Table III). From these clusters, 3,172 EST clones were ordered from Research Genetics, Inc., and were received as frozen glycerol stocks in 96-well plates.

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Table III

Prostate Cluster Summary

Type	# of Superclusters	# of ESTs Ordered
1	688	677
2	2899	2484
3	85	11
4	673	0
Total	4345	3172

5   The EST clone inserts were PCR-amplified using amino-linked PCR primers for Synteni microarray analysis. When more than one PCR product was obtained for a particular clone, that PCR product was not used for expression analysis. In total, 2,528 clones from the electronic subtraction method were analyzed by microarray analysis to identify electronic subtraction breast clones that had high levels 10 of tumor vs. normal tissue mRNA. Such screens were performed using a Synteni (Palo Alto, CA) microarray, according to the manufacturer's instructions (and essentially as described by Schena et al., *Proc. Natl. Acad. Sci. USA 93*:10614-10619, 1996 and Heller et al., *Proc. Natl. Acad. Sci. USA 94*:2150-2155, 1997). Within these analyses, the clones were arrayed on the chip, which was then probed with fluorescent probes 15 generated from normal and tumor prostate cDNA, as well as various other normal tissues. The slides were scanned and the fluorescence intensity was measured.

Clones with an expression ratio greater than 3 (*i.e.*, the level in prostate tumor and normal prostate mRNA was at least three times the level in other normal tissue mRNA) were identified as prostate tumor-specific sequences (Table IV). The 20 sequences of these clones are provided in SEQ ID NO: 401-453, with certain novel sequences shown in SEQ ID NO: 407, 413, 416-419, 422, 426, 427 and 450.

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Table IV

Prostate-tumor Specific Clones

SEQ ID NO.	Sequence Designation	Comments
401	22545	previously identified P1000C
402	22547	previously identified P704P
403	22548	known
404	22550	known
405	22551	PSA
406	22552	prostate secretory protein 94
407	22553	novel
408	22558	previously identified P509S
409	22562	glandular kallikrein
410	22565	previously identified P1000C
411	22567	PAP
412	22568	B1006C (breast tumor antigen)
413	22570	novel
414	22571	PSA
415	22572	previously identified P706P
416	22573	novel
417	22574	novel
418	22575	novel
419	22580	novel
420	22581	PAP
421	22582	prostatic secretory protein 94
422	22583	novel
423	22584	prostatic secretory protein 94
424	22585	prostatic secretory protein 94
425	22586	known
426	22587	novel
427	22588	novel
428	22589	PAP
429	22590	known
430	22591	PSA
431	22592	known
432	22593	Previously identified P777P
433	22594	T cell receptor gamma chain
434	22595	Previously identified P705P
435	22596	Previously identified P707P
436	22847	PAP
437	22848	known
438	22849	prostatic secretory protein 57

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439	22851	PAP
440	22852	PAP
441	22853	' PAP
442	22854	previously identified P509S
443	22855	previously identified P705P
444	22856	previously identified P774P
445	22857	PSA
446	23601	previously identified P777P
447	23602	PSA
448	23605	PSA
449	23606	PSA
450	23612	novel
451	23614	PSA
452	23618	previously identified P1000C
453	23622	previously identified P705P

Further studies on the clone of SEQ ID NO: 407 (also referred to as P1020C) led to the isolation of an extended cDNA sequence provided in SEQ ID NO: 591. This extended cDNA sequence was found to contain an open reading frame that

5 encodes the predicted amino acid sequence of SEQ ID NO: 592. The P1020C cDNA and amino acid sequences were found to show some similarity to the human endogenous retroviral HERV-K pol gene and protein.

EXAMPLE 15

10 FURTHER IDENTIFICATION OF PROSTATE-SPECIFIC ANTIGENS BY MICROARRAY ANALYSIS

This Example describes the isolation of additional prostate-specific polypeptides from a prostate tumor cDNA library.

A human prostate tumor cDNA expression library as described above

15 was screened using microarray analysis to identify clones that display at least a three fold over-expression in prostate tumor and/or normal prostate tissue, as compared to non-prostate normal tissues (not including testis). 142 clones were identified and sequenced. Certain of these clones are shown in SEQ ID NO: 454-467. Of these sequences, SEQ ID NO: 459-460 represent novel genes. The others (SEQ ID NO: 454-

20 458 and 461-467) correspond to known sequences. Comparison of the determined

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cDNA sequence of SEQ ID NO: 461 with sequences in the Genbank database using the BLAST program revealed homology to the previously identified transmembrane protease serine 2 (TMPRSS2). The full-length cDNA sequence for this clone is provided in SEQ ID NO: 894, with the corresponding amino acid sequence being

5   provided in SEQ ID NO: 895. The cDNA sequence encoding the first 209 amino acids of TMPRSS2 is provided in SEQ ID NO: 896, with the first 209 amino acids being provided in SEQ ID NO: 897.

The sequence of SEQ ID NO: 462 (referred to as P835P) was found to correspond to the previously identified clone FLJ13518 (Accession AK023643; SEQ ID

10 . NO: 917), which had no associated open reading frame (ORF). This clone was used to search the Geneseq DNA database and matched a clone previously identified as a G protein-coupled receptor protein (DNA Geneseq Accession A09351; amino acid Geneseq Accession Y92365), that is characterized by the presence of seven transmembrane domains. The sequences of fragments between these domains are

15 provided in SEQ ID NO: 921-928, with SEQ ID NO: 921, 923, 925 and 927 representing extracellular domains and SEQ ID NO: 922, 924, 926 and 928 representing intracellular domains. SEQ ID NO: 921-928 represent amino acids 1-28, 53-61, 83-103, 124-143, 165-201, 226-238, 263-272 and 297-381, respectively, of P835P. The full-length cDNA sequence for P835P is provided in SEQ ID NO: 916. The cDNA

20 sequence of the open reading frame for P835P, including stop codon, is provided in SEQ ID NO: 918, with the open reading frame without stop codon being provided in SEQ ID NO: 919 and the corresponding amino acid sequence being provided in SEQ ID NO: 920.

25   EXAMPLE 16

FURTHER CHARACTERIZATION OF PROSTATE-SPECIFIC ANTIGEN P710P

This Example describes the full length cloning of P710P.

The prostate cDNA library described above was screened with the P710P

30 fragment described above. One million colonies were plated on LB/Ampicillin plates.

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Nylon membrane filters were used to lift these colonies, and the cDNAs picked up by these filters were then denatured and cross-linked to the filters by UV light. The P710P fragment was radiolabeled and used to hybridize with the filters. Positive cDNA clones were selected and their cDNAs recovered and sequenced by an automatic Perkin

5   Elmer/Applied Biosystems Division Sequencer. Four sequences were obtained, and are presented in SEQ ID NO: 468-471. These sequences appear to represent different splice variants of the P710P gene. Subsequent comparison of the cDNA sequences of P710P with those in Genbank releaved homology to the DD3 gene (Genbank accession numbers AF103907 & AF103908). The cDNA sequence of DD3 is provided in SEQ ID

10   NO: 690.

EXAMPLE 17

PROTEIN EXPRESSION OF PROSTATE-SPECIFIC ANTIGENS

15   This example describes the expression and purification of prostate-specific antigens in *E. coli*, baculovirus and mammalian cells.

a)   Expression of P501S in *E. coli*

             Expression of the full-length form of P501S was attempted by first cloning P501S without the leader sequence (amino acids 36-553 of SEQ ID NO: 113)

20   downstream of the first 30 amino acids of the *M. tuberculosis* antigen Ra12 (SEQ ID NO: 484) in pET17b. Specifically, P501S DNA was used to perform PCR using the primers AW025 (SEQ ID NO: 485) and AW003 (SEQ ID NO: 486). AW025 is a sense cloning primer that contains a HindIII site. AW003 is an antisense cloning primer that contains an EcoRI site. DNA amplification was performed using 5 µl 10X Pfu buffer, 1

25   µl 20 mM dNTPs, 1 µl each of the PCR primers at 10 µM concentration, 40 µl water, 1 µl Pfu DNA polymerase (Stratagene, La Jolla, CA) and 1 µl DNA at 100 ng/µl. Denaturation at 95°C was performed for 30 sec, followed by 10 cycles of 95°C for 30 sec, 60°C for 1 min and by 72°C for 3 min. 20 cycles of 95°C for 30 sec, 65°C for 1 min and by 72°C for 3 min, and lastly by 1 cycle of 72°C for 10 min. The PCR product was

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cloned to Ra12m/pET17b using HindIII and EcoRI. The sequence of the resulting fusion construct (referred to as Ra12-P501S-F) was confirmed by DNA sequencing.

The fusion construct was transformed into BL21(DE3)pLysE, pLysS and CodonPlus *E. coli* (Stratagene) and grown overnight in LB broth with kanamycin. The
5   resulting culture was induced with IPTG. Protein was transferred to PVDF membrane and blocked with 5% non-fat milk (in PBS-Tween buffer), washed three times and incubated with mouse anti-His tag antibody (Clontech) for 1 hour. The membrane was washed 3 times and probed with HRP-Protein A (Zymed) for 30 min. Finally, the membrane was washed 3 times and developed with ECL (Amersham). No expression
10 was detected by Western blot. Similarly, no expression was detected by Western blot when the Ra12-P501S-F fusion was used for expression in BL21CodonPlus by CE6 phage (Invitrogen).

An N-terminal fragment of P501S (amino acids 36-325 of SEQ ID NO: 113) was cloned down-stream of the first 30 amino acids of the *M. tuberculosis* antigen
15 Ra12 in pET17b as follows. P501S DNA was used to perform PCR using the primers AW025 (SEQ ID NO: 485) and AW027 (SEQ ID NO: 487). AW027 is an antisense cloning primer that contains an EcoRI site and a stop codon. DNA amplification was performed essentially as described above. The resulting PCR product was cloned to Ra12 in pET17b at the HindIII and EcoRI sites. The fusion construct (referred to as
20 Ra12-P501S-N) was confirmed by DNA sequencing.

The Ra12-P501S-N fusion construct was used for expression in BL21(DE3)pLysE, pLysS and CodonPlus, essentially as described above. Using Western blot analysis, protein bands were observed at the expected molecular weight of 36 kDa. Some high molecular weight bands were also observed, probably due to
25 aggregation of the recombinant protein. No expression was detected by Western blot when the Ra12-P501S-F fusion was used for expression in BL21CodonPlus by CE6 phage.

A fusion construct comprising a C-terminal portion of P501S (amino acids 257-553 of SEQ ID NO: 113) located down-stream of the first 30 amino acids of
30 the *M. tuberculosis* antigen Ra12 (SEQ ID NO: 484) was prepared as follows. P501S

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DNA was used to perform PCR using the primers AW026 (SEQ ID NO: 488) and AW003 (SEQ ID NO: 486). AW026 is a sense cloning primer that contains a HindIII site. DNA amplification was performed essentially as described above. The resulting PCR product was cloned to Ra12 in pET17b at the HindIII and EcoRI sites. The sequence for the fusion construct (referred to as Ra12-P501S-C) was confirmed.

The Ra12-P501S-C fusion construct was used for expression in BL21(DE3)pLysE, pLysS and CodonPlus, as described above. A small amount of protein was detected by Western blot, with some molecular weight aggregates also being observed. Expression was also detected by Western blot when the Ra12-P501S-C fusion was used for expression in BL21CodonPlus induced by CE6 phage.

A fusion construct comprising a fragment of P501 (amino acids 36-298 of SEQ ID NO: 113) located down-stream of the *M. tuberculosis* antigen Ra12 (SEQ ID NO: 848) was prepared as follows. P501S DNA was used to perform PCR using the primers AW042 (SEQ ID NO: 849) and AW053 (SEQ ID NO: 850). AW042 is a sense cloning primer that contains a EcoRI site. AW053 is an antisense primer with stop and Xho I sites. DNA amplification was performed essentially as described above. The resulting PCR product was cloned to Ra12 in pET17b at the EcoRI and Xho I sites. The resulting fusion construct (referred to as Ra12-P501S-E2) was expressed in B834 (DE3) pLys S *E. coli* host cells in TB media for 2 h at room temperature. Expressed protein was purified by washing the inclusion bodies and running on a Ni-NTA column. The purified protein stayed soluble in buffer containing 20 mM Tris-HCl (pH 8), 100 mM NaCl, 10 mM β-Me and 5% glycerol. The determined cDNA and amino acid sequences for the expressed fusion protein are provided in SEQ ID NO: 851 and 852, respectfully.

b)   Expression of P501S in Baculovirus

The Bac-to-Bac baculovirus expression system (BRL Life Technologies, Inc.) was used to express P501S protein in insect cells. Full-length P501S (SEQ ID NO: 113) was amplified by PCR and cloned into the XbaI site of the donor plasmid pFastBacI. The recombinant bacmid and baculovirus were prepared according to the

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manufacturer's instructions. The recombinant baculovirus was amplified in Sf9 cells and the high titer viral stocks were utilized to infect High Five cells (Invitrogen) to make the recombinant protein. The identity of the full-length protein was confirmed by N-terminal sequencing of the recombinant protein and by Western blot analysis (Figure 7). Specifically, 0.6 million High Five cells in 6-well plates were infected with either the unrelated control virus BV/ECD_PD (lane 2), with recombinant baculovirus for P501S at different amounts or MOIs (lanes 4-8), or were uninfected (lane 3). Cell lysates were run on SDS-PAGE under reducing conditions and analyzed by Western blot with the anti-P501S monoclonal antibody P501S-10E3-G4D3 (prepared as described below). Lane 1 is the biotinylated protein molecular weight marker (BioLabs).

The localization of recombinant P501S in the insect cells was investigated as follows. The insect cells overexpressing P501S were fractionated into fractions of nucleus, mitochondria, membrane and cytosol. Equal amounts of protein from each fraction were analyzed by Western blot with a monoclonal antibody against P501S. Due to the scheme of fractionation, both nucleus and mitochondria fractions contain some plasma membrane components. However, the membrane fraction is basically free from mitochondria and nucleus. P501S was found to be present in all fractions that contain the membrane component, suggesting that P501S may be associated with plasma membrane of the insect cells expressing the recombinant protein.

c)   Expression of P501S in mammalian cells

Full-length P501S (553 amino acids; SEQ ID NO: 113) was cloned into various mammalian expression vectors, including pCEP4 (Invitrogen), pVR1012 (Vical, San Diego, CA) and a modified form of the retroviral vector pBMN, referred to as pBIB. Transfection of P501S/pCEP4 and P501S/pVR1012 into HEK293 fibroblasts was carried out using the Fugene transfection reagent (Boehringer Mannheim). Briefly, 2 ul of Fugene reagent was diluted into 100 ul of serum-free media and incubated at room temperature for 5-10 min. This mixture was added to 1 ug of P501S plasmid DNA, mixed briefly and incubated for 30 minutes at room temperature. The

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Fugene/DNA mixture was added to cells and incubated for 24-48 hours. Expression of recombinant P501S in transfected HEK293 fibroblasts was detected by means of Western blot employing a monoclonal antibody to P501S.

Transfection of p501S/pCEP4 into CHO-K cells (American Type Culture Collection, Rockville, MD) was carried out using GenePorter transfection reagent (Gene Therapy Systems, San Diego, CA). Briefly, 15 µl of GenePorter was diluted in 500 µl of serum-free media and incubated at room temperature for 10 min. The GenePorter/media mixture was added to 2 µg of plasmid DNA that was diluted in 500 µl of serum-free media, mixed briefly and incubated for 30 min at room temperature. CHO-K cells were rinsed in PBS to remove serum proteins, and the GenePorter/DNA mix was added and incubated for 5 hours. The transfected cells were then fed an equal volume of 2x media and incubated for 24-48 hours.

FACS analysis of P501S transiently infected CHO-K cells, demonstrated surface expression of P501S. Expression was detected using rabbit polyclonal antisera raised against a P501S peptide, as described below. Flow cytometric analysis was performed using a FaCScan (Becton Dickinson), and the data were analyzed using the Cell Quest program.

d)   Expression of P703P in Baculovirus

The cDNA for full-length P703P-DE5 (SEQ ID NO: 326), together with several flanking restriction sites, was obtained by digesting the plasmid pCDNA703 with restriction endonucleases Xba I and Hind III. The resulting restriction fragment (approx. 800 base pairs) was ligated into the transfer plasmid pFastBacI which was digested with the same restriction enzymes. The sequence of the insert was confirmed by DNA sequencing. The recombinant transfer plasmid pFBP703 was used to make recombinant bacmid DNA and baculovirus using the Bac-To-Bac Baculovirus expression system (BRL Life Technologies). High Five cells were infected with the recombinant virus BVP703, as described above, to obtain recombinant P703P protein.

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e)   Expression of P788P in *E. Coli*

A truncated, N-terminal portion, of P788P (residues 1-644 of SEQ ID NO: 777; referred to as P788P-N) fused with a C-terminal 6xHis Tag was expressed in *E. coli* as follows. P788P cDNA was amplified using the primers AW080 and AW081 (SEQ ID NO: 815 and 816). AW080 is a sense cloning primer with an NdeI site. AW081 is an antisense cloning primer with a XhoI site. The PCR-amplified P788P, as well as the vector pCRX1, were digested with NdeI and XhoI. Vector and insert were ligated and transformed into NovaBlue cells. Colonies were randomly screened for insert and then sequenced. P788P-N clone #6 was confirmed to be identical to the designed construct. The expression construct P788P-N #6/pCRX1 was transformed into *E. coli* BL21 CodonPlus-RIL competent cells. After induction, most of the cells grew well, achieving OD600 of greater than 2.0 after 3 hr. Coomassie stained SDS-PAGE showed an over-expressed band at about 75 kD. Western blot analysis using a 6xHisTag antibody confirmed the band was P788P-N. The determined cDNA sequence for P788P-N is provided in SEQ ID NO: 817, with the corresponding amino acid sequence being provided in SEQ ID NO: 818.

f)   Expression of P510S in *E. coli*

The P510S protein has 9 potential transmembrane domains and is predicted to be located at the plasma membrane. The C-terminal protein of this protein, as well as the predicted third extracellular domain of P510S were expressed in *E. coli* as follows.

The expression construct referred to as Ra12-P501S-C was designed to have a 6 HisTag at the N-terminal enc, followed by the *M. tuberculosis* antigen Ra12 (SEQ ID NO: 819) and then the C-terminal portion of P510S (amino residues 1176-1261 of SEQ ID NO: 538). Full-length P510S was used to amplify the P510S-C fragment by PCR using the primers AW056 and AW057 (SEQ ID NO: 820 and 821, respectively). AW056 is a sense cloning primer with an EcoRI site. AW057 is an antisense primer with stop and XhoI sites. The amplified P501S fragment and Ra12/pCRX1 were digested with EcoRI and XhoI and then purified. The insert and

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vector were ligated together and transformed into NovaBlue. Colonies were randomly screened for insert and sequences. For protein expression, the expression construct was transformed into *E. coli* BL21 (DE3) CodonPlus-RIL competent cells. A mini-induction screen was performed to optimize the expression conditions. After induction the cells grew well, achieving OD 600 nm greater than 2.0 after 3 hours. Coomassie stain SDS-PAGE showed a highly over-expressed band at approx. 30 kD. Though this is higher than the expected molecular weight, western blot analysis was positive, showing this band to be the His tag-containing protein. The optimized culture conditions are as follows. Dilute overnight culture/daytime culture (LB + kanamycin + chloramphenicol) into 2xYT (with kanamycin and chloramphenicol) at a ratio of 25 ml culture to 1 liter 2xYT. Allow to grow at 37 °C until OD600 = 0.6. Take an aliquot out as T0 sample. Add 1 mM IPTG and allow to grow at 30 °C for 3 hours. Take out a T3 sample, spin down cells and store at -80 °C. The determined cDNA and amino acid sequences for the Ra12-P510S-C construct are provided in SEQ ID NO: 822 and 825, respectively.

The expression construct P510S-C was designed to have a 5' added start codon and a glycine (GGA) codon and then the P510S C terminal fragment followed by the in frame 6x histidine tag and stop codon from the pET28b vector. The cloning strategy is similar to that used for Ra12-P510S-C, except that the PCR primers employed were those shown in SEQ ID NO: 828 and 829, respectively and the NcoI/XhoI cut in pET28b was used. The primer of SEQ ID NO: 828 created a 5' NcoI site and added a start codon. The antisense primer of SEQ ID NO: 829 creates a XhoI site on P510S C terminal fragment. Clones were confirmed by sequencing. For protein expression, the expression construct was transformed into *E. coli* BL21 (DE3) CodonPlus-RIL competent cells. An OD600 of greater than 2.0 was obtained 30 hours after induction. Coomassie stained SDS-PAGE showed an over-expressed band at about 11 kD. Western blot analysis confirmed that the band was P510S-C, as did N-terminal protein sequencing. The optimized culture conditions are as follows: dilute overnight culture/daytime culture (LB + kanamycin + chloramphenicol) into 2x YT (+ kanamycin and chloramphenicol) at a ratio of 25 mL culture to 1 liter 2x YT, and allow

to grow at 37 °C until an OD 600 of about 0.5 is reached. Take out an aliquot as T0 sample. Add 1 mM IPTG and allow to grow at 30 °C for 3 hours. Spin down the cells and store at -80 °C until purification. The determined cDNA and amino acid sequences for the P510S-C construct are shown in SEQ ID NO: 823 and 826, respectively.

The predicted third extracellular domain of P510S (P510S-E3; residues 328-676 of SEQ ID NO: 538) was expressed in *E. coli* as follows. The P510S fragment was amplified by PCR using the primers shown in SEQ ID NO: 830 and 831. The primer of SEQ ID NO: 830 is a sense primer with an NdeI site for use in ligating into pPDM. The primer of SEQ ID NO: 831 is an antisense primer with an added XhoI site for use in ligating into pPDM. The resulting fragment was cloned to pPDM at the NdeI and XhoI sites. Clones were confirmed by sequencing. For protein expression, the clone ws transformed into E. coli BL21 (DE3) CodonPlus-RIL competent cells. After induction, an OD600 of greater than 2.0 was achieved after 3 hours. Coomassie stained SDS-PAGE showed an over-expressed band at about 39 kD, and N-terminal sequencing confirmed the N-terminal to be that of P510S-E3. Optimized culture conditions are as follows: dilute overnight culture/daytime culture (LB + kanamycin + chloramphenicol) into 2x YT (kanamycin and chloramphenicol) at a ratio of 25 ml culture to 1 liter 2x YT. Allow to grow at 37 °C until OD 600 equals 0.6. Take out an aliquot as T0 sample. Add 1 mM IPTG and allow to grow at 30 °C for 3 hours. Take out a T3 sample, spin down the cells and store at -80 °C until purification. The determined cDNA and amino acid sequences for the P501S-E3 construct are provided in SEQ ID NO: 824 and 827, respectively.

g)   Expression of P775S in *E. Coli*

The antigen P775P contains multiple open reading frames (ORF). The third ORF, encoding the protein of SEQ ID NO: 483, has the best emotif score. An expression fusion construct containing the *M. tuberculosis* antigen Ra12 (SEQ ID NO: 819) and P775P-ORF3 with an N-terminal 6x HisTag was prepared as follows. P775P-ORF3 was amplified using the sense PCR primers of SEQ ID NO: 832 and the anti-sense PCR primer of SEQ ID NO: 833. The PCR amplified fragment of P775P and

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Ra12/pCRX1 were digested with the restriction enzymes EcoRI and XhoI. Vector and insert were ligated and then transformed into NovaBlue cells. Colonies were randomly screened for insert and then sequenced. A clone having the desired sequence was transformed into E. coli BL21 (DE3) CodonPlus-RIL competent cells. Two hours after

5   induction, the cell density peaked at OD600 of approximately 1.8. Coomassie stained SDS-PAGE showed an over-expressed band at about 31 kD. Western blot using 6x HisTag antibody confirmed that the band was Ra12-P775P-ORF3. The determined cDNA and amino acid sequences for the fusion construct are provided in SEQ ID NO: 834 and 835, respectively.

10

H)   Expression of a P703P His tag fusion protein in *E. coli*

The cDNA for the coding region of P703P was prepared by PCR using the primers of SEQ ID NO: 836 and 837. The PCR product was digested with EcoRI restriction enzyme, gel purified and cloned into a modified pET28 vector with a His tag

15   in frame, which had been digested with Eco72I and EcoRI restriction enzymes. The correct construct was confirmed by DNA sequence analysis and then transformed into *E. coli* BL21 (DE3) pLys S expression host cells. The determined amino acid and cDNA sequences for the expressed recombinant P703P are provided in SEQ ID NO: 838 and 839, respectively.

20

I)   Expression of a P705P His tag fusion protein in *E. coli*

The cDNA for the coding region of P705P was prepared by PCR using the primers of SEQ ID NO: 840 and 841. The PCR product was digested with EcoRI restriction enzyme, gel purified and cloned into a modified pET28 vector with a His tag

25   in frame, which had been digested with Eco72I and EcoRI restriction enzymes. The correct construct was confirmed by DNA sequence analysis and then transformed into *E. coli* BL21 (DE3) pLys S and BL21 (DE3) CodonPlus expression host cells. The determined amino acid and cDNA sequences for the expressed recombinant P705P are provided in SEQ ID NO: 842 and 843, respectively.

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J)   Expression of a P711P His tag fusion protein in *E. coli*

The cDNA for the coding region of P711P was prepared by PCR using
the primers of SEQ ID NO: 844 and 845. The PCR product was digested with EcoRI
restriction enzyme, gel purified and cloned into a modified pET28 vector with a His tag
5   in frame, which had been digested with Eco72I and EcoRI restriction enzymes. The
correct construct was confirmed by DNA sequence analysis and then transformed into
E. coli BL21 (DE3) pLys S and BL21 (DE3) CodonPlus expression host cells. The
determined amino acid and cDNA sequences for the expressed recombinant P711P are
provided in SEQ ID NO: 846 and 847, respectively.

10

K)   Expression of P767P in *E. coli*

The full-length coding region of P767P (amino acids 2-374 of SEQ ID
NO: 590) was amplified by PCR using the primers PDM-468 and PDM-469 (SEQ ID
NO: 935 and 936, respectively). DNA amplification was performed using 10 µl 10X
15   Pfu buffer, 1 µl 10 mM dNTPs, 2 µl each of the PCR primers at 10 µM concentration,
83 µl water, 1.5 µl Pfu DNA polymerase (Stratagene, La Jolla, CA) and 1 µl DNA at
100 ng/µl. Denaturation at 96°C was performed for 2 min, followed by 40 cycles of
96°C for 20 sec, 66°C for 15 sec and by 72°C for 2 min., and lastly by 1 cycle of 72°C
for 4 min. The PCR product was digested with XhoI and cloned into a modified pET28
20   vector with a histidine tag in frame on the 5' end that was digested with Eco72I and
XhoI. The construct was confirmed to be correct through sequence analysis and
transformed into *E. coli* BL21 pLysS and BL21 CodonPlus RP cells. The cDNA coding
region for the recombinant B767P protein is provided in SEQ ID NO: 938, with the
corresponding amino acid sequence being provided in SEQ ID NO: 941. The full-
25   length P767P did not express at high enough levels for detection or purification.

A truncated coding region of P767P (referred to as B767P-B; amino
acids 47-374 of SEQ ID NO: 590) was amplified by PCR using the primers PDM-573
and PDM-469 (SEQ ID NO: 937 and 936, respectively) and the PCR conditions
described above for full-length P767P. The PCR product was digested with XhoI and
30   cloned into the modified pET28 vector that was digested with Eco72I and XhoI. The

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construct was confirmed to be correct through sequence analysis and transformed into
E. coli BL21 pLysS and BL21 CodonPlus RP cells. The protein was found to be
expressed in the inclusion body pellet. The coding region for the expressed B767P-B
protein is provided in SEQ ID NO: 939, with the corresponding amino acid sequence
5   being provided in SEQ ID NO: 940.

EXAMPLE 18

PREPARATION AND CHARACTERIZATION OF ANTIBODIES
AGAINST PROSTATE-SPECIFIC POLYPEPTIDES

10

a)   Preparation and Characterization of Polyclonal Antibodies against P703P,
P504S and P509S

Polyclonal antibodies against P703P, P504S and P509S were prepared as
follows.

15   Each prostate tumor antigen expressed in an *E. coli* recombinant
expression system was grown overnight in LB broth with the appropriate antibiotics at
37°C in a shaking incubator. The next morning, 10 ml of the overnight culture was
added to 500 ml to 2x YT plus appropriate antibiotics in a 2L-baffled Erlenmeyer flask.
When the Optical Density (at 560 nm) of the culture reached 0.4-0.6, the cells were
20   induced with IPTG (1 mM). Four hours after induction with IPTG, the cells were
harvested by centrifugation. The cells were then washed with phosphate buffered saline
and centrifuged again. The supernatant was discarded and the cells were either frozen
for future use or immediately processed. Twenty ml of lysis buffer was added to the
cell pellets and vortexed. To break open the *E. coli* cells, this mixture was then run
25   through the French Press at a pressure of 16,000 psi. The cells were then centrifuged
again and the supernatant and pellet were checked by SDS-PAGE for the partitioning of
the recombinant protein. For proteins that localized to the cell pellet, the pellet was
resuspended in 10 mM Tris pH 8.0, 1% CHAPS and the inclusion body pellet was
washed and centrifuged again. This procedure was repeated twice more. The washed

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inclusion body pellet was solubilized with either 8 M urea or 6 M guanidine HCl containing 10 mM Tris pH 8.0 plus 10 mM imidazole. The solubilized protein was added to 5 ml of nickel-chelate resin (Qiagen) and incubated for 45 min to 1 hour at room temperature with continuous agitation. After incubation, the resin and protein

5   mixture were poured through a disposable column and the flow through was collected. The column was then washed with 10-20 column volumes of the solubilization buffer. The antigen was then eluted from the column using 8M urea, 10 mM Tris pH 8.0 and 300 mM imidazole and collected in 3 ml fractions. A SDS-PAGE gel was run to determine which fractions to pool for further purification.

10   As a final purification step, a strong anion exchange resin such as HiPrepQ (Biorad) was equilibrated with the appropriate buffer and the pooled fractions from above were loaded onto the column. Each antigen was eluted off the column with a increasing salt gradient. Fractions were collected as the column was run and another SDS-PAGE gel was run to determine which fractions from the column to pool. The

15   pooled fractions were dialyzed against 10 mM Tris pH 8.0. The proteins were then vialed after filtration through a 0.22 micron filter and the antigens were frozen until needed for immunization.

Four hundred micrograms of each prostate antigen was combined with 100 micrograms of muramyldipeptide (MDP). Every four weeks rabbits were boosted

20   · with 100 micrograms mixed with an equal volume of Incomplete Freund's Adjuvant (IFA). Seven days following each boost, the animal was bled. Sera was generated by incubating the blood at 4°C for 12-4 hours followed by centrifugation.

Ninety-six well plates were coated with antigen by incubating with 50 microliters (typically 1 microgram) of recombinant protein at 4 °C for 20 hours. 250

25   microliters of BSA blocking buffer was added to the wells and incubated at room temperature for 2 hours. Plates were washed 6 times with PBS/0.01% Tween. Rabbit sera was diluted in PBS. Fifty microliters of diluted sera was added to each well and incubated at room temperature for 30 min. Plates were washed as described above before 50 microliters of goat anti-rabbit horse radish peroxidase (HRP) at a 1:10000

30   dilution was added and incubated at room temperature for 30 min. Plates were again

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washed as described above and 100 microliters of TMB microwell peroxidase substrate was added to each well. Following a 15 min incubation in the dark at room temperature, the colorimetric reaction was stopped with 100 microliters of 1N H_2SO_4 and read immediately at 450 nm. All polyclonal antibodies showed immunoreactivity
5   to the appropriate antigen.

b)   Preparation and Characterization of Antibodies against P501S

A murine monoclonal antibody directed against the carboxy-terminus of the prostate-specific antigen P501S was prepared as follows.

A truncated fragment of P501S (amino acids 355-526 of SEQ ID NO:
10   113) was generated and cloned into the pET28b vector (Novagen) and expressed in *E. coli* as a thioredoxin fusion protein with a histidine tag. The trx-P501S fusion protein was purified by nickel chromatography, digested with thrombin to remove the trx fragment and further purified by an acid precipitation procedure followed by reverse phase HPLC.

15   Mice were immunized with truncated P501S protein. Serum bleeds from mice that potentially contained anti-P501S polyclonal sera were tested for P501S-specific reactivity using ELISA assays with purified P501S and trx-P501S proteins. Serum bleeds that appeared to react specifically with P501S were then screened for P501S reactivity by Western analysis. Mice that contained a P501S-specific antibody
20   component were sacrificed and spleen cells were used to generate anti-P501S antibody producing hybridomas using standard techniques. Hybridoma supernatants were tested for P501S-specific reactivity initially by ELISA, and subsequently by FACS analysis of reactivity with P501S transduced cells. Based on these results, a monoclonal hybridoma referred to as 10E3 was chosen for further subcloning. A number of subclones were
25   generated, tested for specific reactivity to P501S using ELISA and typed for IgG isotype. The results of this analysis are shown below in Table V. Of the 16 subclones tested, the monoclonal antibody 10E3-G4-D3 was selected for further study.

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Table V

Isotype analysis of murine anti-P501S monoclonal antibodies

Hybridoma clone	Isotype	Estimated [Ig] in supernatant (μg/ml)
4D11	IgG1	14.6
1G1	IgG1	0.6
4F6	IgG1	72
4H5	IgG1	13.8
4H5-E12	IgG1	10.7
4H5-EH2	IgG1	9.2
4H5-H2-A10	IgG1	10
4H5-H2-A3	IgG1	12.8
4H5-H2-A10-G6	IgG1	13.6
4H5-H2-B11	IgG1	12.3
10E3	IgG2a	3.4
10E3-D4	IgG2a	3.8
10E3-D4-G3	IgG2a	9.5
10E3-D4-G6	IgG2a	10.4
10E3-E7	IgG2a	6.5
8H12	IgG2a	0.6

The specificity of 10E3-G4-D3 for P501S was examined by FACS analysis. Specifically, cells were fixed (2% formaldehyde, 10 minutes), permeabilized (0.1% saponin, 10 minutes) and stained with 10E3-G4-D3 at 0.5 – 1 μg/ml, followed by incubation with a secondary, FITC-conjugated goat anti-mouse Ig antibody (Pharmingen, San Diego, CA). Cells were then analyzed for FITC fluorescence using an Excalibur fluorescence activated cell sorter. For FACS analysis of transduced cells, B-LCL were retrovirally transduced with P501S. For analysis of infected cells, B-LCL were infected with a vaccinia vector that expresses P501S. To demonstrate specificity in these assays, B-LCL transduced with a different antigen (P703P) and uninfected B-LCL vectors were utilized. 10E3-G4-D3 was shown to bind with P501S-transduced B-LCL and also with P501S-infected B-LCL, but not with either uninfected cells or P703P-transduced cells.

To determine whether the epitope recognized by 10E3-G4-D3 was found on the surface or in an intracellular compartment of cells, B-LCL were transduced with P501S or HLA-B8 as a control antigen and either fixed and permeabilized as described

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above or directly stained with 10E3-G4-D3 and analyzed as above. Specific recognition of P501S by 10E3-G4-D3 was found to require permeabilization, suggesting that the epitope recognized by this antibody is intracellular.

5   The reactivity of 10E3-G4-D3 with the three prostate tumor cell lines Lncap, PC-3 and DU-145, which are known to express high, medium and very low levels of P501S, respectively, was examined by permeabilizing the cells and treating them as described above. Higher reactivity of 10E3-G4-D3 was seen with Lncap than with PC-3, which in turn showed higher reactivity that DU-145. These results are in agreement with the real time PCR and demonstrate that the antibody specifically 10   recognizes P501S in these tumor cell lines and that the epitope recognized in prostate tumor cell lines is also intracellular.

Specificity of 10E3-G4-D3 for P501S was also demonstrated by Western blot analysis. Lysates from the prostate tumor cell lines Lncap, DU-145 and PC-3, from P501S-transiently transfected HEK293 cells, and from non-transfected HEK293 cells 15   were generated. Western blot analysis of these lysates with 10E3-G4-D3 revealed a 46 kDa immunoreactive band in Lncap, PC-3 and P501S-transfected HEK cells, but not in DU-145 cells or non-transfected HEK293 cells. P501S mRNA expression is consistent with these results since semi-quantitative PCR analysis revealed that P501S mRNA is expressed in Lncap, to a lesser but detectable level in PC-3 and not at all in DU-145 20   cells. Bacterially expressed and purified recombinant P501S (referred to as P501SStr2) was recognized by 10E3-G4-D3 (24 kDa), as was full-length P501S that was transiently expressed in HEK293 cells using either the expression vector VR1012 or pCEP4. Although the predicted molecular weight of P501S is 60.5 kDa, both transfected and "native" P501S run at a slightly lower mobility due to its hydrophobic nature.

25   Immunohistochemical analysis was performed on prostate tumor and a panel of normal tissue sections (prostate, adrenal, breast, cervix, colon, duodenum, gall bladder, ileum, kidney, ovary, pancreas, parotid gland, skeletal muscle, spleen and testis). Tissue samples were fixed in formalin solution for 24 hours and embedded in paraffin before being sliced into 10 micron sections. Tissue sections were 30   permeabilized and incubated with 10E3-G4-D3 antibody for 1 hr. HRP-labeled anti-

mouse followed by incubation with DAB chromogen was used to visualize P501S immunoreactivity. P501S was found to be highly expressed in both normal prostate and prostate tumor tissue but was not detected in any of the other tissues tested.

To identify the epitope recognized by 10E3-G4-D3, an epitope mapping approach was pursued. A series of 13 overlapping 20-21 mers (5 amino acid overlap; SEQ ID NO: 489-501) was synthesized that spanned the fragment of P501S used to generate 10E3-G4-D3. Flat bottom 96 well microtiter plates were coated with either the peptides or the P501S fragment used to immunize mice, at 1 microgram/ml for 2 hours at 37 °C. Wells were then aspirated and blocked with phosphate buffered saline containing 1% (w/v) BSA for 2 hours at room temperature, and subsequently washed in PBS containing 0.1% Tween 20 (PBST). Purified antibody 10E3-G4-D3 was added at 2 fold dilutions (1000 ng – 16 ng) in PBST and incubated for 30 minutes at room temperature. This was followed by washing 6 times with PBST and subsequently incubating with HRP-conjugated donkey anti-mouse IgG (H+L)Affinipure F(ab') fragment (Jackson Immunoresearch, West Grove, PA) at 1:20000 for 30 minutes. Plates were then washed and incubated for 15 minutes in tetramethyl benzidine. Reactions were stopped by the addition of 1N sulfuric acid and plates were read at 450 nm using an ELISA plate reader. As shown in Fig. 8, reactivity was seen with the peptide of SEQ ID NO: 496 (corresponding to amino acids 439-459 of P501S) and with the P501S fragment but not with the remaining peptides, demonstrating that the epitope recognized by 10E3-G4-D3 is localized to amino acids 439-459 of SEQ ID NO: 113.

In order to further evaluate the tissue specificity of P501S, multi-array immunohistochemical analysis was performed on approximately 4700 different human tissues encompassing all the major normal organs as well as neoplasias derived from these tissues. Sixty-five of these human tissue samples were of prostate origin. Tissue sections 0.6 mm in diameter were formalin-fixed and paraffin embedded. Samples were pretreated with HIER using 10 mM citrate buffer pH 6.0 and boiling for 10 min. Sections were stained with 10E3-G4-D3 and P501S immunoreactivity was visualized with HRP. All the 65 prostate tissues samples (5 normal, 55 untreated prostate tumors,

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5 hormone refractory prostate tumors) were positive, showing distinct perinuclear staining. All other tissues examined were negative for P501S expression.

c)   Preparation and Characterization of Antibodies against P503S

5   A fragment of P503S (amino acids 113-241 of SEQ ID NO: 114) was expressed and purified from bacteria essentially as described above for P501S and used to immunize both rabbits and mice. Mouse monoclonal antibodies were isolated using standard hybridoma technology as described above. Rabbit monoclonal antibodies were isolated using Selected Lymphocyte Antibody Method (SLAM) technology at

10 Immgenics Pharmaceuticals (Vancouver, BC, Canada). Table VI, below, lists the monoclonal antibodies that were developed against P503S.

Table VI

Antibody	Species
20D4	Rabbit
JA1	Rabbit
1A4·	Mouse
1C3	Mouse
1C9	Mouse
1D12	Mouse
2A11	Mouse
2H9	Mouse
4H7	Mouse
8A8	Mouse
8D10	Mouse
9C12	Mouse
6D12	Mouse

15

           The DNA sequences encoding the complementarity determining regions (CDRs) for the rabbit monoclonal antibodies 20D4 and JA1 were determined and are provided in SEQ ID NO: 502 and 503, respectively.

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In order to better define the epitope binding region of each of the antibodies, a series of overlapping peptides were generated that span amino acids 109-213 of SEQ ID NO: 114. These peptides were used to epitope map the anti-P503S monoclonal antibodies by ELISA as follows. The recombinant fragment of P503S that

5   was employed as the immunogen was used as a positive control. Ninety-six well microtiter plates were coated with either peptide or recombinant antigen at 20 ng/well overnight at 4 °C. Plates were aspirated and blocked with phosphate buffered saline containing 1% (w/v) BSA for 2 hours at room temperature then washed in PBS containing 0.1% Tween 20 (PBST). Purified rabbit monoclonal antibodies diluted in

10   PBST were added to the wells and incubated for 30 min at room temperature. This was followed by washing 6 times with PBST and incubation with Protein-A HRP conjugate at a 1:2000 dilution for a further 30 min. Plates were washed six times in PBST and incubated with tetramethylbenzidine (TMB) substrate for a further 15 min. The reaction was stopped by the addition of 1N sulfuric acid and plates were read at 450 nm using at

15   ELISA plate reader. ELISA with the mouse monoclonal antibodies was performed with supernatants from tissue culture run neat in the assay.

All of the antibodies bound to the recombinant P503S fragment, with the exception of the negative control SP2 supernatant. 20D4, JA1 and 1D12 bound strictly to peptide #2101 (SEQ ID NO: 504), which corresponds to amino acids 151-169 of

20   SEQ ID NO: 114. 1C3 bound to peptide #2102 (SEQ ID NO: 505), which corresponds to amino acids 165-184 of SEQ ID NO: 114. 9C12 bound to peptide #2099 (SEQ ID NO: 522), which corresponds to amino acids 120-139 of SEQ ID NO: 114. The other antibodies bind to regions that were not examined in these studies.

Subsequent to epitope mapping, the antibodies were tested by FACS

25   analysis on a cell line that stably expressed P503S to confirm that the antibodies bind to cell surface epitopes. Cells stably transfected with a control plasmid were employed as a negative control. Cells were stained live with no fixative. 0.5 ug of anti-P503S monoclonal antibody was added and cells were incubated on ice for 30 min before being washed twice and incubated with a FITC-labelled goat anti-rabbit or mouse secondary

30   antibody for 20 min. After being washed twice, cells were analyzed with an Excalibur

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fluorescent activated cell sorter. The monoclonal antibodies 1C3, 1D12, 9C12, 20D4 and JA1, but not 8D3, were found to bind to a cell surface epitope of P503S.

In order to determine which tissues express P503S, immunohistochemical analysis was performed, essentially as described above, on a
5   panel of normal tissues (prostate, adrenal, breast, cervix, colon, duodenum, gall bladder, ileum, kidney, ovary, pancreas, parotid gland, skeletal muscle, spleen and testis). HRP-labeled anti-mouse or anti-rabbit antibody followed by incubation with TMB was used to visualize P503S immunoreactivity. P503S was found to be highly expressed in prostate tissue, with lower levels of expression being observed in cervix, colon, ileum
10   and kidney, and no expression being observed in adrenal, breast, duodenum, gall bladder, ovary, pancreas, parotid gland, skeletal muscle, spleen and testis.

Western blot analysis was used to characterize anti-P503S monoclonal antibody specificity. SDS-PAGE was performed on recombinant (rec) P503S expressed in and purified from bacteria and on lysates from HEK293 cells transfected with full
15   length P503S. Protein was transferred to nitrocellulose and then Western blotted with each of the anti-P503S monoclonal antibodies (20D4, JA1, 1D12, 6D12 and 9C12) at an antibody concentration of 1 ug/ml. Protein was detected using horse radish peroxidase (HRP) conjugated to either a goat anti-mouse monoclonal antibody or to protein A-sepharose. The monoclonal antibody 20D4 detected the appropriate
20   molecular weight 14 kDa recombinant P503S (amino acids 113-241) and the 23.5 kDa species in the HEK293 cell lysates transfected with full length P503S. Other anti-P503S monoclonal antibodies displayed similar specificity by Western blot.

d)   Preparation and Characterization of Antibodies against P703P

Rabbits were immunized with either a truncated (P703Ptr1; SEQ ID NO:
25   172) or full-length mature form (P703Pfl; SEQ ID NO: 523) of recombinant P703P protein was expressed in and purified from bacteria as described above. Affinity purified polyclonal antibody was generated using immunogen P703Pfl or P703Ptr1 attached to a solid support. Rabbit monoclonal antibodies were isolated using SLAM

technology at Immgenics Pharmaceuticals. Table VII below lists both the polyclonal
and monoclonal antibodies that were generated against P703P.

Table VII

5

Antibody	Immunogen	Species/type
Aff. Purif. P703P (truncated); #2594	P703Ptrl	Rabbit polyclonal
Aff. Purif. P703P (full length); #9245	P703Pfl	Rabbit polyclonal
2D4	P703Ptrl	Rabbit monoclonal
8H2	P703Ptrl	Rabbit monoclonal
7H8	P703Ptrl	Rabbit monoclonal

The DNA sequences encoding the complementarity determining regions
(CDRs) for the rabbit monoclonal antibodies 8H2, 7H8 and 2D4 were determined and
are provided in SEQ ID NO: 506-508, respectively.

10   Epitope mapping studies were performed as described above.
Monoclonal antibodies 2D4 and 7H8 were found to specifically bind to the peptides of
SEQ ID NO: 509 (corresponding to amino acids 145-159 of SEQ ID NO: 172) and SEQ
ID NO: 510 (corresponding to amino acids 11-25 of SEQ ID NO: 172), respectively.
The polyclonal antibody 2594 was found to bind to the peptides of SEQ ID NO: 511-

15   514, with the polyclonal antibody 9427 binding to the peptides of SEQ ID NO: 515-517.

The specificity of the anti-P703P antibodies was determined by Western
blot analysis as follows. SDS-PAGE was performed on (1) bacterially expressed
recombinant antigen; (2) lysates of HEK293 cells and Ltk-/- cells either untransfected or
transfected with a plasmid expressing full length P703P; and (3) supernatant isolated

20   from these cell cultures. Protein was transferred to nitrocellulose and then Western
blotted using the anti-P703P polyclonal antibody #2594 at an antibody concentration of
1 ug/ml. Protein was detected using horse radish peroxidase (HRP) conjugated to an
anti-rabbit antibody. A 35 kDa immunoreactive band could be observed with
recombinant P703P. Recombinant P703P runs at a slightly higher molecular weight

25   since it is epitope tagged. In lysates and supernatants from cells transfected with full
length P703P, a 30 kDa band corresponding to P703P was observed. To assure

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specificity, lysates from HEK293 cells stably transfected with a control plasmid were
also tested and were negative for P703P expression. Other anti-P703P antibodies
showed similar results.

     Immunohistochemical studies were performed as described above, using
5 anti-P703P monoclonal antibody. P703P was found to be expressed at high levels in
normal prostate and prostate tumor tissue but was not detectable in all other tissues
tested (breast tumor, lung tumor and normal kidney).

     e)   Preparation and Characterization of Antibodies against P504S

     Full-length P504S (SEQ ID NO: 108) was expressed and purified from
10 bacteria essentially as described above for P501S and employed to raise rabbit
monoclonal antibodies using Selected Lymphocyte Antibody Method (SLAM)
technology at Immgenics Pharmaceuticals (Vancouver, BC, Canada). The anti-P504S
monoclonal antibody 13H4 was shown by Western blot to bind to both expressed
recombinant P504S and to native P504S in tumor cells.

15   Immunohistochemical studies using 13H4 to assess P504S expression in
various prostate tissues were performed as described above. A total of 104 cases,
including 65 cases of radical prostatectomies with prostate cancer (PC), 26 cases of
prostate biopsies and 13 cases of benign prostate hyperplasia (BPH), were stained with
the anti-P504S monoclonal antibody 13H4. P504S showed strongly cytoplasmic
20 granular staining in 64/65 (98.5%) of PCs in prostatectomies and 26/26 (100%) of PCs
in prostatic biopsies. P504S was stained strongly and diffusely in carcinomas (4+ in
91.2% of cases of PC; 3+ in 5.5%; 2+ in 2.2% and 1+ in 1.1%) and high grade prostatic
intraepithelial neoplasia (4+ in all cases). The expression of P504S did not vary with
Gleason score. Only 17/91 (18.7%) of cases of NP/BPH around PC and 2/13 (15.4%) of
25 BPH cases were focally (1+, no 2+ to 4+ in all cases) and weakly positive for P504S in
large glands. Expression of P504S was not found in small atrophic glands, postatrophic
hyperplasia, basal cell hyperplasia and transitional cell metaplasia in either biopsies or
prostatectomies. P504S was thus found to be over-expressed in all Gleason scores of
prostate cancer (98.5 to 100% of sensitivity) and exhibited only focal positivities in

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large normal glands in 19/104 of cases (82.3% of specificity). These findings indicate
that P504S may be usefully employed for the diagnosis of prostate cancer.

EXAMPLE 19

5   CHARACTERIZATION OF CELL SURFACE EXPRESSION AND
        CHROMOSOME LOCALIZATION OF THE PROSTATE-SPECIFIC ANTIGEN P501S

        This example describes studies demonstrating that the prostate-specific
antigen P501S is expressed on the surface of cells, together with studies to determine
10   the probable chromosomal location of P501S.
        The protein P501S (SEQ ID NO: 113) is predicted to have 11
transmembrane domains. Based on the discovery that the epitope recognized by the anti-
P501S monoclonal antibody 10E3-G4-D3 (described above in Example 17) is
intracellular, it was predicted that following transmembrane determinants would allow
15   the prediction of extracellular domains of P501S. Fig. 9 is a schematic representation
of the P501S protein showing the predicted location of the transmembrane domains and
the intracellular epitope described in Example 17. Underlined sequence represents the
predicted transmembrane domains, bold sequence represents the predicted extracellular
domains, and italicized sequence represents the predicted intracellular domains.
20   Sequence that is both bold and underlined represents sequence employed to generate
polyclonal rabbit serum.   The location of the transmembrane domains was predicted
using HHMTOP as described by Tusnady and Simon (Principles Governing Amino
Acid Composition of Integral Membrane Proteins: Applications to Topology Prediction,
J. Mol. Biol. 283:489-506, 1998).
25   Based on Fig. 9, the P501S domain flanked by the transmembrane
domains corresponding to amino acids 274-295 and 323-342 is predicted to be
extracellular. The peptide of SEQ ID NO: 518 corresponds to amino acids 306-320 of
P501S and lies in the predicted extracellular domain. The peptide of SEQ ID NO: 519,
which is identical to the peptide of SEQ ID NO: 518 with the exception of the
30   substitution of the histidine with an asparginine, was synthesized as described above. A

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Cys-Gly was added to the C-terminus of the peptide to facilitate conjugation to the carrier protein. Cleavage of the peptide from the solid support was carried out using the following cleavage mixture: trifluoroacetic acid:ethanediol:thioanisol:water:phenol (40:1:2:2:3). After cleaving for two hours, the peptide was precipitated in cold ether. The peptide pellet was then dissolved in 10% v/v acetic acid and lyophilized prior to purification by C18 reverse phase hplc. A gradient of 5-60% acetonitrile (containing 0.05% TFA) in water (containing 0.05% TFA) was used to elute the peptide. The purity of the peptide was verified by hplc and mass spectrometry, and was determined to be >95%. The purified peptide was used to generate rabbit polyclonal antisera as described above.

Surface expression of P501S was examined by FACS analysis. Cells were stained with the polyclonal anti-P501S peptide serum at 10 µg/ml, washed, incubated with a secondary FITC-conjugated goat anti-rabbit Ig antibody (ICN), washed and analyzed for FITC fluorescence using an Excalibur fluorescence activated cell sorter. For FACS analysis of transduced cells, B-LCL were retrovirally transduced with P501S. To demonstrate specificity in these assays, B-LCL transduced with an irrelevant antigen (P703P) or nontransduced were stained in parallel. For FACS analysis of prostate tumor cell lines, Lncap, PC-3 and DU-145 were utilized. Prostate tumor cell lines were dissociated from tissue culture plates using cell dissociation medium and stained as above. All samples were treated with propidium iodide (PI) prior to FACS analysis, and data was obtained from PI-excluding (i.e., intact and non-permeabilized) cells. The rabbit polyclonal serum generated against the peptide of SEQ ID NO: 519 was shown to specifically recognize the surface of cells transduced to express P501S, demonstrating that the epitope recognized by the polyclonal serum is extracellular.

To determine biochemically if P501S is expressed on the cell surface, peripheral membranes from Lncap cells were isolated and subjected to Western blot analysis. Specifically, Lncap cells were lysed using a dounce homogenizer in 5 ml of homogenization buffer (250 mM sucrose, 10 mM HEPES, 1mM EDTA, pH 8.0, 1 complete protease inhibitor tablet (Boehringer Mannheim)). Lysate samples were spun at 1000 g for 5 min at 4 °C. The supernatant was then spun at 8000g for 10 min at 4 °C.

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Supernatant from the 8000g spin was recovered and subjected to a 100,000g spin for 30
min at 4 °C to recover peripheral membrane. Samples were then separated by SDS-
PAGE and Western blotted with the mouse monoclonal antibody 10E3-G4-D3
(described above in Example 17) using conditions described above. Recombinant
5   purified P501S, as well as HEK293 cells transfected with and over-expressing P501S
were included as positive controls for P501S detection. LCL cell lysate was included as
a negative control. P501S could be detected in Lncap total cell lysate, the 8000g
(internal membrane) fraction and also in the 100,000g (plasma membrane) fraction.
These results indicate that P501S is expressed at, and localizes to, the peripheral
10   membrane.

To demonstrate that the rabbit polyclonal antiserum generated to the
peptide of SEQ ID NO: 519 specifically recognizes this peptide as well as the
corresponding native peptide of SEQ ID NO: 518, ELISA analyses were performed.
For these analyses, flat-bottomed 96 well microtiter plates were coated with either the
15   peptide of SEQ ID NO: 519, the longer peptide of SEQ ID NO: 520 that spans the entire
predicted extracellular domain, the peptide of SEQ ID NO: 521 which represents the
epitope recognized by the P501S-specific antibody 10E3-G4-D3, or a P501S fragment
(corresponding to amino acids 355-526 of SEQ ID NO: 113) that does not include the
immunizing peptide sequence, at 1 μg/ml for 2 hours at 37 °C. Wells were aspirated,
20   blocked with phosphate buffered saline containing 1% (w/v) BSA for 2 hours at room
temperature and subsequently washed in PBS containing 0.1% Tween 20 (PBST).
Purified anti-P501S polyclonal rabbit serum was added at 2 fold dilutions (1000 ng -
125 ng) in PBST and incubated for 30 min at room temperature. This was followed by
washing 6 times with PBST and incubating with HRP-conjugated goat anti-rabbit IgG
25   (H+L) Affinipure F(ab') fragment at 1:20000 for 30 min. Plates were then washed and
incubated for 15 min in tetramethyl benzidine. Reactions were stopped by the addition
of 1N sulfuric acid and plates were read at 450 nm using an ELISA plate reader. As
shown in Fig. 11, the anti-P501S polyclonal rabbit serum specifically recognized the
peptide of SEQ ID NO: 519 used in the immunization as well as the longer peptide of

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SEQ ID NO: 520, but did not recognize the irrelevant P501S-derived peptides and fragments.

In further studies, rabbits were immunized with peptides derived from the P501S sequence and predicted to be either extracellular or intracellular, as shown in Fig. 9. Polyclonal rabbit sera were isolated and polyclonal antibodies in the serum were purified, as described above. To determine specific reactivity with P501S, FACS analysis was employed, utilizing either B-LCL transduced with P501S or the irrelevant antigen P703P, of B-LCL infected with vaccinia virus-expressing P501S. For surface expression, dead and non-intact cells were excluded from the analysis as described above. For intracellular staining, cells were fixed and permeabilized as described above. Rabbit polyclonal serum generated against the peptide of SEQ ID NO: 548, which corresponds to amino acids 181-198 of P501S, was found to recognize a surface epitope of P501S. Rabbit polyclonal serum generated against the peptide SEQ ID NO: 551, which corresponds to amino acids 543-553 of P501S, was found to recognize an epitope that was either potentially extracellular or intracellular since in different experiments intact or permeabilized cells were recognized by the polyclonal sera. Based on similar deductive reasoning, the sequences of SEQ ID NO: 541-547, 549 and 550, which correspond to amino acids 109-122, 539-553, 509-520, 37-54, 342-359, 295-323, 217-274, 143-160 and 75-88, respectively, of P501S, can be considered to be potential surface epitopes of P501S recognized by antibodies.

In further studies, mouse monoclonal antibodies were raised against amino acids 296 to 322 to P501S, which are predicted to be in an extracellular domain. A/J mice were immunized with P501S/adenovirus, followed by subsequent boosts with an *E. coli* recombinant protein, referred to as P501N, that contains amino acids 296 to 322 of P501S, and with peptide 296-322 (SEQ ID NO: 898) coupled with KLH. The mice were subsequently used for splenic B cell fusions to generate anti-peptide hybridomas. The resulting 3 clones, referred to as 4F4 (IgG1,kappa), 4G5 (IgG2a,kappa) and 9B9 (IgG1,kappa), were grown for antibody production. The 4G5 mAb was purified by passing the supernatant over a Protein A-sepharose column,

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followed by antibody elution using 0.2M glycine, pH 2.3. Purified antibody was neutralized by the addition of 1M Tris, pH 8, and buffer exchanged into PBS.

For ELISA analysis, 96 well plates were coated with P501S peptide 296-322 (referred to as P501-long), an irrelevant P775 peptide, P501S-N, P501TR2, P501S-

5   long-KLH, P501S peptide 306-319 (referred to as P501-short)-KLH, or the irrelevant peptide 2073-KLH, all at a concentration of 2 ug/ml and allowed to incubate for 60 minutes at 37 °C. After coating, plates were washed 5X with PBS + 0.1% Tween and then blocked with PBS, 0.5% BSA, 0.4% Tween20 for 2 hours at room temperature. Following the addition of supernatants or purified mAb, the plates were incubated for

10   60 minutes at room temperature. Plates were washed as above and donkey anti-mouse IgHRP-linked secondary antibody was added and incubated for 30 minutes at room temperature, followed by a final washing as above. TMB peroxidase substrate was added and incubated 15 minutes at room temperature in the dark. The reaction was stopped by the addition of 1N H_2SO_4 and the OD was read at 450 nM. All three hybrid

15   clones secreted mAb that recognized peptide 296-322 and the recombinant protein P501N.

For FACS analysis, HEK293 cells were transiently transfected with a P501S/VR1012 expression constructs using Fugene 6 reagent. After 2 days of culture, cells were harvested and washed, then incubated with purified 4G5 mAb for 30 minutes

20   on ice. After several washes in PBS, 0.5% BSA, 0.01% azide, goat anti-mouse Ig-FITC was added to the cells and incubated for 30 minutes on ice. Cells were washed and resuspended in wash buffer including 1% propidium iodide and subjected to FACS analysis. The FACS analysis confirmed that amino acids 296-322 of P501S are in an extracellular domain and are cell surface expressed.

25   The chromosomal location of P501S was determined using the GeneBridge 4 Radiation Hybrid panel (Research Genetics). The PCR primers of SEQ ID NO: 528 and 529 were employed in PCR with DNA pools from the hybrid panel according to the manufacturer's directions. After 38 cycles of amplification, the reaction products were separated on a 1.2% agarose gel, and the results were analyzed

30   through the Whitehead Institute/MIT Center for Genome Research web server

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(http://www-genome.wi.mit.edu/cgi-bin/contig/rhmapper.pl) to determine the probable chromosomal location. Using this approach, P501S was mapped to the long arm of chromosome 1 at WI-9641 between q32 and q42. This region of chromosome 1 has been linked to prostate cancer susceptibility in hereditary prostate cancer (Smith *et al.*

5   *Science 274*:1371-1374, 1996 and Berthon *et al. Am. J. Hum. Genet. 62*:1416-1424, 1998). These results suggest that P501S may play a role in prostate cancer malignancy.

EXAMPLE 20

REGULATION OF EXPRESSION OF THE PROSTATE-SPECIFIC ANTIGEN P501S

10

Steroid (androgen) hormone modulation is a common treatment modality in prostate cancer. The expression of a number of prostate tissue-specific antigens have previously been demonstrated to respond to androgen. The responsiveness of the prostate-specific antigen P501S to androgen treatment was examined in a tissue culture

15   system as follows.

Cells from the prostate tumor cell line LNCaP were plated at 1.5 x 10^6 cells/T75 flask (for RNA isolation) or 3 x 10^5 cells/well of a 6-well plate (for FACS analysis) and grown overnight in RPMI 1640 media containing 10% charcoal-stripped fetal calf serum (BRL Life Technologies, Gaithersburg, MD). Cell culture was

20   continued for an additional 72 hours in RPMI 1640 media containing 10% charcoal-stripped fetal calf serum, with 1 nM of the synthetic androgen Methyltrienolone (R1881; New England Nuclear) added at various time points. Cells were then harvested for RNA isolation and FACS analysis at 0, 1, 2, 4, 8, 16, 24, 28 and 72-hours post androgen addition. FACS analysis was performed using the anti-P501S antibody 10E3-

25   G4-D3 and permeabilized cells.

For Northern analysis, 5-10 micrograms of total RNA was run on a formaldehyde denaturing gel, transferred to Hybond-N nylon membrane (Amersham Pharmacia Biotech, Piscataway, NJ), cross-linked and stained with methylene blue. The filter was then prehybridized with Church's Buffer (250 mM Na_2HPO_4, 70 mM H_3PO_4,

30   1 mM EDTA, 1% SDS, 1% BSA in pH 7.2) at 65 °C for 1 hour. P501S DNA was

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labeled with 32P using High Prime random-primed DNA labeling kit (Boehringer Mannheim). Unincorporated label was removed using MicroSpin S300-HR columns (Amersham Pharmacia Biotech). The RNA filter was then hybridized with fresh Church's Buffer containing labeled cDNA overnight, washed with 1X SCP (0.1 M

5   NaCl, 0.03 M $Na_2HPO_4.7H_2O$, 0.001 M Na_2EDTA), 1% sarkosyl (n-lauroylsarcosine) and exposed to X-ray film.

Using both FACS and Northern analysis, P501S message and protein levels were found in increase in response to androgen treatment.

10   ·   EXAMPLE 21

PREPARATION OF FUSION PROTEINS OF PROSTATE-SPECIFIC ANTIGENS

The example describes the preparation of a fusion protein of the prostate-specific antigen P703P and a truncated form of the known prostate antigen PSA. The

15   truncated form of PSA has a 21 amino acid deletion around the active serine site. The expression construct for the fusion protein also has a restriction site at 3' end, immediately prior to the termination codon, to aid in adding cDNA for additional antigens.

The full-length cDNA for PSA was obtained by RT-PCR from a pool of

20   RNA from human prostate tumor tissues using the primers of SEQ ID NO: 607 and 608, and cloned in the vector pCR-Blunt II-TOPO. The resulting cDNA was employed as a template to make two different fragments of PSA by PCR with two sets of primers (SEQ ID NO: 609 and 610; and SEQ ID NO: 611 and 612). The PCR products having the expected size were used as templates to make truncated forms of PSA by PCR with

25   the primers of SEQ ID NO: 611 and 613, which generated PSA (delta 208-218 in amino acids). The cDNA for the mature form of P703P with a 6X histidine tag at the 5' end, was prepared by PCR with P703P and the primers of SEQ ID NO: 614 and 615. The cDNA for the fusion of P703P with the truncated form of PSA (referred to as FOPP) was then obtained by PCR using the modified P703P cDNA and the truncated form of

30   PSA cDNA as templates and the primers of SEQ ID NO: 614 and 615. The FOPP

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cDNA was cloned into the NdeI site and XhoI site of the expression vector pCRX1, and confirmed by DNA sequencing. The determined cDNA sequence for the fusion construct FOPP is provided in SEQ ID NO: 616, with the amino acid sequence being provided in SEQ ID NO: 617.

5   The fusion FOPP was expressed as a single recombinant protein in *E. coli* as follows. The expression plasmid pCRX1FOPP was transformed into the *E. coli* strain BL21-CodonPlus RIL. The transformant was shown to express FOPP protein upon induction with 1 mM IPTG. The culture of the corresponding expression clone was inoculated into 25 ml LB broth containing 50 ug/ml kanamycin and 34 ug/ml

10   chloramphenicol, grown at 37 °C to OD600 of about 1, and stored at 4 °C overnight. The culture was diluted into 1 liter of TB LB containing 50 ug/ml kanamycin and 34 ug/ml chloramphenicol, and grown at 37 °C to OD600 of 0.4. IPTG was added to a final concentration of 1 mM, and the culture was incubated at 30 °C for 3 hours. The cells were pelleted by centrifugation at 5,000 RPM for 8 min. To purify the protein, the

15   cell pellet was suspended in 25 ml of 10 mM Tris-Cl pH 8.0, 2mM PMSF, complete protease inhibitor and 15 ug lysozyme. The cells were lysed at 4 °C for 30 minutes, sonicated several times and the lysate centrifuged for 30 minutes at 10,000 x g. The precipitate, which contained the inclusion body, was washed twice with 10 mM Tris-Cl pH 8.0 and 1% CHAPS. The inclusion body was dissolved in 40 ml of 10 mM Tris-Cl

20   pH 8.0, 100 mM sodium phosphate and 8 M urea. The solution was bound to 8 ml Ni-NTA (Qiagen) for one hour at room temperature. The mixture was poured into a 25 ml column and washed with 50 ml of 10 mM Tris-Cl pH 6.3, 100 mM sodium phosphate, 0.5% DOC and 8M urea. The bound protein was eluted with 350 mM imidazole, 10 mM Tris-Cl pH 8.0, 100 mM sodium phosphate and 8 M urea. The fractions containing

25   FOPP proteins were combined and dialyzed extensively against 10 mM Tris-Cl pH 4.6, aliquoted and stored at - 70 °C.

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EXAMPLE 22

REAL-TIME PCR CHARACTERIZATION OF THE PROSTATE-SPECIFIC ANTIGEN P501S IN
PERIPHERAL BLOOD OF PROSTATE CANCER PATIENTS

5   Circulating epithelial cells were isolated from fresh blood of normal
individuals and metastatic prostate cancer patients, mRNA isolated and cDNA prepared
using real-time PCR procedures. Real-time PCR was performed with the Taqman^{TM}
procedure using both gene specific primers and probes to determine the levels of gene
expression.

10   Epithelial cells were enriched from blood samples using an
immunomagnetic bead separation method (Dynal A.S., Oslo, Norway). Isolated cells
were lysed and the magnetic beads removed. The lysate was then processed for poly A+
mRNA isolation using magnetic beads coated with Oligo(dT)25. After washing the
beads in buffer, bead/poly A+ RNA samples were suspended in 10 mM Tris HCl pH 8.0
15   and subjected to reversed transcription. The resulting cDNA was subjected to real-time
PCR using gene specific primers. Beta-actin content was also determined and used for
normalization. Samples with P501S copies greater than the mean of the normal
samples + 3 standard deviations were considered positive. Real time PCR on blood
samples was performed using the Taqman^{TM} procedure but extending to 50 cycles using
20   forward and reverse primers and probes specific for P501S. Of the eight samples tested,
6 were positive for P501S and β-actin signal. The remaining 2 samples had no
detectable β-actin or P501S. No P501S signal was observed in the four normal blood
samples tested.

25   EXAMPLE 23

EXPRESSION OF THE PROSTATE-SPECIFIC ANTIGENS P703P AND P501S IN
SCID MOUSE-PASSAGED PROSTATE TUMORS

          When considering the effectiveness of antigens in the treatment of
30   prostate cancer, the continued presence of the antigens in tumors during androgen

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ablation therapy is important. The presence of the prostate-specific antigens P703P and P501S in prostate tumor samples grown in SCID mice in the presence of testosterone was evaluated as follows.

Two prostate tumors that had metastasized to the bone were removed 5 from patients, implanted into SCID mice and grown in the presence of testosterone. Tumors were evaluated for mRNA expression of P703P, P501S and PSA using quantitative real time PCR with the SYBR green assay method. Expression of P703P and P501S in a prostate tumor was used as a positive control and the absence in normal intestine and normal heart as negative controls. In both cases, the specific mRNA was 10 present in late passage tumors. Since the bone metastases were grown in the presence of testosterone, this implies that the presence of these genes would not be lost during androgen ablation therapy.

EXAMPLE 24

15   ANTI-P503S MONOCLONAL ANTIBODY INHIBITS TUMOR GROWTH *IN VIVO*

The ability of the anti-P503S monoclonal antibody 20D4 to suppress tumor formation in mice was examined as follows.

Ten SCID mice were injected subcutaneously with HEK293 cells that expressed P503S. Five mice received 150 micrograms of 20D4 intravenously at day 0 20 (time of tumor cell injection), day 5 and day 9. Tumor size was measured for 50 days. Of the five animals that received no 20D4, three formed detectable tumors after about 2 weeks which continued to enlarge throughout the study. In contrast, none of the five mice that received 20D4 formed tumors. These results demonstrate that the anti-P503S Mab 20D4 displays potent anti-tumor activity *in vivo*.

25

EXAMPLE 25

CHARACTERIZATION OF A T CELL RECEPTOR CLONE FROM A
P501S-SPECIFIC T CELL CLONE

30   T cells have a limited lifespan. However, cloning of T cell receptor (TCR) chains and subsequent transfer essentially enables infinite propagation of the T

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cell specificity. Cloning of tumor-antigen TCR chains allows the transfer of the specificity into T cells isolated from patients that share the TCR MHC-restricting allele. Such T cells could then be expanded and used in adoptive transfer settings to introduce the tumor antigen specificity into patients carrying tumors that express the antigen. T

5   cell receptor alpha and beta chains from a CD8 T cell clone specific for the prostate-specific antigen P501S were isolated and sequenced as follows.

Total mRNA from 2 x 10^6 cells from CTL clone 4E5 (described above in Example 12) was isolated using Trizol reagent and cDNA was synthesized. To determine Va and Vb sequences in this clone, a panel of Va and Vb subtype-specific

10   primers was synthesized and used in RT-PCR reactions with cDNA generated from each of the clones. The RT-PCR reactions demonstrated that each of the clones expressed a common Vb sequence that corresponded to the Vb7 subfamily. Futhermore, using cDNA generated from the clone, the Va sequence expressed was determined to be Va6. To clone the full TCR alpha and beta chains from clone 4E5,

15   primers were designed that spanned the initiator and terminator-coding TCR nucleotides. The primers were as follows: TCR Valpha-6 5'(sense): GGATCC---GCCGCCACC—ATGTCACTTTCTAGCCTGCT (SEQ ID NO: 899) BamHI site Kozak TCR alpha sequence TCR alpha 3' (antisense): GTCGAC---TCAGCTGGACCACAGCCGCAG (SEQ ID NO: 900) SalI site TCR alpha constant

20   sequence TCR Vbeta-7. 5'(sense): GGATCC---GCCGCCACC--ATGGGCTGCAGGCTGCTCT (SEQ ID NO: 901) BamHI site Kozak TCR alpha sequence TCR beta 3' (antisense): GTCGAC---TCAGAAATCCTTTCTCTTGAC (SEQ ID NO: 902) SalI site TCR beta constant sequence. Standard 35 cycle RT-PCR reactions were established using cDNA synthesized from the CTL clone and the above

25   primers, employing the proofreading thermostable polymerase PWO (Roche, Nutley, NJ).

The resultant specific bands (approx. 850 bp for alpha and approx. 950 for beta) were ligated into the PCR blunt vector (Invitrogen) and transformed into *E. coli*. *E .coli* transformed with plasmids containing full-length alpha and beta chains

30   were identified, and large scale preparations of the corresponding plasmids were generated. Plasmids containing full-length TCR alpha and beta chains were submitted

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for sequencing. The sequencing reactions demonstrated the cloning of full-length TCR
alpha and beta chains with the determined cDNA sequences for the Vb and Va chains
being shown in SEQ ID NO: 903 and 904, respectively. The corresponding amino acid
sequences are shown in SEQ ID NO: 905 and 906, respectively. The Va sequence was
5   shown by nucleotide sequence alignment to be 99% identical (347/348) to Va6.2, and
the Vb to be 99% identical to Vb7 (336/338).

EXAMPLE 26

CAPTURE OF PROSTATE SPECIFIC CELLS USING
10   THE PROSTATE ANTIGEN P503S

As described above, P503S is found on the surface of prostate cells.
Secondary coated microsphere beads specific for mouse IgG were coupled with the
purified P503S-specific monoclonal antibody 1D12. The bound P503S antibody was
then used to capture HEK cells expressing recombinant P503S. This provides a model
15   system for prostate-specific cell capture which may be usefully employed in the
detection of prostate cells in blood, and therefore in the detection of prostate cancer.

P503S-transfected HEK cells were harvested and redissolved in wash
buffer (PBS, 0.1% BSA, 0.6% sodium citrate) at an appropriate volume to give at least
5^4 cells per sample. Round bottom Eppendorf tubes were used for all procedures
20   involving beads. The stock concentrations were as shown below in Table VIII.

Table VIII

Stock concentrations	Sample concentration	Amount needed
Epithelial enrich beads 4^8 beads/ml (Dynal Biotech Inc. Lake Success, NY)	1^7 beads/ml	125 ul stock per 5 ml volume
1D12 ascites antibody 2 mg/ml	0.1 ug/ml (0.1X) to 5 ug/ml (5X) titrations	0.05 ul to 2.5 ul stock per sample
α- Mamma Mu 0.9 mg/ml	1 ug/ml (1X)	1.1 ul stock per sample
Pan-mouse IgG beads 4^8 beads/ml (Dynal Biotech)	1^7 beads/ml	125 ul stock per 5 ml volume

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Blocked immunomagnetic beads were pre-washed as follows: all beads needed were pooled and washed once with 1 ml wash buffer. The beads were resuspended din a 3X volume of 1% BSA (v/v) in wash buffer and incubated for 15 min rotating at 4 °C. The beads were then washed three times with 2X volume of wash

5   buffer and resuspended to original volume. Non-blocked beads were pooled, washed three times with 2X volume of wash buffer and resuspended to original volume.

Primary antibody was incubated with secondary beads in a fresh Eppendorf for 30 minutes, rotating at 4 °C. Approximately 200 ul wash buffer was added to increase the total volume for even mixing of the sample. The antibody-bead

10   solution was transferred to a fresh Eppendorf, washed twice with an equal volume of wash buffer and resuspended to original volume. Target cells were added to each sample and incubated for 45 minutes, rotating at 4 °C. The tubes were transferred to a magnet, the supernatant removed, taking care not the agitate the beads, and the samples were washed twice with 1 ml wash buffer. The samples were then ready for RT-PCR

15   using a Dynabeads mRNA direct microkit (Dynal Biotech).

Epithelial cell enrichment was placed in a magnet and supernant was removed. The epithelial enrichment beads were then resuspendedin 100 ul lysis/binding buffer fortified with Rnasin (2 U/ul per sample), and sotred at −70 °C until use. Oligo (dT$_{25}$) Dynabeads were pre-washed as follows: all beads needed were pooled (23

20   ul/sample), washed three times with an excess volume of lysis/binding buffer, and resuspsended ot original volume. The lysis supernant was separated with a magnet and transferred to a fresh Eppendorf. 20 ul oligo(dT25) Dynabeads were added per samplem ad rolled for 5 min at room temperature. Supernant was separated using a magnet and discarded, leaving the mRNA annealed ot the beads. The bead/mRNA

25   complex was washed with buffer and resuspended in cold Tris-HCl.

For RT-PCR, the Tris-HCl supernatant was separated and discarded using MPS. For each sample containing 1^5 cells or less, the following was added to give a total volume of 30 ul: 14.25 ul H$_2$O; 1.5 ul BSA; 6 ul first strand buffer; 0.75 mL 10 mM dNTP mix; 3 ul Rnasin; 3 ul 0.1M dTT; and 1.5 ul Superscript II. The resulting

30   solution was incubated for 1 hour at 42 °C, diluted 1:5 in H2O, heated at 80°C for 2 min

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to detach cDNA from the beads, and immediately placed on MPS. The supernatant containing cDNA was transferred to a new tube and stored at –20 °C.

Table IX shows the percentage of capture of P503S-transfected HEK cells as determined by RT-PCR.

5

Table IX

	% capture P503S-transfected HEK cells	% capture LnCAP cells
0.1 ug/ml P503S Mab	36.90	0.00
0.5 ug/ml P503S Mab	67.40	2.93
1 ug/ml P503S Mab	40.22	0.00
5 ug/ml P503S Mab	13.11	0.00
Anti-Mu beads only, non-blocked	1.42	0.00
Anti-Mu beads only, blocked	15.65	20.21
Absolute control, non-capture cells	100.00	100.00

10   From the foregoing it will be appreciated that, although specific embodiments of the invention have been described herein for purposes of illustration, various modifications may be made without deviating from the spirit and scope of the invention. Accordingly, the invention is not limited except as by the appended claims.

CLAIMS

What is Claimed:

1.   An isolated polynucleotide comprising a sequence selected from
the group consisting of:

(a)   sequences provided in SEQ ID NO: 1-111, 115-171, 173-175,
177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524,
526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-705, 709-774, 777,
789, 817, 823, 824, 878, 880-882, 894, 896, 907, 908, 916-919, 929-931, 938, 939 and
942;

(b)   complements of the sequences provided in SEQ ID NO: 1-111,
115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382
and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-
705, 709-774, 777, 789, 817, 823, 824, 878, 880-882, 894, 896, 907, 908, 916-919, 929-
931, 938, 939 and 942;

(c)   sequences consisting of at least 20 contiguous residues of a
sequence provided in SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315,
326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535,
536, 552, 569-572, 587, 591, 593-606, 618-705, 709-774, 777, 789, 817, 823, 824, 878,
880-882, 894, 896, 907, 908, 916-919, 929-931, 938, 939 and 942;

(d)   sequences that hybridize to a sequence provided in SEQ ID NO:
1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375,
381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-
606, 618-705, 709-774, 777, 789, 817, 823, 824, 878, 880-882, 894, 896, 907, 908, 916-
919, 929-931, 938, 939 and 942 under moderately stringent conditions;

(e)   sequences having at least 75% identity to a sequence of SEQ ID
NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-
375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591,
593-606, 618-705, 709-774, 777, 789, 817, 823, 824, 878, 880-882, 894, 896, 907, 908,
916-919, 929-931, 938, 939 and 942;

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(f)   sequences having at least 90% identity to a sequence of SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-705, 709-774, 777, 789, 817, 823, 824, 878, 880-882, 894, 896, 907, 908, 916-919, 929-931, 938, 939 and 942; and

(g)   degenerate variants of a sequence provided in SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-705, 709-774, 777, 789, 817, 823, 824, 878, 880-882, 894, 896, 907, 908, 916-919, 929-931, 938, 939 and 942.

2.   An isolated polypeptide comprising an amino acid sequence selected from the group consisting of:

(a)   sequences recited in SEQ ID NO: 112-114, 172, 176, 178, 327, 329, 331, 336, 339, 376-380, 383, 477-483, 496, 504, 505, 519, 520, 522, 525, 527, 532, 534, 537-551, 553-568, 573-586, 588-590, 592, 706-708, 775, 776, 778, 780, 781, 811, 814, 818, 826, 827, 853, 855, 858, 860-862, 866-877, 879, 883-893, 895, 897, 898, 909-915, 920-928, 932-934, 940, 941 and 943;

(b)   sequences having at least 70% identity to a sequence of SEQ ID NO: 112-114, 172, 176, 178, 327, 329, 331, 336, 339, 376-380, 383, 477-483, 496, 504, 505, 519, 520, 522, 525, 527, 532, 534, 537-551, 553-568, 573-586, 588-590, 592, 706-708, 775, 776, 778, 780, 781, 811, 814, 818, 826, 827, 853, 855, 858, 860-862, 866-877, 879, 883-893, 895, 897, 898, 909-915, 920-928, 932-934, 940, 941 and 943;

(c)   sequences having at least 90% identity to a sequence of SEQ ID NO: 112-114, 172, 176, 178, 327, 329, 331, 336, 339, 376-380, 383, 477-483, 496, 504, 505, 519, 520, 522, 525, 527, 532, 534, 537-551, 553-568, 573-586, 588-590, 592, 706-708, 775, 776, 778, 780, 781, 811, 814, 818, 826, 827, 853, 855, 858, 860-862, 866-877, 879, 883-893, 895, 897, 898, 909-915, 920-928, 932-934, 940, 941 and 943;

(d)   sequences encoded by a polynucleotide of claim 1;

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(e)   sequences having at least 70% identity to a sequence encoded by a polynucleotide of claim 1; and

(f)   sequences having at least 90% identity to a sequence encoded by a polynucleotide of claim 1.

3.   An expression vector comprising a polynucleotide of claim 1 operably linked to an expression control sequence.

4.   A host cell transformed or transfected with an expression vector according to claim 3.

5.   An isolated antibody, or antigen-binding fragment thereof, that specifically binds to a polypeptide of claim 2.

6.   A method for detecting the presence of a cancer in a patient, comprising the steps of:

(a)   obtaining a biological sample from the patient;

(b)   contacting the biological sample with a binding agent that binds to a polypeptide of claim 2;

(c)   detecting in the sample an amount of polypeptide that binds to the binding agent; and

(d)   comparing the amount of polypeptide to a predetermined cut-off value and therefrom determining the presence of a cancer in the patient.

7.   A fusion protein comprising at least one polypeptide according to claim 2.

8.   An oligonucleotide that hybridizes to a sequence recited in SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591,

593-606, 618-705, 709-774, 777, 789, 817, 823, 824, 878, 880-882, 894, 896, 907, 908, 916-919, 929-931, 938, 939 and 942 under moderately stringent conditions.

9.   A method for stimulating and/or expanding T cells specific for a tumor protein, comprising contacting T cells with at least one component selected from the group consisting of:

(a)   polypeptides according to claim 2;

(b)   polynucleotides according to claim 1; and

(c)   antigen-presenting cells that express a polypeptide according to claim 2,

under conditions and for a time sufficient to permit the stimulation and/or expansion of T cells.

10.   An isolated T cell population, comprising T cells prepared according to the method of claim 9.

11.   A composition comprising a first component selected from the group consisting of physiologically acceptable carriers and immunostimulants, and a second component selected from the group consisting of:

(a)   polypeptides according to claim 2;

(b)   polynucleotides according to claim 1;

(c)   antibodies according to claim 5;

(d)   fusion proteins according to claim 7;

(e)   T cell populations according to claim 10; and

(f)   antigen presenting cells that express a polypeptide according to claim 2.

12.   A method for stimulating an immune response in a patient, comprising administering to the patient a composition of claim 11.

13.   A method for the treatment of a cancer in a patient, comprising administering to the patient a composition of claim 11.

14.   A method for determining the presence of a cancer in a patient, comprising the steps of:

(a)   obtaining a biological sample from the patient;

(b)   contacting the biological sample with an oligonucleotide according to claim 8;

(c)   detecting in the sample an amount of a polynucleotide that hybridizes to the oligonucleotide; and

(d)   compare the amount of polynucleotide that hybridizes to the oligonucleotide to a predetermined cut-off value, and therefrom determining the presence of the cancer in the patient.

15.   A diagnostic kit comprising at least one oligonucleotide according to claim 8.

16.   A diagnostic kit comprising at least one antibody according to claim 5 and a detection reagent, wherein the detection reagent comprises a reporter group.

17.   A method for inhibiting the development of a cancer in a patient, comprising the steps of:

(a)   incubating CD4+ and/or CD8+ T cells isolated from a patient with at least one component selected from the group consisting of: (i) polypeptides according to claim 2; (ii) polynucleotides according to claim 1; and (iii) antigen presenting cells that express a polypeptide of claim 2, such that T cell proliferate;

(b)   administering to the patient an effective amount of the proliferated T cells,

and thereby inhibiting the development of a cancer in the patient.
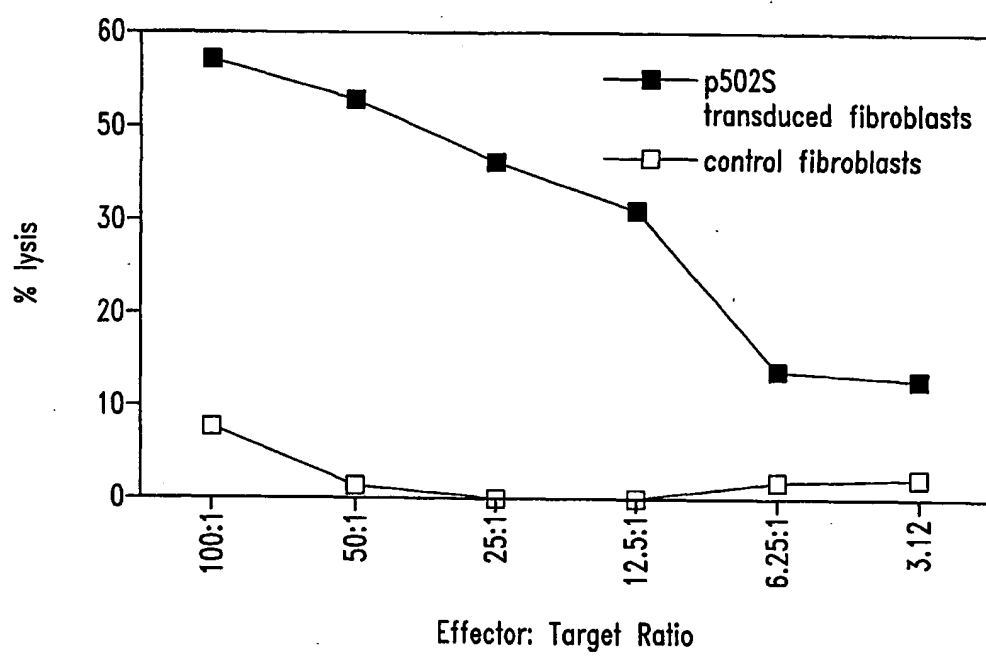
Fig. 1
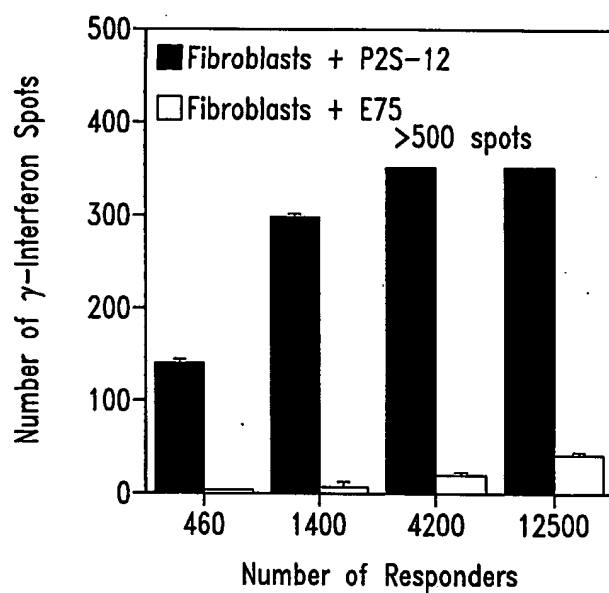
Fig. 2A
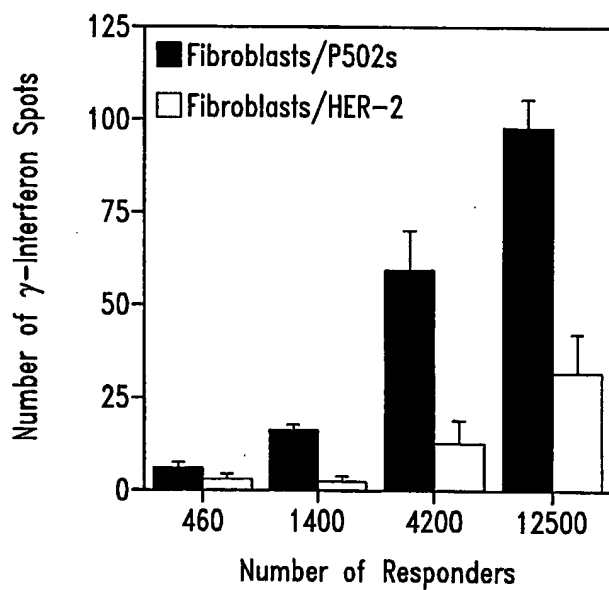
Fig. 2B
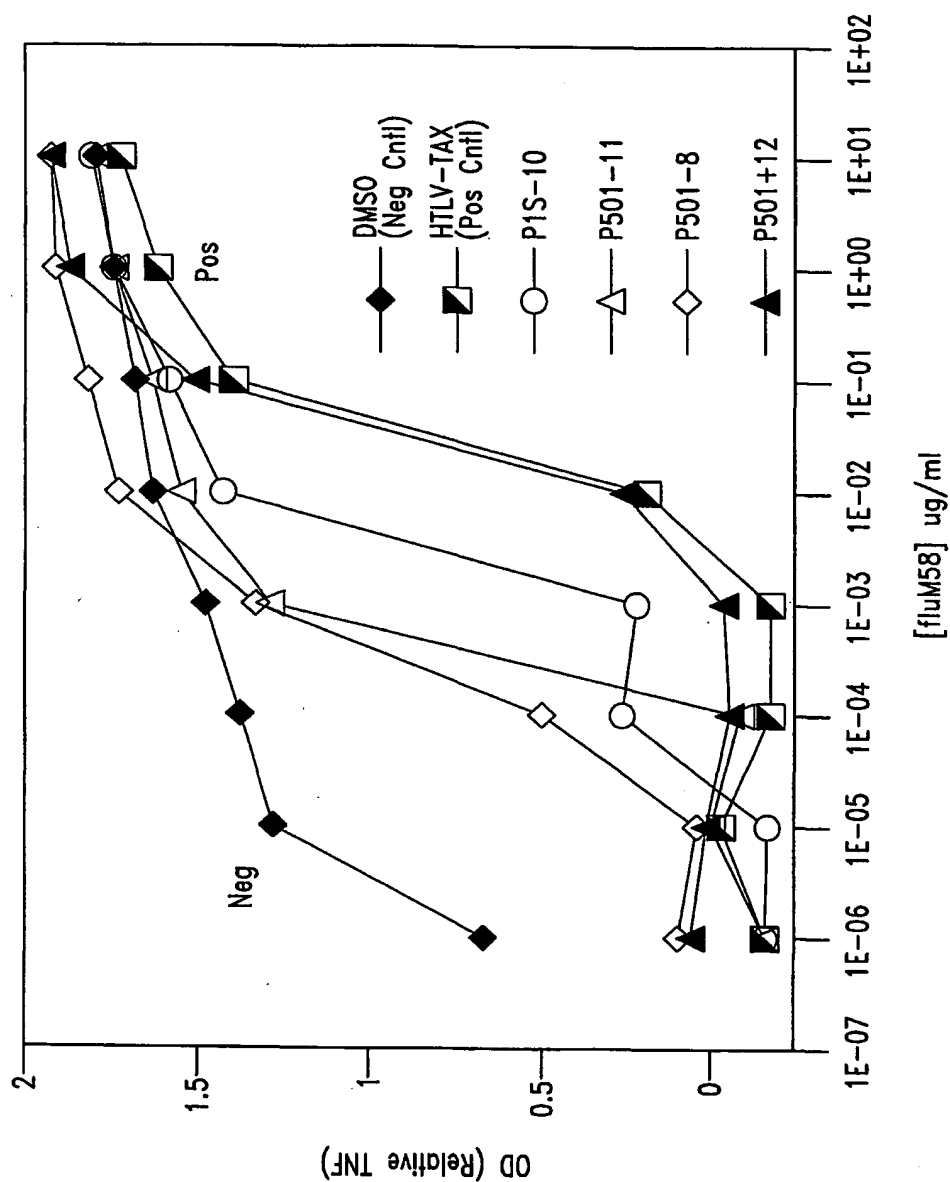
Fig. 3
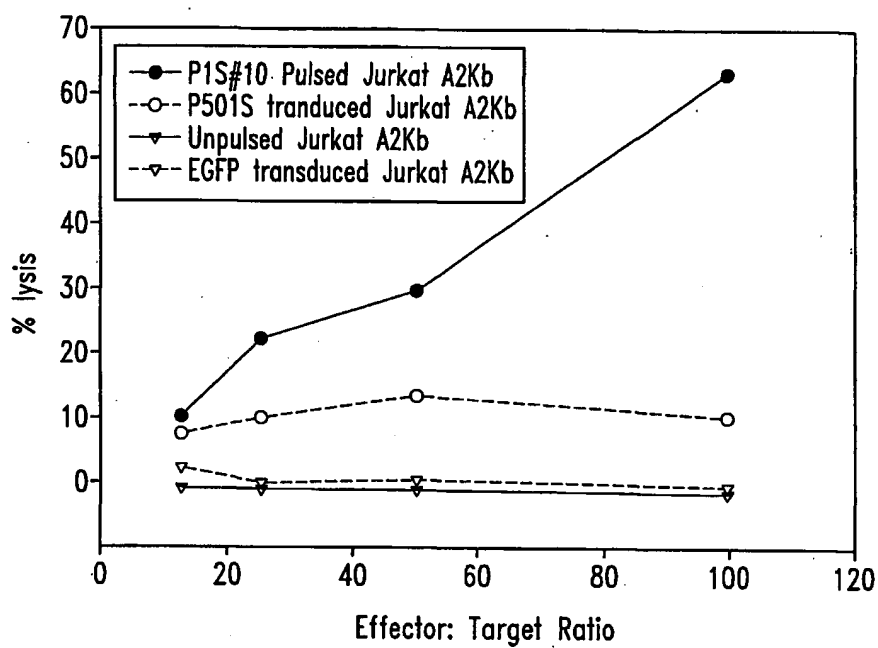
Fig. 4
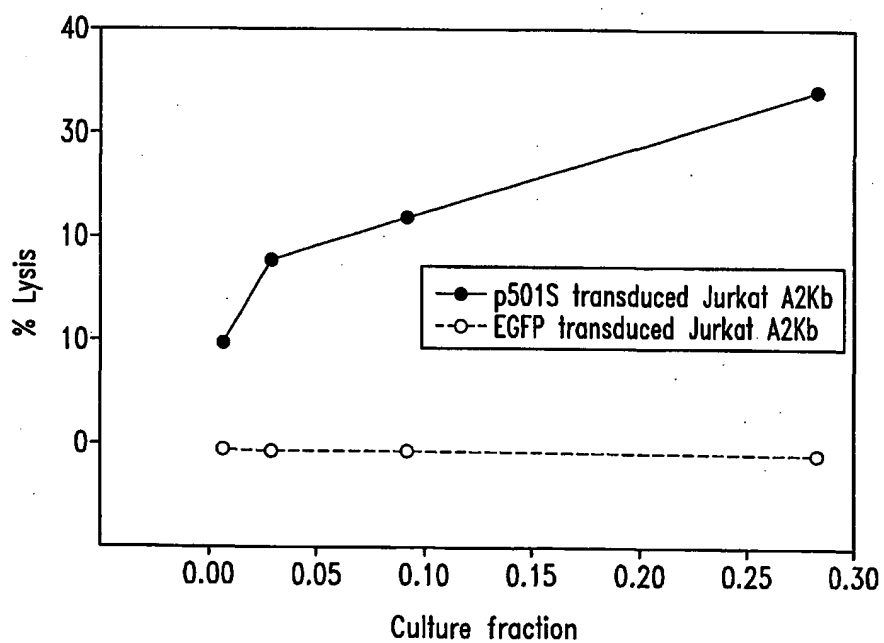
Fig. 5

5/14
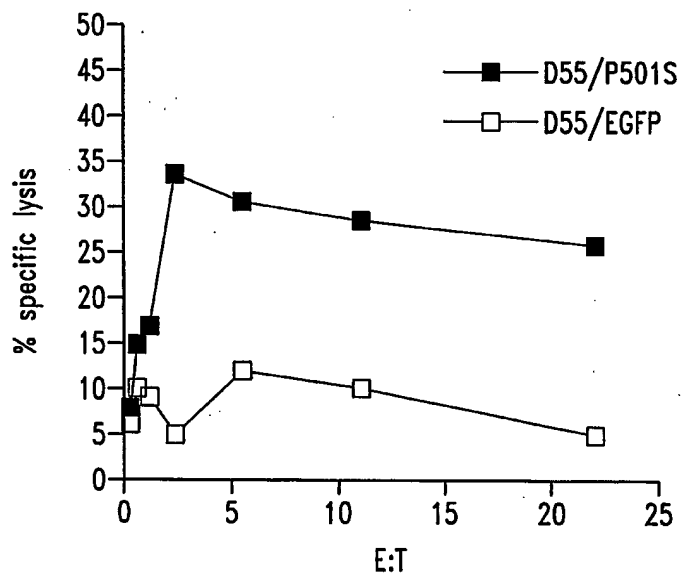
Fig. 6A
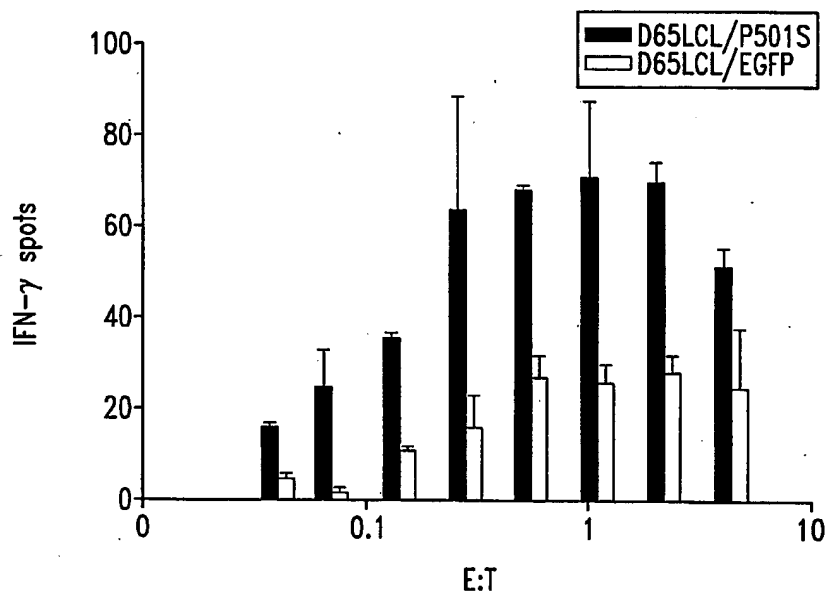
Fig. 6B

Expression of P501S
by the Baculovirus Expression System
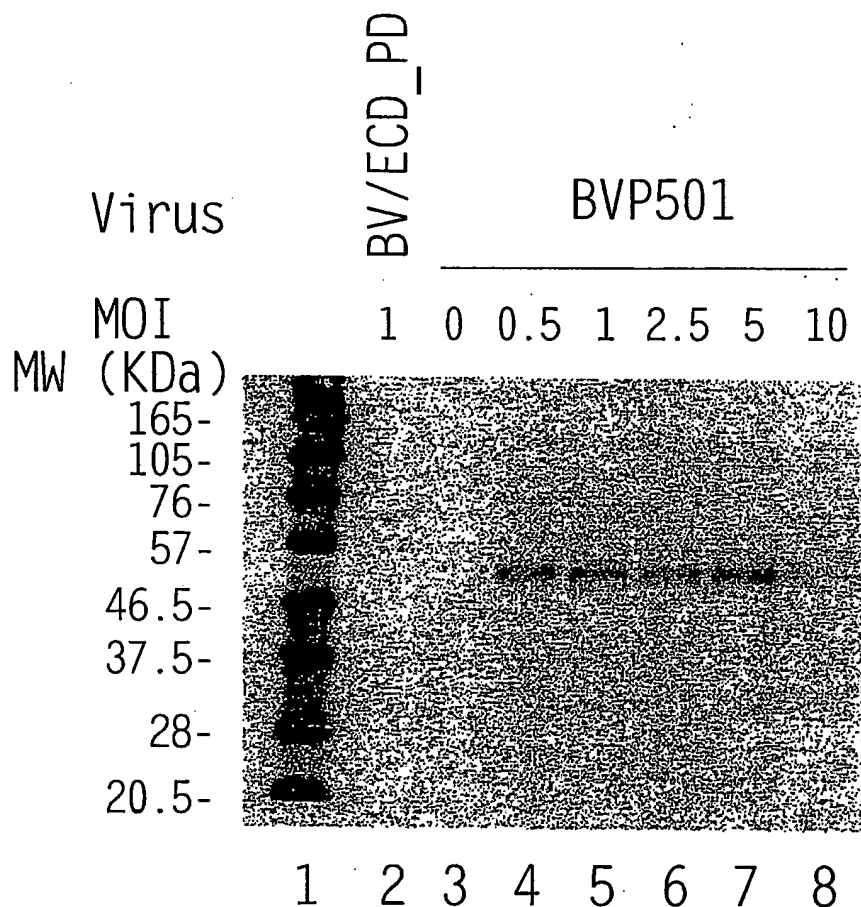
0.6 million high 5 cells in 6-well plate were infected with an unrelated control virus BV/ECD_PD (lane2), without virus (lane3), or with recombinant baculovirus for P501 at different MOIs (lane 4-8). Cell lysates were run on SDS-PAGE under the reducing conditions and analyzed by Western blot with a monoclonal antibody against P501S (P501S-10E3-G4D3). Lane 1 is the biotinylated protein molecular weight marker (BioLabs).

Fig. 7

FIGURE 8. Mapping of the epitope recognized by 10E3-G4-D3
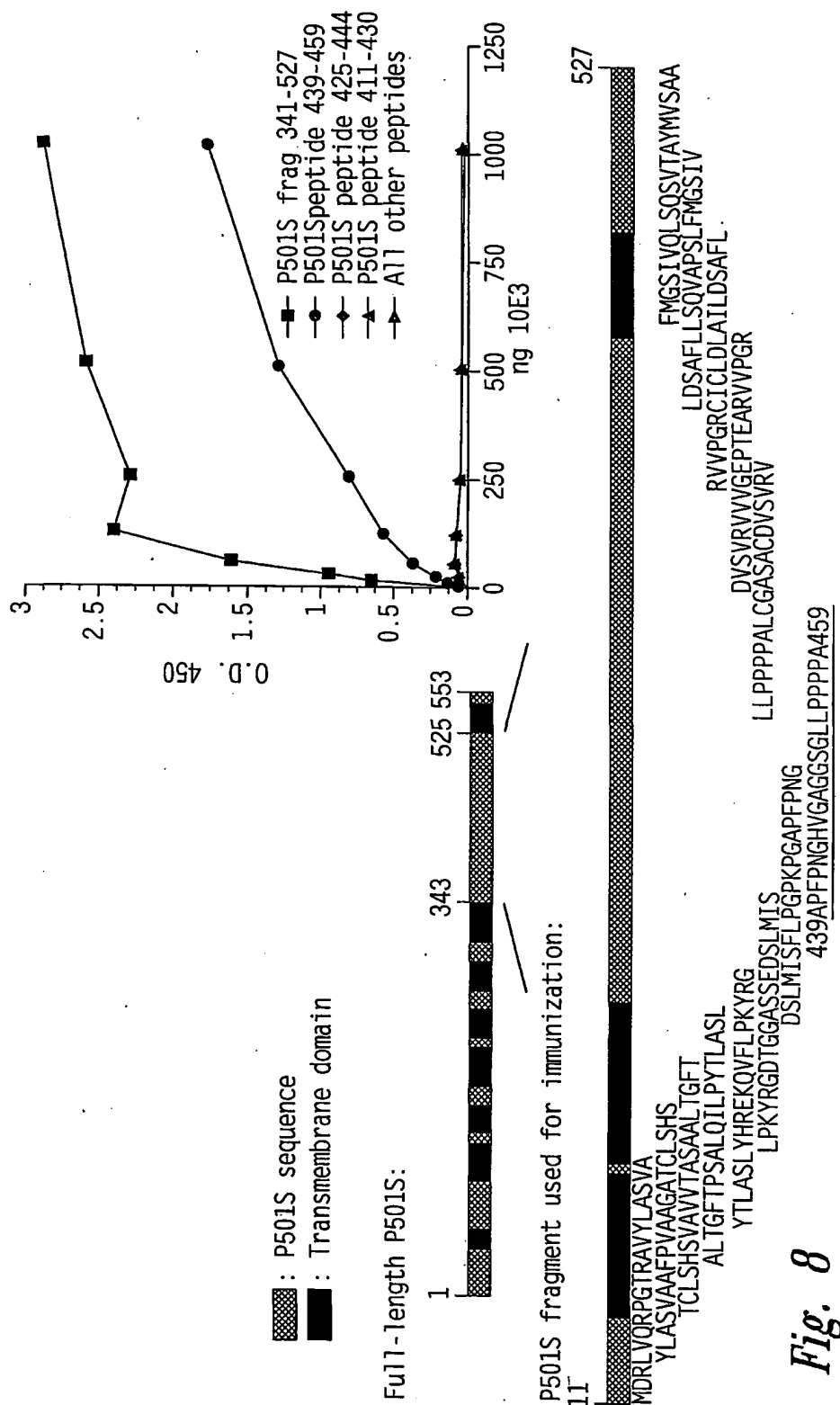
Fig. 8

Schematic of P501S with predicted
transmembrane, cytoplasmic, and extracellular regions

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CLFGLLTLIFLTCVAATLLV *AEEAALGPTEPAEGLSAPSLSPHCCPCRARLAFRNLGALLPRL*

HQLCCRMPRTLRR LFVAELCSWMALMTFTLFYTDF **VGEGLYQGVPRAEPGTEARRHYDEGVR**

MGSLGLFLQCAISLVFSLVM *DRLVQRFGTRAVYLAS* VAAFPVAAGATCLSHSVAVVTA **SAA**

LTGFTFSALQILPYTLASLY *HREKQVFLPKYRGDTGGASSEDSLMTSFLPGPKPGAPFPNGHVGAGGSGL*

LPPPPALCGASACDVSVRVVVGEPTEARVVPGRG ICLDLAILDSAFLLSQVAPSLF **MGSIVQLSQS**

VTAYMVSAAGLGLVAIYFAT *QVVFDKSDLAKYSA*

Underlined sequence: Predicted transmembrane domain; **Bold sequence**:
Predicted extracellular domain; *Italic sequence*: Predicted intracellular
domain. Sequence in bold/underlined: used generate polyclonal rabbit
serum

Localization of domains predicted using HMMTOP (G.E. Tusnady an I. Simon
(1998) Principles Governing Amino Acid Composition of Integral Membrane
Proteins: Applications to topology Prediction.J.Mol Biol. 283, 489-506.

Fig. 9
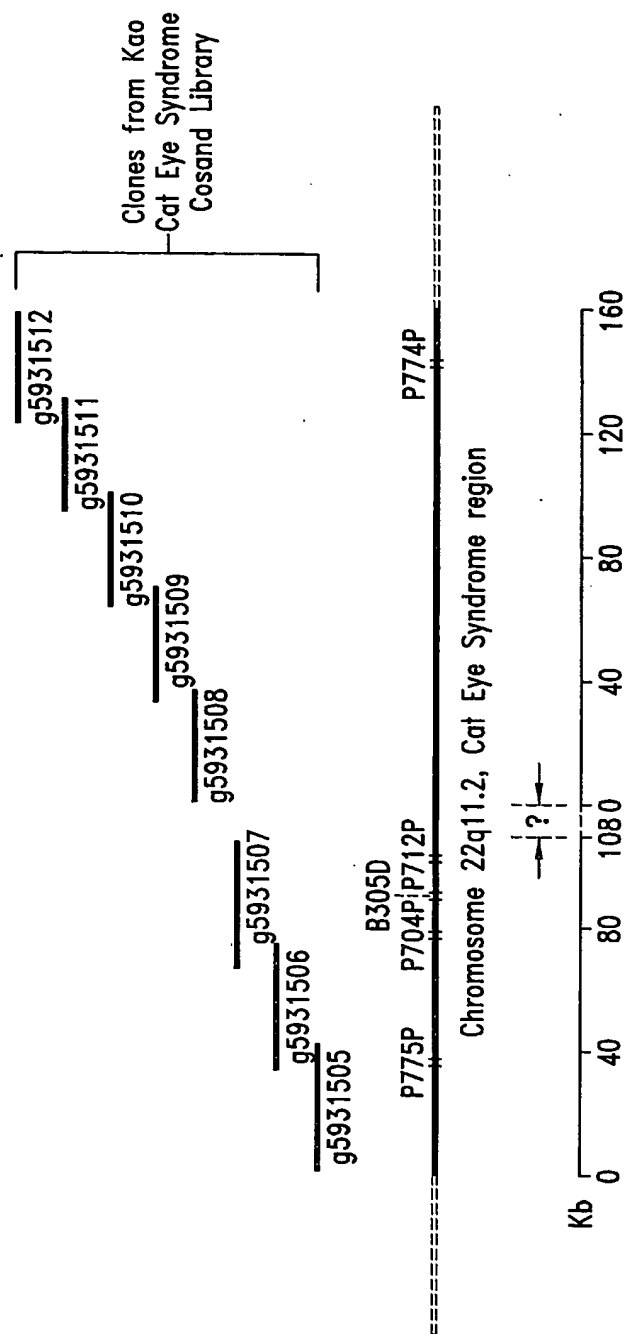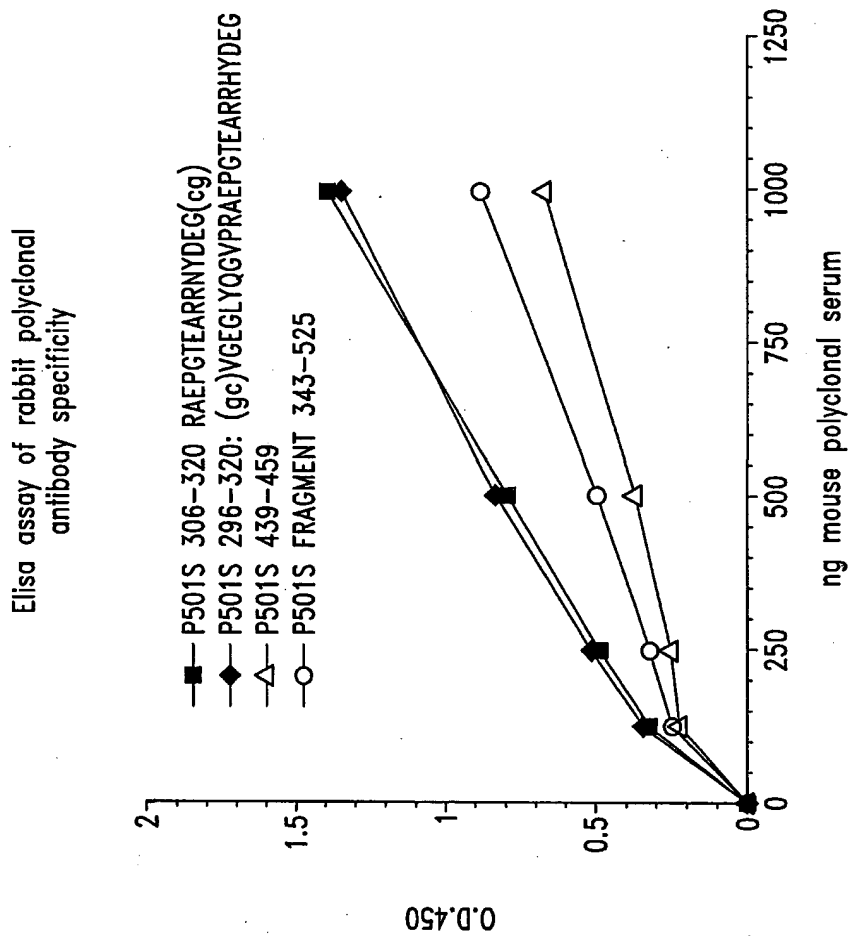
Fig. 10

Elisa assay of rabbit polyclonal
antibody specificity

—■— P501S 306–320 RAEPGTEARRNYDEG(cg)
—◆— P501S 296–320: (gc)VGEGLYQGVPRAEPGTEARRHYDEG
—△— P501S 439–459
—○— P501S FRAGMENT 343–525

O.D.450

ng mouse polyclonal serum

Fig. 11

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Fig. 12A (1)

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Fig. 12A (2)

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Fig. 12A (3)

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Fig. 12B

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<110> Corixa Corporation
      Xu, Jiangchun
      Dillon, Davin C.
      Mitcham, Jennifer L.
      Harlocker, Susan L.
      Yuqui, Jiang
      Kalos, Michael D.
      Fanger, Gary R.
      Retter, Marc W.
      Stolk, John A.
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gatattggtc attttttacca gcttctaaat ctnaactttc aggcttttga actggaacat    720
tgnatnacag tgttccanag ttncaaccta ctggaacatt acagtgtgct tgattcaaaa    780
tgttattttg ttaaaaatta aattttaacc tggtggaaaa ataatttgaa atna           834

    <210> 6
    <211> 818
    <212> DNA
    <213> Homo sapien

    <220>
    <221> misc_feature
    <222> (1)...(818)
    <223> n = A,T,C or G

    <400> 6
```

4

```
ttttttttttt ttttttttttt aagaccctca tcaatagatg gagacataca gaaatagtca    60
aaccacatct acaaaatgcc agtatcaggc ggcggcttcg aagccaaagt gatgtttgga   120
tgtaaagtga aatattagtt ggcggatgaa gcagatagtg aggaaagttg agccaataat   180
gacgtgaagt ccgtggaagc ctgtggctac aaaaaatgtt gagccgtaga tgccgtcgga   240
aatggtgaag ggagactcga agtactctga ggcttgtagg agggtaaaat agagacccag   300
taaaattgta ataagcagtg cttgaattat ttggtttcgg ttgtttttcta ttagactatg   360
gtgagctcag gtgattgata ctcctgatgc gagtaatacg gatgtgttta ggagtgggac   420
ttctagggga tttagcgggg tgatgcctgt tggggggccag tgccctccta gttgggggt   480
aggggctagg ctggagtggt aaaaggctca gaaaaatcct gcgaagaaaa aaacttctga   540
ggtaataaat aggattatcc cgtatcgaag gccttttttgg acaggtggtg tgtggtggcc   600
ttggtatgtg ctttctcgtg ttacatcgcg ccatcattgg tatatggtta gtgtgttggg   660
ttantanggc ctantatgaa gaactttggg antggaatta aatcaatngc ttggccggaa   720
gtcattanga nggctnaaaa ggccctgtta ngggtctggg ctnggtttta cccnacccat   780
ggaatncncc ccccggacna ntgnatccct attcttaa                            818
```

<210> 7
<211> 817
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(817)
<223> n = A,T,C or G

<400> 7
```
ttttttttttt ttttttttttt tggctctaga gggggtagag ggggtgctat agggtaaata    60
cgggccctat ttcaaagatt tttaggggaa ttaattctag gacgatgggt atgaaactgt   120
ggtttgctcc acagatttca gagcattgac cgtagtatac ccccggtcgt gtagcggtga   180
aagtggtttg gtttagacgt ccgggaattg catctgtttt taagcctaat gtggggacag   240
ctcatgagtg caagacgtct tgtgatgtaa ttattatacn aatgggggct tcaatcggga   300
gtactactcg attgtcaacg tcaaggagtc gcaggtcgcc tggttctagg aataatgggg   360
gaagtatgta ggaattgaag attaatccgc cgtagtcggt gttctcctag gttcaatacc   420
attggtggcc aattgatttg atggtaaggg gagggatcgt tgaactcgtc tgttatgtaa   480
aggatncctt ngggatggga aggcnatnaa ggactangga tnaatggcgg gcangatatt   540
tcaaacngtc tctanttcct gaaacgtctg aaatgttaat aanaattaan tttngttatt   600
gaatnttnng gaaaagggct tacaggacta gaaaccaaat angaaaanta atnntaangg   660
cnttatcntn aaaggtnata accnctccta tnatcccacc caatngnatt ccccacncnn   720
acnattggat ncccccanttc cananaangge cncccccccgg tgnanncenc cttttgttcc   780
cttnantgan ggttattcnc ccctngcntt atcancc                             817
```

<210> 8
<211> 799
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(799)
<223> n = A,T,C or G

<400> 8
```
catttccggg tttactttct aaggaaagcc gagcggaagc tgctaacgtg ggaatcggtg    60
cataaggaga actttctgct ggcacgcgct agggacaagc gggagagcga ctccgagcgt   120
ctgaagcgca cgtcccagaa ggtggacttg gcactgaaac agctgggaca catccgcgag   180
tacgaacagc gcctgaaagt gctggagcgg gaggtccagc agtgtagccg cgtcctgggg   240
tgggtggccg angcctganc cgctctgcct tgctgccccc angtgggccg ccacccctg   300
acctgcctgg gtccaaacac tgagccctgc tggcggactt caaggananac ccccacangg   360
```

5

```
ggatttttgct cctanantaa ggctcatctg ggcctcggcc cccccacctg gttggccttg     420
tctttgangt gagccccatg tccatctggg ccactgtcng gaccaccttt ngggagtgtt     480
ctccttacaa ccacannatg cccggctcct cccggaaacc antcccancc tgngaaggat     540
caagncctgn atccactnnt nctanaaccg gccnccnccg cngtggaacc cnccttntgt     600
tcctttttcnt tnagggttaa tnncgccttg gccttnccan ngtcctncnc nttttccnnt     660
gttnaaattg ttangcnccc nccnntcccn cnncnncnan cccgacccnn annttnnann     720
ncctgggggt nccnncngat tgacccnncc nccctntant tgcnttnggg nncnntgccc     780
ctttccctct nggganncg                                                  799
```

        <210> 9
        <211> 801
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(801)
        <223> n = A,T,C or G

        <400> 9
```
acgccttgat cctcccaggc tgggactggt tctgggagga gccgggcatg ctgtggtttg      60
taangatgac actcccaaag gtggtcctga cagtggccca gatggacatg gggctcacct     120
caaggacaag gccaccaggt gcgggggccg aagcccacat gatccttact ctatgagcaa     180
aatccccctgt gggggcttct ccttgaagtc cgccancagg gctcagtctt tggacccang     240
caggtcatgg ggttgtngnc caactggggg ccncaacgca aaanggcnca gggcctcngn     300
cacccatccc angacgcggc tacactnctg gacctcccnc tccaccactt tcatgcgctg     360
ttcntacccg cgnatntgtc ccanctgttt cngtgccnac tccancttct nggacgtgcg     420
ctacatacgc ccggantcnc nctcccgctt tgtccctatc cacgtnccan caacaaattt     480
cnccntantg caccnattcc cacntttnnc agntttccnc nncgngcttc cttntaaaag     540
ggttgancccc cggaaaatnc cccaaggggg gggggccngg tacccaactn ccccctnata     600
gctgaantcc ccatnaccnn gnctcnatgg anccntccnt tttaannacn ttctnaactt     660
gggaananccc ctcgncccntn cccccnttaa tcccnccttg cnagnnncnt cccccnntcc     720
ncccnnntng gcntntnann cnaaaaaggc ccnnnancaa tctcctnncn cctcanttcg     780
ccancccctcg aaatcggccn c                                               801
```

        <210> 10
        <211> 789
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(789)
        <223> n = A,T,C or G

        <400> 10
```
cagtctatnt ggccagtgtg gcagctttcc ctgtggctgc cggtgccaca tgcctgtccc      60
acagtgtggc cgtggtgaca gcttcagccg ccctcaccgg gttcaccttc tcagccctgc     120
agatcctgcc ctacacactg gcctccctct accaccggga gaagcaggtg ttcctgccca     180
aataccgagg ggacactgga ggtgctagca gtgaggacag cctgatgacc agcttcctgc     240
caggccctaa gcctggagct cccttcccta atggacacgt gggtgctgga ggcagtggcc     300
tgctcccacc tccaccgcg ctctgcgggg cctctgcctg tgatgtctcc gtacgtgtgg     360
tggtgggtga gcccaccgan gccagggtgg ttccgggccg gggcatctgc ctggacctcg     420
ccatcctgga tagtgcttcc tgctgtccca ngtggcccca tccctgttta tgggctccat     480
tgtccagctc agccagtctg tcactgccta tatggtgtct gccgcaggcc tgggtctggt     540
cccatttact ttgctacaca ggtantattt gacaagaacg anttggccaa atactcagcg     600
ttaaaaaatt ccagcaacat tggggggtgga aggcctgcct cactgggtcc aactccccgc     660
tcctgttaac cccatggggc tgccggcttg gccgccaatt tctgttgctg ccaaantnat     720
```

6

```
gtggctctct gctgccacct gttgctggct gaagtgcnta cngcncanct nggggggtng      780
ggngttccc                                                             789
```

    <210> 11
    <211> 772
    <212> DNA
    <213> Homo sapien

    <220>
    <221> misc_feature
    <222> (1)...(772)
    <223> n = A,T,C or G

    <400> 11

```
cccaccctac ccaaatatta gacaccaaca cagaaaagct agcaatggat tcccttctac       60
tttgttaaat aaataagtta aatatttaaa tgcctgtgtc tctgtgatgg caacagaagg      120
accaacaggc cacatcctga taaaaggtaa gaggggggtg gatcagcaaa aagacagtgc      180
tgtgggctga ggggacctgg ttcttgtgtg ttgcccctca ggactcttcc cctacaaata      240
actttcatat gttcaaatcc catggaggag tgtttcatcc tagaaactcc catgcaagag      300
ctacattaaa cgaagctgca ggttaagggg cttanagatg ggaaaccagg tgactgagtt      360
tattcagctc ccaaaaaccc ttctctaggt gtgtctcaac taggaggcta gctgttaacc      420
ctgagcctgg gtaatccacc tgcagagtcc ccgcattcca gtgcatggaa cccttctggc      480
ctccctgtat aagtccagac tgaaaccccc ttggaaggnc tccagtcagg cagccctana      540
aactggggaa aaaagaaaag gacgccccan cccccagctg tgcanctacg cacctcaaca      600
gcacaggtg gcagcaaaaa aaccacttta ctttggcaca aacaaaaact nggggggggca      660
accccggcac cccnangggg gttaacagga ancnggnaa cntggaaccc aattnaggca      720
ggcccnccac cccnaatntt gctgggaaat ttttcctccc ctaaattntt tc              772
```

    <210> 12
    <211> 751
    <212> DNA
    <213> Homo sapien

    <220>
    <221> misc_feature
    <222> (1)...(751)
    <223> n = A,T,C or G

    <400> 12

```
gccccaattc cagctgccac accacccacg gtgactgcat tagttcggat gtcatacaaa       60
agctgattga agcaaccctc tacttttttgg tcgtgagcct tttgcttggt gcaggtttca      120
ttggctgtgt tggtgacgtt gtcattgcaa cagaatgggg gaaaggcact gttctctttg      180
aagtanggtg agtcctcaaa atccgtatag ttggtgaagc cacagcactt gagccctttc      240
atggtggtgt tccacacttg agtgaagtct tcctgggaac cataatcttt cttgatggca      300
ggcactacca gcaacgtcag ggaagtgctc agccattgtg gtgtacacca aggcgaccac      360
agcagctgcn acctcagcaa tgaagatgan gaggangatg aagaagaacg tcncgagggc      420
acacttgctc tcagtcttan caccatanca gcccntgaaa accaananca aagaccacna      480
cnccggctgc gatgaagaaa tnaccccncg ttgacaaact tgcatggcac tgggannccac     540
agtggcccna aaaatcttca aaaggatgc cccatcnatt gacccccaa atgcccactg      600
ccaacagggg ctgccccacn cncnnaacga tganccnatt gnacaagatc tncntggtct      660
tnatnaacnt gaaccctgcn tngtggctcc tgttcaggnc cnnggcctga cttctnaann      720
aangaactcn gaagnccccca cngganannc g                                    751
```

    <210> 13
    <211> 729
    <212> DNA
    <213> Homo sapien

7

```
      <220>
      <221> misc_feature
      <222> (1)...(729)
      <223> n = A,T,C or G

      <400> 13
gagccaggcg tccctctgcc tgcccactca gtggcaacac ccgggagctg ttttgtcctt        60
tgtggancct cagcagtncc ctctttcaga actcantgcc aaganccctg aacaggagcc       120
accatgcagt gcttcagctt cattaagacc atgatgatcc tcttcaattt gctcatcttt       180
ctgtgtggtg cagccctgtt ggcagtgggc atctgggtgt caatcgatgg ggcatccttt       240
ctgaagatct tcgggccact gtcgtccagt gccatgcagt ttgtcaacgt gggctacttc .     300
ctcatcgcag ccggcgttgt ggtcttagct ctaggtttcc tgggctgcta tggtgctaag       360
actgagagca agtgtgccct cgtgacgttc ttcttcatcc tcctcctcat cttcattgct       420
gaggttgcaa tgctgtggtc gccttggtgt acaccacaat ggctgagcac ttcctgacgt       480
tgctggtaat gcctgccatc aanaaaagat tatgggttcc caggaanact tcactcaagt       540
gttggaacac caccatgaaa gggctcaagt gctgtggctt cnnccaacta tacggatttt       600
gaagantcac ctacttcaaa gaaaanagtg cctttcccc atttctgttg caattgacaa       660
acgtccccaa cacagccaat tgaaaacctg cacccaaccc aaangggtcc ccaaccanaa       720
attnaaggg                                                                729

      <210> 14
      <211> 816
      <212> DNA
      <213> Homo sapien

      <220>
      <221> misc_feature
      <222> (1)...(816)
      <223> n = A,T,C or G

      <400> 14
tgctcttcct caaagttgtt cttgttgcca taacaaccac cataggtaaa gcgggcgcag        60
tgttcgctga aggggttgta gtaccagcgc gggatgctct ccttgcagag tcctgtgtct       120
ggcaggtcca cgcagtgccc tttgtcactg gggaaatgga tgcgctggag ctcgtcaaag       180
ccactcgtgt attttcaca ggcagcctcg tccgacgcgt cggggcagtt gggggtgtct        240
tcacactcca ggaaactgtc natgcagcag ccattgctgc agcggaactg ggtgggctga       300
cangtgccag agcacactgg atggcgcctt tccatgnnan gggccctgng ggaaagtccc       360
tgancccan anctgcctct caaangcccc accttgcaca ccccgacagg ctagaatgga       420
atcttcttcc cgaaaggtag ttnttcttgt tgcccaancc anccccntaa acaaactctt       480
gcanatctgc tccgnggggg tcntantacc ancgtgggaa aagaacccca ggcngcgaac       540
caancttgtt tggatncgaa gcnataatct nctnttctgc ttggtggaca gcaccantna       600
ctgtnnanct ttagnccntg gtcctcntgg gttgnncttg aacctaatcn ccnntcaact       660
gggacaaggt aantngccnt cctttnaatt cccnancntn ccccctggtt tggggttttn       720
cncnctccta ccccacccac ggggtcngnt ggttng                                  780
cacaaccctn ccccacccac gggttcngnt ggttng                                  816

      <210> 15
      <211> 783
      <212> DNA
      <213> Homo sapien

      <220>
      <221> misc_feature
      <222> (1)...(783)
      <223> n = A,T,C or G

      <400> 15
ccaaggcctg ggcaggcata nacttgaagg tacaacccca ggaacccctg gtgctgaagg        60
```

8

```
atgtggaaaa cacagattgg cgcctactgc ggggtgacac ggatgtcagg gtagagagga    120
aagacccaaa ccaggtggaa ctgtggggac tcaaggaang cacctacctg ttccagctga    180
cagtgactag ctcagaccac ccagaggaca cggccaacgt cacagtcact gtgctgtcca    240
ccaagcagac agaagactac tgcctcgcat ccaacaangt gggtcgctgc cggggctctt    300
tcccacgctg gtactatgac cccacggagc agatctgcaa gagtttcgtt tatggaggct    360
gcttgggcaa caagaacaac taccttcggg aagaagagtg cattctancc tgtcngggtg    420
tgcaaggtgg gcctttgana ngcanctctg gggctcangc gactttcccc cagggcccct    480
ccatggaaag gcgccatcca ntgttctctg gcacctgtca gcccacccag ttccgctgca    540
ncaatggctg ctgcatcnac antttcctng aattgtgaca acacccccca ntgcccccaa    600
ccctcccaac aaagcttccc tgttnaaaaa tacnccantt ggcttttnac aaacnccggg    660
cnctccnttt ttccccnntn aacaaagggc nctngcnttt gaactgcccn aacccnggaa    720
tctnccnngg aaaaantncc cccctggtt cctnnaancc cctccncnaa anctncccc    780
ccc                                                                783
```

```
        <210> 16
        <211> 80ľ
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(801)
        <223> n = A,T,C or G

        <400> 16
gccccaattc cagctgccac accacccacg gtgactgcat tagttcggat gtcatacaaa     60
agctgattga agcaaccctc tacttttttgg tcgtgagcct tttgcttggt gcaggtttca    120
ttggctgtgt tggtgacgtt gtcattgcaa cagaatgggg gaaaggcact gttctctttg    180
aagtagggtg agtcctcaaa atccgtatag ttggtgaagc cacagcactt gagcccttc     240
atggtggtgt tccacacttg agtgaagtct tcctgggaac cataatcttt cttgatggca    300
ggcactacca gcaacgtcag gaagtgctca gccattgtgg tgtacaccaa ggcgaccaca    360
gcagctgcaa cctcagcaat gaagatgagg aggaggatga agaagaacgt cncgagggca    420
cacttgctct ccgtcttagc accatagcag cccangaaac caagagcaaa gaccacaacg    480
ccngctgcga atgaaagaaa ntacccacgt tgacaaactg catggccact ggacgacagt     540
tggcccgaan atcttcagaa aagggatgcc ccatcgattg aacacccana tgcccactgc    600
cnacagggct gcnccncncn gaaagaatga gccattgaag aaggatcntc ntggtcttaa    660
tgaactgaaa ccntgcatgg tggcccctgt tcagggctct tggcagtgaa ttctganaaa    720
aaggaacngc ntnagccccc ccaaangana aaacacccccc gggtgttgcc ctgaattggc    780
ggccaaggan ccctgcccccn g                                            801
```

```
        <210> 17
        <211> 740
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(740)
        <223> n = A,T,C or G

        <400> 17
gtgagagcca ggcgtccctc tgcctgccca ctcagtggca acacccggga gctgttttgt     60
cctttgtgga gcctcagcag ttccctcttt cagaactcac tgccaagagc cctgaacagg    120
agccaccatg cagtgcttca gcttcattaa gaccatgatg atcctcttca atttgctcat    180
ctttctgtgt ggtgcagccc tgttggcagt gggcatctgg gtgtcaatcg atggggcatc    240
ctttctgaag atcttcgggc cactgtcgtc cagtgccatg cagtttgtca acgtgggcta    300
cttcctcatc gcagccggcg ttgtggtctt tgctcttggt ttcctgggct gctatggtgc    360
taagacggag agcaagtgtg ccctcgtgac gttcttcttc atcctcctcc tcatcttcat    420
```

9

```
tgctgaagtt gcagctgctg tggtcgcctt ggtgtacacc acaatggctg aaccattcct    480
gacgttgctg gtantgcctg ccatcaanaa agattatggg ttcccaggaa aaattcactc    540
aantntggaa caccnccatg aaaagggctc caatttctgn tggcttcccc aactataccg    600
gaattttgaa agantcnccc tacttccaaa aaaaaanant tgcctttncc cccnttctgt    660
tgcaatgaaa acntcccaan acngccaatn aaaacctgcc cnnncaaaaa ggntcncaaa    720
caaaaaaant nnaagggttn                                                 740
```

        <210> 18
        <211> 802
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(802)
        <223> n = A,T,C or G

        <400> 18
```
ccgctggttg .cgctggtcca gngnagccac gaagcacgtc agcatacaca gcctcaatca    60
caaggtcttc cagctgccgc acattacgca gggcaagagc ctccagcaac actgcatatg    120
ggatacactt tactttagca gccagggtga caactgagag gtgtcgaagc ttattcttct    180
gagcctctgt tagtggagga agattccggg cttcagctaa gtagtcagcg tatgtcccat    240
aagcaaacac tgtgagcagc cggaaggtag aggcaaagtc actctcagcc agctctctaa    300
cattgggcat gtccagcagt tctccaaaca cgtagacacc agnggcctcc agcacctgat    360
ggatgagtgt ggccagcgct gccccccttgg ccgacttggc taggagcaga aattgctcct   420
ggttctgccc tgtcaccttc acttccgcac tcatcactgc actgagtgtg ggggacttgg    480
gctcaggatg tccagagacg tggttccgcc ccctcnctta atgacaccgn ccanncaacc    540
gtcggctccc gccgantgng ttcgtcgtnc ctgggtcagg gtctgctggc cnctacttgc    600
aancttcgtc nggcccatgg aattcaccnc accggaactn gtangatcca ctnnttctat    660
aaccggncgc cacctcnnnt ggaactccac tcttnttncc tttacttgag ggttaaggtc    720
accctttnncg ttaccttggt ccaaacccntn ccntgtgtcg anatngtnaa tcnggnccna   780
tnccanccnc atangaagcc ng                                              802
```

        <210> 19
        <211> 731
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(731)
        <223> n = A,T,C or G

        <400> 19
```
cnaagcttcc aggtnacggg ccgcnaancc tgacccnagg tancanaang cagncngcgg    60
gagcccaccg tcacgnggng gngtctttat nggagggggc ggagccacat cnctggacnt    120
cntgaccccca actcccncc ncncantgca gtgatgagtg cagaactgaa ggtnacgtgg    180
caggaaccaa gancaaannc tgctccnntc caagtcggcn naggggggcgg ggctggccac   240
gcncatccnt cnagtgctgn aaagcccccnn cctgtctact tgtttggaga acngcnnnga    300
catgcccagn gttanataac nggcngagag tnantttgcc tctcccttcc ggctgcgcan    360
cgngtntgct tagnggacat aacctgacta cttaactgaa cccnngaatc tncncccct    420
ccactaagct cagaacaaaa aacttcgaca ccactcantt gtcacctgnc tgctcaagta    480
aagtgtaccc catncccaat gtntgctnga ngctctgncc tgcnttangt tcggtcctgg    540
gaagacctat caattnaagc tatgtttctg actgcctctt gctccctgna acaancnacc    600
cnncnntcca aggggggggnc ggccccccaat ccccccaacc ntnaattnan tttanccccn   660
ccccnggcc cggcctttta cnancntcnn nnacngggna aaaccnnngc tttncccaac     720
nnaatccncc t                                                          731
```

10

```
            <210> 20
            <211> 754
            <212> DNA
            <213> Homo sapien

            <220>
            <221> misc_feature
            <222> (1)...(754)
            <223> n = A,T,C or G

            <400> 20
tttttttttt tttttttttt taaaaacccc ctccattnaa tgnaaacttc cgaaattgtc          60
caacccccctc ntccaaatnn ccntttccgg gnggggttc caaacccaan ttannttttgg        120
annttaaatt aaatnttnnt tggnggnnna anccnaatgt nangaaagtt naacccanta         180
tnancttnaa tncctggaaa ccngtngntt ccaaaaatnt ttaacccctta antccctccg        240
aaatngttna nggaaaaccc aanttctcnt aaggttgttt gaaggntnaa tnaaaanccc         300
nnccaattgt ttttngccac gcctgaatta attggnttcc gntgtttttcc nttaaaanaa        360
ggnnancccc ggttantnaa tcccccccnnc cccaattata ccganttttt ttngaattgg        420
ganccncgg gaattaacgg ggnnnntccc tnttggggggg cnggnncccc cccntcggg          480
ggttngggnc aggncnnaat tgtttaaggg tccgaaaaat ccctccnaga aaaaaanctc         540
ccaggntgag nntnggggttt ncccccccccc canggccccct ctcgnanagt tggggtttgg      600
ggggcctggg attttntttc ccctnttncc tccccccccc ccngggganag aggttngngt        660
tttgntcnnc ggccccnccn aaganctttn ccganttnan ttaaatccnt gcctnggcga        720
agtccnttgn agggntaaan ggccccctnn cggg                                     754

            <210> 21
            <211> 755
            <212> DNA
            <213> Homo sapien

            <220>
            <221> misc_feature
            <222> (1)...(755)
            <223> n = A,T,C or G

            <400> 21
atcancccat gaccccnaac nngggaccnc tcanccggnc nnncnaccnc cggccnatca          60
nngtnagnnc actncnnttn natcacnccc cnccnactac gcccncnanc cnacgcncta         120
nncanatncc actganngcg cgangtngan ngagaaanct nataccanag ncaccanacn         180
ccagctgtcc nanaangcct nnnatacngg nnnatccaat ntgnancctc cnaagtattn         240
nncnncanat gattttcctn anccgattac ccntnccccc tanccccctcc cccccaacna        300
cgaaggcnct ggnccnaagg nngcgncncc ccgctagntc cccnncaagt cncncncccta        360
aactcanccn nattacncgc ttcntgagta tcactccccg aatctcaccc tactcaactc        420
aaaaanatcn gatacaaaat aatncaagcc tgnttatnac actntgactg ggtctctatt        480
ttagnggtcc ntnaancntc ctaatacttc cagtctncct tcnccaattt ccnaanggct        540
ctttcngaca gcatnttttg gttcccnntt gggttcttan ngaattgccc ttcntngaac        600
gggctcntct tttccttcgg ttanccctggn ttcnnccggc cagttattat ttcccnttttt       660
aaattcntnc cntttanttt tggcnttcna aaccccccggc cttgaaaacg gcccccctggt      720
aaaaggttgt tttganaaaa tttttgtttt gttcc                                    755

            <210> 22
            <211> 849
            <212> DNA
            <213> Homo sapien

            <220>
            <221> misc_feature
            <222> (1)...(849)
```

11

<223> n = A,T,C or G

<400> 22
```
tttttttttt tttttangtg tngtcgtgca ggtagaggct tactacaant gtgaanacgt      60
acgctnggan taangcgacc cganttctag ganncnccct aaaatcanac tgtgaagatn     120
atcctgnnna cggaanggtc accggnngat nntgctaggg tgnccnctcc cannncnttn     180
cataactcng nggccctgcc caccaccttc ggcggcccng ngnccgggcc cgggtcattn     240
gnnttaaccn cactnngcna ncggtttccn nccccnncng acccnggcga tccggggtnc     300
tctgtcttcc cctgnagncn anaaantggg ccncggnccc ctttacccct nnacaagcca     360
cngccntcta nccncngccc ccctccant nnggggact gccnanngct ccgttnctng     420
nnaccccnnn gggtncctcg gttgtcgant cnaccgnang ccanggattc cnaaggaagg     480
tgcgttnttg gcccctaccc ttcgctncgg nncacccttc ccgacnanga nccgctcccg     540
cncnncgnng cctcncctcg caacacccgc nctcntcgt ncggnnnccc ccccacccgc     600
nccctcncnc ngncgnancn ctccnccncc gtctcannca ccacccgcc ccgccaggcc     660
ntcancacn ggnngacnng nagcncnntc gcnccgcgcn gcgncnccct cgccncngaa     720
ctncntcngg ccantnncgc tcaanccnna cnaaacgccg ctgcgcggcc cgnagcgncc     780
ncctcccga gtcctcccgn cttccnaccc angnnttccn cgaggacacn nnaccccgcc     840
nncangcgg                                                            849
```

<210> 23
<211> 872
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(872)
<223> n = A,T,C or G

<400> 23
```
gcgcaaacta tacttcgctc gnactcgtgc gcctcgctnc tcttttcctc cgcaaccatg      60
tctgacnanc ccgattnggc ngatatcnan aagntcganc agtccaaact gantaacaca     120
cacacncnan aganaaatcc nctgccttcc anagtanacn attgaacnng agaaccangc     180
nggcgaatcg taatnaggcg tgcgccgcca atntgtcncc gtttattntn ccagcntcnc     240
ctnccnaccc tacntcttcn nagctgtcnn acccctngtn cgnacccccc naggtcggga     300
tcgggtttnn natgaccgng cnnccctcc ccccntccat nacganccnc ccgcaccacc     360
nanngcncgc nccccgnnct cttcgccncc ctgtcctntn ccctgtngc ctggcncngn     420
accgcattga ccctcgccnn ctncnngaaa ncgnanacgt ccgggttgnn annancgctg     480
tgggnnngcg tctgcnccgc gttccttccn ncnncttcca ccatcttcnt tacnggtct     540
ccncgcccntc tcnnncacnc cctgggacgc tntcctntgc ccccccttac tcccccccctt     600
cgncgtgncc cgnccccacc ntcatttnca nacgntcttc acaannncct ggntnnctcc     660
cnancngncn gtcanccnag ggaaggnggg ggnnccnntg nttgacgttg nggngangtc     720
cgaanantcc tcnccntcan cnctacccct cgggcgnnct ctcngttncc aacttancaa     780
ntctcccccg ngngcncntc tcagcctcnc ccncccccnct ctctgcantg tnctctgctc     840
tnaccnntac gantnttcgn cnccctcttt cc                                    872
```

<210> 24
<211> 815
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(815)
<223> n = A,T,C or G

<400> 24
```
gcatgcaagc ttgagtattc tatagngtca cctaaatanc ttggcntaat catggtcnta      60
```

12

```
nctgncttcc tgtgtcaaat gtatacnaan tanatatgaa tctnatntga caaganngta    120
tcntncatta gtaacaantg tnntgtccat cctgtcngan canattccca tnnattncgn    180
cgcattcncn gcncantatn taatngggaa ntcnnntnnn ncaccnncat ctatcntncc    240
gcnccctgac tggnagagat ggatnanttc tnntntgacc nacatgttca tcttggattn    300
aananccccc cgcngnccac cggttngnng cnagccnntc ccaagacctc ctgtggaggt    360
aacctgcgtc aganncatca aacntgggaa acccgcnncc angtnnaagt ngnnncanan    420
gatcccgtcc aggnttnacc atcccttcnc agcgcccct ttngtgcctt anagngnagc    480
gtgtccnanc cnctcaacat ganacgcgcc agnccanccg caattnggca caatgtcgnc    540
gaacccccta gggggantna tncaaanccc caggattgtc cncncangaa atcccncanc    600
cccnccctac ccnnctttgg gacngtgacc aantcccgga gtnccagtcc ggccngnctc    660
ccccaccggt nnccntgggg gggtgaanct cngnntcanc cngncgaggn ntcgnaagga    720
accggnccth ggncgaanng ancnntcnga agngccncnt cgtataaccc ccctcncca     780
nccnacngnt agntcccccc cngggtncgg aangg                              815
```

        <210> 25
        <211> 775
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(775)
        <223> n = A,T,C or G

        <400> 25
```
ccgagatgtc tcgctccgtg gccttagctg tgctcgcgct actctctctt tctggcctgg    60
aggctatcca gcgtactcca aagattcagg tttactcacg tcatccagca gagaatggaa    120
agtcaaattt cctgaattgc tatgtgtctg ggtttcatcc atccgacatt gaanttgact    180
tactgaagaa tgganagaga attgaaaaag tggagcattc agacttgtct ttcagcaagg    240
actggtcttt ctatctcntg tactacactg aattcacccc cactgaaaaa gatgagtatg    300
cctgccgtgt gaaccatgtg actttgtcac agcccaagat agttaagtgg gatcgagaca    360
tgtaagcagn cnncatggaa gtttgaagat gccgcatttg gattggatga attccaaatt    420
ctgcttgctt gcnttttaat antgatatgc ntatacaccc taccctttat gncccccaaat    480
tgtaggggtt acatnantgt tcncntngga catgatcttc ctttataant ccnccnttcg    540
aattgcccgt cncccngttn ngaatgtttc cnnaaccacg gttggctccc ccaggtcncc    600
tcttacgggaa gggcctgggc cncttncaa ggttggggga accnaaaatt tcncttntgc    660
ccncccncca cnntcttgng nncncanttt ggaacccttc cnattcccct tggcctcnna    720
nccttnncta anaaaacttn aaancgtngc naaannttn acttcccccc ttacc           775
```

        <210> 26
        <211> 820
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(820)
        <223> n = A,T,C or G

        <400> 26
```
anattantac agtgtaatct tttcccagag gtgtgtanag ggaacggggc ctagaggcat    60
cccanagata ncttatanca acagtgcttt gaccaagagc tgctgggcac atttcctgca    120
gaaaaggtgg cggtccccat cactcctcct ctcccatagc catcccagag gggtgagtag    180
ccatcangcc ttcggtggga gggagtcang gaaacaacan accacagagc anacagacca    240
ntgatgacca tgggcgggag cgagcctctt ccctgnaccg gggtggcana nganagccta    300
nctgaggggt cacactataa acgttaacga ccnagatnan cacctgcttc aagtgcaccc    360
ttcctacctg acnaccagng accnnnaact gcngcctggg gacagcnctg ggancagcta    420
acnnagcact cacctgcccc cccatggccg tncgcntccc tggtcctgnc aagggaagct    480
```

```
ccctgttgga attncgggga naccaaggga nccccctcct ccanctgtga aggaaaaann       540
gatggaattt tncccttccg gccnntcccc tcttccttta cacgccccct nntactcntc       600
tccctctntt ntcctgncnc acttttnacc ccnnnatttc ccttnattga tcggannctn       660
ganattccac tnncgcctnc cntcnatcng naanacnaaa nactntctna cccnggggat       720
gggnncctcg ntcatcctct cttttcnct accnccnntt ctttgcctct ccttngatca        780
tccaaccntc gntggccntn ccccccnnn tcctttnccc                              820
```

        <210> 27
        <211> 818
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(818)
        <223> n = A,T,C or G

        <400> 27
```
tctgggtgat ggcctcttcc tcctcaggga cctctgactg ctctgggcca aagaatctct       60
tgtttcttct ccgagcccca ggcagcggtg attcagccct gcccaacctg attctgatga       120
ctgcggatgc tgtgacggac ccaaggggca aatagggtcc cagggtccag ggaggggcgc       180
ctgctgagca cttccgcccc tcaccctgcc cagcccctgc catgagctct gggctgggtc       240
tccgcctcca gggttctgct cttccangca ngccancaag tggcgctggg ccacactggc       300
ttcttcctgc cccntccctg gctctgantc tctgtcttcc tgtcctgtgc angcnccttg       360
gatctcagtt tccctcnctc anngaactct gtttctgann tcttcantta actntgantt       420
tatnaccnan tggnctgtnc tgtcnnactt taatgggccn gaccggctaa tccctccctc       480
nctcccttcc anttcnnnna accngcttnc cntcntctct ccntancceg ccngggaanc       540
ctcctttgcc ctnaccangg gccnnnaccg cccntnnctn gggggcnng gtnnctncnc        600
ctgntnncce cnctcncnnt tncctcgtcc cnncnncgcn nngcannttc ncngtcccnn       660
tnnctcttcn ngtntcgnaa ngntcncntn tnnnnngncn ngntnntncn tccctctcnc       720
cnnntgnang tnnttnnnnc ncngnncccc nnnncnnnnn nggnnntnnn tctncncngc        780
cccnnccccc ngnattaagg cctccnntct ccggccnc                              818
```

        <210> 28
        <211> 731
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(731)
        <223> n = A,T,C or G

        <400> 28
```
aggaagggcg gagggatatt gtangggatt gagggatagg agnataangg gggaggtgtg       60
tcccaacatg anggtgnngt tctcttttga angagggttg ngtttttann ccnggtgggt       120
gattnaaccc cattgtatgg agnnaaaggn tttnagggat ttttcggctc ttatcagtat       180
ntanattcct gtnaatcgga aaatnatntt tcnncnggaa aatnttgctc ccatccgnaa       240
attnctcccg ggtagtgcat nttnggggggn cngccangtt tcccaggctg ctanaatcgt       300
actaaagntt naagtgggan tncaaatgaa aacctnncac agagnatccn tacccgactg       360
tnnnttncct tcgccctntg actctgcnng agcccaatac ccnngngnat gtcnccngn        420
nnngcgncnc tgaaannnnc tcgnggctnn gancatcang gggtttcgca tcaaaagcnn       480
cgtttcncat naaggcactt tngcctcatc caaccnctng ccctcnncca tttngccgtc       540
nggttcncct acgctnntng cncctnnntn ganattttnc ccgcctnggg naancctcct      600
gnaatgggta gggncttntc ttttnaccnn gnggtntact aatcnnctnc acgcntnctt       660
tctcnacccc cccccttttt caatcccanc ggcnaatggg gtctccccnn cgangggggg      720
nnncccannc c                                                           731
```

14

```
<210> 29
<211> 822
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(822)
<223> n = A,T,C or G

<400> 29
actagtccag tgtggtggaa ttccattgtg ttggggncnc ttctatgant antnttagat        60
cgctcanacc tcacancctc ccnacnangc ctataangaa nannaataga nctgtncnnt       120
atntntacnc tcatanncct cnnacccac tccctcttaa cccntactgt gcctatngcn       180
tnnctantct ntgccgcctn cnanccaccn gtgggccnac cncnngnatt ctcnatctcc       240
tcnccatntn gcctananta ngtncatacc ctatacctac nccaatgcta nnnctaancn       300
tccatnantt annntaacta ccactgacnt ngactttcnc atnanctcct aatttgaatc       360
tactctgact cccacngcct annnattagc ancntccccc nacnatntct caaccaaatc       420
ntcaacaacc tatctanctg ttcnccaacc nttncctccg atcccnnac aaccccctc        480
ccaaataccc nccacctgac ncctaacccn caccatcccg gcaagccnan ggncatttan       540
ccactggaat cacnatngga naaaaaaaac ccnaactctc tancncnnat ctccctaana       600
aatnctcctn naatttactn ncantnccat caancccacn tgaaacnnaa cccctgtttt       660
tanatccctt ctttcgaaaa ccnacccttt annncccaac ctttngggcc ccccnctnc       720
ccnaatgaag gncncccaat cnangaaacg nccntgaaaa ancnaggcna anannntccg       780
canatcctat cccttanttn ggggncccctt ncccngggcc cc                       822

<210> 30
<211> 787
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(787)
<223> n = A,T,C or G

<400> 30
cggccgcctg ctctggcaca tgcctcctga atggcatcaa aagtgatgga ctgcccattg        60
ctagagaaga ccttctctcc tactgtcatt atggagccct gcagactgag ggctcccctt       120
gtctgcagga tttgatgtct gaagtcgtgg agtgtggctt ggagctcctc atctacatna       180
gctggaagcc ctggagggcc tctctcgcca gcctcccccct tctctccacg ctctccangg       240
acaccagggg ctccaggcag cccattattc ccagnangac atggtgtttc tccacgcgga       300
cccatggggc ctgnaaggcc agggtctcct ttgacaccat ctctcccgtc ctgcctggca       360
ggccgtggga tccactantt ctanaacggn cgccacccg gtgggagctc cagcttttgt       420
tcccnttaat gaaggttaat tgcncgcttg gcgtaatcat nggtcanaac tntttcctgt       480
gtgaaattgt ttntcccctc ncnattccnc ncnacatacn aacccggaan cataaagtgt       540
taaagcctgg gggtngcctn nngaatnaac tnaactcaat taattgcgtt ggctcatggc       600
ccgctttccn ttcnggaaaa ctgtcntccc ctgcnttnnt gaatcggcca cccccnnggg       660
aaaagcggtt tgcnttttng ggggntcctt ccncttcccc cctcnctaan ccctncgcct       720
cggtcgttnc nggtngcggg gaangggnat nnnctcccnc naagggggng agnnngntat       780
ccccaaa                                                               787

<210> 31
<211> 799
<212> DNA
<213> Homo sapien

<220>
```

15

```
        <221> misc_feature
        <222> (1)...(799)
        <223> n = A,T,C or G

    <400> 31
tttttttttt tttttttggc gatgctactg tttaattgca ggaggtgggg gtgtgtgtac      60
catgtaccag ggctattaga agcaagaagg aaggagggag ggcagagcgc cctgctgagc     120
aacaaaggac tcctgcagcc ttctctgtct gtctcttggc gcaggcacat ggggaggcct     180
cccgcagggt gggggccacc agtccagggg tggagcact acangggtg ggagtggggtg     240
gtggctggtn cnaatggcct gncacanatc cctacgattc ttgacacctg gatttcacca     300
ggggaccttc tgttctccca nggnaacttc ntnnatctcn aaagaacaca actgtttctt     360
cngcanttct ggctgttcat ggaaagcaca ggtgtccnat ttnggctggg acttggtaca     420
tatggttccg gcccacctct cccntcnaan aagtaattca cccccccccn ccntctnttg     480
cctgggccct taantaccca caccggaact canttantta ttcatcttng gntgggcttg     540
ntnatcnccn cctgaangcg ccaagttgaa aggccacgcc gtncccnctc cccatagnan     600
nttttnncnt canctaatgc ccccccnggc aacatccaa tcccccccccn tggggccccc     660
agcccanggc ccccgnctcg ggnnnccngn cncgnantcc ccaggntctc ccantcngnc     720
ccnnngcncc cccgcacgca gaacanaagg ntngagccnc cgcannnnnn nggtnncnac     780
ctcgcccccc ccnncgnng                                                  799
```

```
        <210> 32
        <211> 789
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(789)
        <223> n = A,T,C or G

    <400> 32
tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt      60
ttttnccnag ggcaggttta ttgacaacct cncgggacac aancaggctg gggacaggac     120
ggcaacaggc tccggcggcg gcggcggcgg ccctacctgc ggtaccaaat ntgcagcctc     180
cgctcccgct tgatnttcct ctgcagctgc aggatgccnt aaacagggc ctcggccntn     240
ggtgggcacc ctgggatttn aatttccacg ggcacaatgc ggtcgcancc cctcaccacc     300
nattaggaat agtggtntta cccnccnccg ttggcncact ccccntggaa accacttntc     360
gcggctccgg catctggtct taaaccttgc aaacnctggg gccctctttt tggttantnt     420
nccngccaca atcatnactc agactggcnc gggctggccc caaaaaancn ccccaaaacc     480
ggnccatgtc ttnncggggt tgctgcnatn tncatcacct cccgggcnca ncaggncaac     540
ccaaaagttc ttgnggcccn caaaaaanct ccggggggnc ccagtttcaa caaagtcatc     600
cccttggcc cccaaatcct cccccgntt nctgggtttg ggaacccacg cctctnnctt     660
tggnnggcaa gntggntccc ccttcgggcc cccggtgggc ccnnctctaa ngaaaacncc     720
ntcctnnnca ccatccccc nngnnacgnc tancaangna tccctttttt tanaaacggg     780
ccccccncg                                                            789
```

```
        <210> 33
        <211> 793
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(793)
        <223> n = A,T,C or G

    <400> 33
gacagaacat gttggatggt ggagcacctt tctatacgac ttacaggaca gcagatgggg      60
```

16

```
aattcatggc tgttggagca atanaacccc agttctacga gctgctgatc aaaggacttg      120
gactaaagtc tgatgaactt cccaatcaga tgagcatgga tgattggcca gaaatgaana      180
agaagtttgc agatgtattt gcaaagaaga cgaaggcaga gtggtgtcaa atctttgacg      240
gcacagatgc ctgtgtgact ccggttctga cttttgagga ggttgttcat catgatcaca      300
acaangaacg gggctcgttt atcaccantg aggagcagga cgtgagcccc cgccctgcac      360
ctctgctgtt aaacacccca gccatccctt ctttcaaaag ggatccacta cttctagagc      420
ggncgccacc gcggtggagc tccagctttt gttcccttta gtgagggtta attgcgcgct      480
tggcgtaatc atggtcatan ctgtttcctg tgtgaaattg ttatccgctc acaattccac      540
acaacatacg anccggaagc atnaaatttt aaagcctggg ggtngcctaa tgantgaact      600
nactcacatt aattggcttt gcgctcactg cccgctttcc agtccggaaa acctgtcctt      660
gccagctgcc nttaatgaat cnggccaccc cccgggggaaa aggcngtttg cttnttgggg      720
cgcncttccc gctttctcgc ttcctgaant ccttcccccc ggtctttcgg cttgcggcna      780
acggtatcna cct                                                        793
```

```
        <210> 34
        <211> 756
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(756)
        <223> n = A,T,C or G

        <400> 34
gccgcgaccg gcatgtacga gcaactcaag ggcgagtgga accgtaaaag ccccaatctt       60
ancaagtgcg gggaanagct gggtcgactc aagctagttc ttctggagct caacttcttg      120
ccaaccacag ggaccaagct gaccaaacag cagctaattc tggcccgtga catactggag      180
atcggggccc aatggagcat cctacgcaan gacatccct ccttcgagcg ctacatggcc      240
cagctcaaat gctactactt tgattacaan gagcagctcc ccgagtcagc ctatatgcac      300
cagctcttgg gcctcaacct cctcttcctg ctgtcccaga accgggtggc tgantnccac      360
acgganttgg ancggctgcc tgcccaanga catacanacc aatgtctaca tcnaccacca      420
gtgtcctgga gcaatactga tgganggcag ctaccncaaa gtnttctgg ccnagggtaa      480
catccccgc cgagagctac accttcttca ttgacatcct gctcgacact atcagggatg      540
aaaatcgcng ggttgctcca gaaaggctnc aanaanatcc ttttcnctga aggccccgg      600
atncnctagt nctagaatcg gcccgccatc gcggtgganc ctccaacctt tcgttncct      660
ttactgaggg ttnattgccg cccttggcgt tatcatggtc acnccngttn cctgtgttga      720
aattnttaac cccccacaat tccacgccna cattng                               756
```

```
        <210> 35
        <211> 834
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(834)
        <223> n = A,T,C or G

        <400> 35
ggggatctct anatcnacct gnatgcatgg ttgtcggtgt ggtcgctgtc gatgaanatg       60
aacaggatct tgcccttgaa gctctcggct gctgtnttta agttgctcag tctgccgtca      120
tagtcagaca cnctcttggg caaaaaacan caggatntga gtcttgattt cacctccaat      180
aatcttcngg gctgtctgct cggtgaactc gatgacnang ggcagctggt tgtgtntgat      240
aaantccanc angttctcct tggtgacctc cccttcaaag ttgttccggc cttcatcaaa      300
cttctnnaan angannancc canctttgtc gagctggnat ttgganaaca cgtcactgtt      360
ggaaactgat cccaaatggt atgtcatcca tcgcctctgc tgcctgcaaa aaacttgctt      420
ggcncaaatc cgactcccn tccttgaaag aagccnatca cacccccctc cctggactcc      480
```

17

```
nncaangact ctnccgctnc cccntccnng cagggttggt ggcannccgg gcccntgcgc      540
ttcttcagcc agttcacnat nttcatcagc ccctctgcca gctgttntat tccttggggg      600
ggaanccgtc tctcccttcc tgaannaact ttgaccgtng gaatagccgc gcntcnccnt      660
acntnctggg ccgggttcaa antccctccn ttgncnntcn cctcgggcca ttctggattt      720
nccnaacttt ttccttcccc cnccccncgg ngtttggntt tttcatnggg ccccaactct      780
gctnttggcc antcccctgg gggcntntan cnccccctnt ggtcccntng ggcc           834
```

        `<210> 36`
        `<211> 814`
        `<212> DNA`
        `<213> Homo sapien`

        `<220>`
        `<221> misc_feature`
        `<222> (1)...(814)`
        `<223> n = A,T,C or G`

        `<400> 36`
```
cggncgcttt ccngccgcgc cccgtttcca tgacnaaggc tccttcang ttaaatacnn       60
cctagnaaac attaatgggt tgctctacta atacatcata cnaaccagta agcctgccca      120
naacgccaac tcaggccatt cctaccaaag gaagaaaggc tggtctctcc accccctgta      180
ggaaaggcct gccttgtaag acaccacaat ncggctgaat ctnaagtctt gtgttttact      240
aatggaaaaa aaaaataaac aanaggtttt gttctcatgg ctgcccaccg cagcctggca      300
ctaaaacanc ccagcgctca cttctgcttg ganaaatatt ctttgctctt ttggacatca      360
ggcttgatgg tatcactgcc acntttccac ccagctgggc ncccttcccc catntttgtc      420
antganctgg aaggcctgaa ncttagtctc caaaagtctc ngcccacaag accggccacc      480
aggggangtc ntttncagtg gatctgccaa anantacccn tatcatcnnt gaataaaaag      540
gcccctgaac ganatgcttc cancancctt taagacccat aatcctngaa ccatggtgcc      600
cttccggtct gatccnaaag gaatgttcct gggtcccant ccctcctttg ttncttacgt      660
tgtnttggac ccntgctngn atnacccaan tganatcccc ngaagcaccc tncccctggc      720
atttganttt cntaaattct ctgccctacn nctgaaagca cnattccctn ggcnccnaan      780
ggngaactca agaaggtctn ngaaaaacca cncn                                 814
```

        `<210> 37`
        `<211> 760`
        `<212> DNA`
        `<213> Homo sapien`

        `<220>`
        `<221> misc_feature`
        `<222> (1)...(760)`
        `<223> n = A,T,C or G`

        `<400> 37`
```
gcatgctgct cttcctcaaa gttgttcttg ttgccataac aaccaccata ggtaaagcgg       60
gcgcagtgtt cgctgaaggg gttgtagtac cagcgcggga tgctctcctt gcagagtcct      120
gtgtctggca ggtccacgca atgccctttg tcactgggga aatggatgcg ctggagctcg      180
tcnaanccac tcgtgtattt ttcacangca gcctcctccg aagcntccgg gcagttgggg      240
gtgtcgtcac actccactaa actgtcgatn cancagccca ttgctgcagc ggaactgggt      300
gggctgacag gtgccagaac acactggatn ggcctttcca tggaagggcc tgggggaaat      360
cncctnancc caaactgcct ctcaaaggcc accttgcaca ccccgacagg ctagaaatgc      420
actcttcttc ccaaaggtag ttgttcttgt tgcccaagca ncctccanca aaccaaaanc      480
ttgcaaaatc tgctccgtgg gggtcatnnm taccanggtt ggggaaanaa accggcngn      540
ganccncctt gtttgaatgc naaggnaata atcctcctgt cttgcttggg tggaanagca      600
caattgaact gttaacnttg ggccgngttc cnctngggtg gtctgaaact aatcaccgtc      660
actggaaaaa ggtangtgcc ttccttgaat tcccaaantt cccctngntt tgggtnnttt      720
ctcctctncc ctaaaaatcg tnttcccccc ccntanggcg                           760
```

18

```
<210> 38
<211> 724
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(724)
<223> n = A,T,C or G

<400> 38
tttttttttt tttttttttt tttttttttt tttttaaaaa cccccctccat tgaatgaaaa      60
cttccnaaat tgtccaaccc cctcnnccaa atnnccattt ccggggggggg gttccaaacc     120
caaattaatt ttgganttta aattaaatnt tnattngggg aanaanccaa atgtnaagaa     180
aatttaaccc attatnaact taaatncctn gaaacccntg gnttccaaaa attttttaacc    240
cttaaatccc tccgaaattg ntaanggaaa accaaattcn cctaaggctn tttgaaggtt     300
ngatttaaac ccccttnant tnttttnacc cnngnctnaa ntatttngnt tccggtgttt     360
tcctnttaan cntnggtaac tcccgntaat gaannnccct aanccaatta aaccgaattt     420
ttttgaatt ggaaattccn ngggaattna ccggggtttt tcccntttgg gggccatncc      480
cccnctttcg gggtttgggn ntaggttgaa tttttnnang ncccaaaaaa nccccccaana   540
aaaaaactcc caagnnttaa ttngaatntc ccccttccca ggccttttgg gaaaggnggg    600
tttntggggg ccngggantt cnttcccccn ttnccncccc cccccnggt aaanggttat     660
ngnntttggt ttttgggccc cttnanggac cttccggatn gaaattaaat ccccgggncg    720
gccg                                                                        724
```

```
<210> 39
<211> 751
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(751)
<223> n = A,T,C or G

<400> 39
tttttttttt ttttctttg ctcacattta attttattt tgattttttt taatgctgca      60
caacacaata tttatttcat ttgtttcttt tatttcattt tatttgtttg ctgctgctgt     120
tttatttatt tttactgaaa gtgagaggga acttttgtgg cctttttttcc ttttttctgta  180
ggccgcctta agctttctaa atttggaaca tctaagcaag ctgaanggaa aaggggggttt   240
cgcaaaatca ctcgggggaa nggaaaggtt gctttgttaa tcatgcccta tggtgggtga    300
ttaactgctt gtacaattac ntttcacttt taattaattg tgctnaangc tttaattana    360
cttggggggtt ccctccccan accaaccccn ctgacaaaaa gtgccngccc tcaaatnatg    420
tcccggcnnt cnttgaaaca cacngcngaa ngttctcatt ntccccncnc caggtnaaaa    480
tgaagggtta ccatntttaa cnccacctcc acntggcnnn gcctgaatcc tcnaaaancn    540
ccctcaancn aattnctnng cccccggtcnc gcntnngtcc cnccccgggct ccgggaantn   600
caccccccnga annccnntnnc naacnaaatt ccgaaaatat tcccccntcnc tcaattcccc   660
cnnagactnt cctcnncnan cncaattttc ttttnntcac gaacncgnnc cnnaaaatgn    720
nnnncncctc cnctngtccn naatcnccan c                                          751
```

```
<210> 40
<211> 753
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(753)
```

19

```
    <223> n = A,T,C or G

    <400> 40
gtggtatttt ctgtaagatc aggtgttcct ccctcgtagg tttagaggaa acaccctcat      60
agatgaaaac cccccgaga cagcagcact gcaactgcca agcagccggg gtaggaggggg     120
cgccctatgc acagctgggc ccttgagaca gcagggcttc gatgtcaggc tcgatgtcaa     180
tggtctggaa gcggcggctg tacctgcgta ggggcacacc gtcagggccc accaggaact     240
tctcaaagtt ccaggcaacn tcgttgcgac acaccggaga ccaggtgatn agcttggggt     300
cggtcataan cgcggtggcg tcgtcgctgg gagctggcag ggcctcccgc aggaaggcna     360
ataaaaggtg cgccccgca ccgttcanct cgcacttctc naanaccatg angttgggct      420
cnaacccacc accannccgg acttccttga nggaattccc aaatctcttc gntcttgggc     480
ttctnctgat gccctanctg gttgcccngn atgccaanca ncccaanccc ccggggtcct     540
aaancacccn cctcctcntt tcatctgggt tnttntcccc ggaccntggt tcctctcaag     600
ggancccata tctcnaccan tactcaccnt nccccccnt gnnacccanc cttctanngn      660
ttcccncccg ncctctggcc cntcaaanan gcttncacna cctgggtctg ccttccccc      720
tncctatct gnaccccncn tttgtctcan tnt                                   753

    <210> 41
    <211> 341
    <212> DNA
    <213> Homo sapien

    <400> 41
actatatcca tcacaacaga catgcttcat cccatagact tcttgacata gcttcaaatg      60
agtgaaccca tccttgattt atatacatat atgttctcag tattttggga gcctttccac     120
ttctttaaac cttgttcatt atgaacactg aaaataggaa tttgtgaaga gttaaaaagt     180
tatagcttgt ttacgtagta agttttttgaa gtctacattc aatccagaca cttagttgag     240
tgttaaactg tgatttttaa aaaatatcat ttgagaatat tctttcagag gtattttcat     300
ttttactttt tgattaattg tgttttatat attagggtag t                         341

    <210> 42
    <211> 101
    <212> DNA
    <213> Homo sapien

    <400> 42
acttactgaa tttagttctg tgctcttcct tatttagtgt tgtatcataa atactttgat      60
gtttcaaaca ttctaaataa ataattttca gtggcttcat a                         101

    <210> 43
    <211> 305
    <212> DNA
    <213> Homo sapien

    <400> 43
acatctttgt tacagtctaa gatgtgttct taaatcacca ttccttcctg gtcctcaccc      60
tccagggtgg tctcacactg taattagagc tattgaggag tctttacagc aaattaagat     120
tcagatgcct tgctaagtct agagttctag agttatgttt cagaaagtct aagaaaccca     180
cctcttgaga ggtcagtaaa gaggacttaa tatttcatat ctacaaaatg accacaggat     240
tggatacaga acgagagtta tcctggataa ctcagagctg agtacctgcc cgggggccgc     300
tcgaa                                                                 305

    <210> 44
    <211> 852
    <212> DNA
    <213> Homo sapien

    <220>
```

20

```
<221> misc_feature
<222> (1)...(852)
<223> n = A,T,C or G

    <400> 44
acataaatat cagagaaaag tagtctttga aatatttacg tccaggagtt ctttgtttct    60
gattatttgg tgtgtgtttt ggtttgtgtc caaagtattg gcagcttcag ttttcatttt    120
ctctccatcc tcgggcattc ttcccaaatt tatataccag tcttcgtcca tccacacgct    180
ccagaatttc tcttttgtag taatatctca tagctcggct gagcttttca taggtcatgc    240
tgctgttgtt cttcttttta ccccatagct gagccactgc ctctgatttc aagaacctga    300
agacgccctc agatcggtct tcccatttta ttaatcctgg gttcttgtct gggttcaaga    360
ggatgtcgcg gatgaattcc cataagtgag tccctctcgg gttgtgcttt ttggtgtggc    420
acttggcagg ggggtcttgc tcctttttca tatcaggtga ctctgcaaca ggaaggtgac    480
tggtggttgt catggagatc tgagcccggc agaaagtttt gctgtccaac aaatctactg    540
tgctaccata gttggtgtca tataaatagt tctngtcttt ccaggtgttc atgatggaag    600
gctcagtttg ttcagtcttg acaatgacat tgtgtgtgga ctggaacagg tcactactgc    660
actggccgtt ccacttcaga tgctgcaagt tgctgtagag gagntgcccc gccgtccctg    720
ccgcccgggt gaactcctgc aaactcatgc tgcaaaggtg ctcgccgttg atgtcgaact    780
cntggaaagg gatacaattg gcatccagct ggttggtgtc caggaggtga tggagccact    840
cccacacctg gt                                                        852

    <210> 45
    <211> 234
    <212> DNA
    <213> Homo sapien

    <400> 45
acaacagacc cttgctcgct aacgacctca tgctcatcaa gttggacgaa tccgtgtccg    60
agtctgacac catccggagc atcagcattg cttcgcagtg ccctaccgcg gggaactctt    120
gcctcgtttc tggctggggt ctgctggcga acggcagaat gcctaccgtg ctgcagtgcg    180
tgaacgtgtc ggtggtgtct gaggaggtct gcagtaagct ctatgacccg ctgt          234

    <210> 46
    <211> 590
    <212> DNA
    <213> Homo sapien

    <220>
    <221> misc_feature
    <222> (1)...(590)
    <223> n = A,T,C or G

    <400> 46
acttttattt taaatgttta taaggcagat ctatgagaat gatagaaaac atggtgtgta    60
atttgatagc aatattttg agattacaga gttttagtaa ttaccaatta cacagttaaa    120
aagaagataa tatattccaa gcanatacaa aatatctaat gaaagatcaa ggcaggaaaa    180
tgantataac taattgacaa tggaaaatca attttaatgt gaattgcaca ttatccttta    240
aaagctttca aaanaaanaa ttattgcagt ctanttaatt caaacagtgt taaatggtat    300
caggataaan aactgaaggg canaagaat taatttcac ttcatgtaac ncacccanat    360
ttacaatggc ttaaatgcan ggaaaaagca gtggaagtag ggaagtantc aaggtctttc    420
tggtctctaa tctgccttac tctttgggtg tggctttgat cctctggaga cagctgccag    480
ggctcctgtt atatccacaa tcccagcagc aagatgaagg gatgaaaaag gacacatgct    540
gccttccttt gaggagactt catctcactg gccaacactc agtcacatgt                590

    <210> 47
    <211> 774
    <212> DNA
    <213> Homo sapien
```

21

```
<220>
<221> misc_feature
<222> (1)...(774)
<223> n = A,T,C or G

  <400> 47·
acaaggggc ataatgaagg agtggggana gattttaaag aaggaaaaaa aacgaggccc        60
tgaacagaat tttcctgnac aacggggctt caaaataatt ttcttgggga ggttcaagac       120
gcttcactgc ttgaaactta aatggatgtg ggacanaatt ttctgtaatg accctgaggg       180
cattacagac gggactctgg gaggaaggat aaacagaaag gggacaaagg ctaatcccaa       240
aacatcaaag aaaggaaggt ggcgtcatac ctcccagcct acacagttct ccagggctct       300
cctcatccct ggaggacgac agtggaggaa caactgacca tgtccccagg ctcctgtgtg       360
ctggctcctg gtcttcagcc cccagctctg gaagcccacc ctctgctgat cctgcgtggc       420
ccacactcct tgaacacaca tccccaggtt atattcctgg acatggctga acctcctatt       480
cctacttccg agatgccttg ctccctgcag cctgtcaaaa tcccactcac cctccaaacc       540
acggcatggg aagcctttct gacttgcctg attactccag catcttggaa caatccctga       600
ttccccactc cttagaggca agatagggtg gttaagagta gggctggacc acttggagcc       660
aggctgctgg cttcaaattn tggctcattt acgagctatg ggaccttggg caagtnatct       720
tcacttctat gggcntcatt ttgttctacc tgcaaaatgg gggataataa tagt            774
```

```
<210> 48
<211> 124
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(124)
<223> n = A,T,C or G

  <400> 48
canaaattga aattttataa aaaggcattt ttctcttata tccataaaat gatataattt       60
ttgcaantat anaaatgtgt cataaattat aatgttcctt aattacagct caacgcaact      120
tggt                                                                    124
```

```
<210> 49
<211> 147·
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(147)
<223> n = A,T,C or G

 ·<400> 49
gccgatgcta ctattttatt gcaggaggtg ggggtgtttt tattattctc tcaacagctt       60
tgtggctaca ggtggtgtct gactgcatna aaaanttttt tacgggtgat tgcaaaaatt      120
ttagggcacc catatcccaa gcantgt                                          147
```

```
<210> 50
<211> 107
<212> DNA
<213> Homo sapien

  <400> 50
acattaaatt aataaaagga ctgttggggt tctgctaaaa cacatggctt gatatattgc       60
```

22

```
atggtttgag gttaggagga gttaggcata tgtttttggga gaggggt                    107

        <210> 51
        <211> 204
        <212> DNA
        <213> Homo sapien

        <400> 51
gtcctaggaa gtctagggga cacacgactc tggggtcacg gggccgacac acttgcacgg        60
cgggaaggaa aggcagagaa gtgacaccgt caggggggaaa tgacagaaag gaaaatcaag      120
gccttgcaag gtcagaaagg ggactcaggg cttccaccac agccctgccc cacttggcca      180
cctccctttt gggaccagca atgt                                            204

        <210> 52
        <211> 491
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(491)
        <223> n = A,T,C or G

        <400> 52
acaaagataa catttatctt ataacaaaaa tttgatagtt ttaaaggtta gtattgtgta        60
gggtattttc caaaagacta aagagataac tcaggtaaaa agttagaaat gtataaaaca      120
ccatcagaca ggtttttaaa aaacaacata ttacaaaatt agacaatcat ccttaaaaaa      180
aaaacttctt gtatcaattt cttttgttca aaatgactga cttaantatt tttaaatatt      240
tcanaaacac ttccctcaaaa attttcaana tggtagcttt canatgtncc ctcagtccca      300
atgttgctca gataaataaa tctcgtgaga acttaccacc caccacaagc tttctgggggc      360
atgcaacagt gtcttttctt tncttttttct ttttttttttt ttacaggcac agaaactcat      420
caattttatt tggataacaa agggtctcca aattatattg aaaaataaat ccaagttaat      480
atcactcttg t                                                          491

        <210> 53
        <211> 484
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(484)
        <223> n = A,T,C or G

        <400> 53
acataattta gcagggctaa ttaccataag atgctattta ttaanaggtn tatgatctga        60
gtattaacag ttgctgaagt ttggtatttt tatgcagcat tttctttttg ctttgataac      120
actacagaac ccttaaggac actgaaaatt agtaagtaaa gttcagaaac attagctgct      180
caatcaaatc tctacataac actatagtaa ttaaaacgtt aaaaaaaagt gttgaaatct      240
gcactagtat anaccgctcc tgtcaggata anactgcttt ggaacagaaa gggaaaaanc      300
agctttgant ttctttgtgc tgatangagg aaaggctgaa ttaccttgtt gcctctccct      360
aatgattggc aggtcnggta aatnccaaaa catattccaa ctcaacactt cttttccncg      420
tancttgant ctgtgtattc caggancagg cggatggaat gggccagccc ncggatgttc      480
cant                                                                  484

        <210> 54
        <211> 151
        <212> DNA
```

23

```
<213> Homo sapien

<400> 54
actaaacctc gtgcttgtga actccataca gaaaacggtg ccatccctga acacggctgg      60
ccactgggta tactgctgac aaccgcaaca acaaaaacac aaatccttgg cactggctag     120
tctatgtcct ctcaagtgcc tttttgtttg t                                    151

<210> 55
<211> 91
<212> DNA
<213> Homo sapien

<400> 55
acctggcttg tctccgggtg gttcccggcg cccccacgg tccccagaac ggacactttc       60
gccctccagt ggatactcga gccaaagtgg t                                     91

<210> 56
<211> 133
<212> DNA
<213> Homo sapien

<400> 56
ggcggatgtg cgttggttat atacaaatat gtcattttat gtaagggact tgagtatact      60
tggatttttg gtatctgtgg gttgggggga cggtccagga accaataccc catggatacc     120
aagggacaac tgt                                                        133

<210> 57
<211> 147
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(147)
<223> n = A,T,C or G

<400> 57
actctggaga acctgagccg ctgctccgcc tctgggatga ggtgatgcan gcngtggcgc      60
gactgggagc tgagcccttc cctttgcgcc tgcctcagag gattgttgcc gacntgcana     120
tctcantggg ctggatncat gcagggt                                         147

<210> 58
<211> 198
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(198)
<223> n = A,T,C or G

<400> 58
acagggatat aggtttnaag ttattgtnat tgtaaaatac attgaatttt ctgtatactc      60
tgattacata catttatcct ttaaaaaaga tgtaaatctt aatttttatg ccatctatta     120
atttaccaat gagttacctt gtaaatgaga agtcatgata gcactgaatt ttaactagtt     180
ttgacttcta agtttggt                                                   198

<210> 59
```

24

```
        <211> 330
        <212> DNA
        <213> Homo sapien

        <400> 59
acaacaaatg ggttgtgagg aagtcttatc agcaaaactg gtgatggcta ctgaaaagat     60
ccattgaaaa ttatcattaa tgattttaaa tgacaagtta tcaaaaactc actcaatttt    120
cacctgtgct agcttgctaa aatgggagtt aactctagag caaatatagt atcttctgaa    180
tacagtcaat aaatgacaaa gccagggcct acaggtggtt tccagacttt ccagacccag    240
cagaaggaat ctattttatc acatggatct ccgtctgtgc tcaaaatacc taatgatatt    300
tttcgtcttt attggacttc tttgaagagt                                      330

        <210> 60
        <211> 175
        <212> DNA
        <213> Homo sapien

        <400> 60
accgtgggtg ccttctacat tcctgacggc tccttcacca acatctggtt ctacttcggc     60
gtcgtgggct ccttcctctt catcctcatc cagctggtgc tgctcatcga ctttgcgcac    120
tcctggaacc agcggtggct gggcaaggcc gaggagtgcg attcccgtgc ctggt         175

        <210> 61
        <211> 154
        <212> DNA
        <213> Homo sapien

        <400> 61
accccacttt tcctcctgtg agcagtctgg acttctcact gctacatgat gagggtgagt     60
ggttgttgct cttcaacagt atcctcccct ttccggatct gctgagccgg acagcagtgc    120
tggactgcac agccccgggg ctccacattg ctgt                                 154

        <210> 62
        <211> 30
        <212> DNA
        <213> Homo sapien

        <400> 62
cgctcgagcc ctatagtgag tcgtattaga                                      30

        <210> 63
        <211> 89
        <212> DNA
        <213> Homo sapien

        <400> 63
acaagtcatt tcagcaccct ttgctcttca aaactgacca tcttttatat ttaatgcttc     60
ctgtatgaat aaaaatggtt atgtcaagt                                       89

        <210> 64
        <211> 97
        <212> DNA
        <213> Homo sapien

        <400> 64
accggagtaa ctgagtcggg acgctgaatc tgaatccacc aataaataaa ggttctgcag     60
aatcagtgca tccaggattg gtccttggat ctggggt                              97
```

25

```
<210> 65
<211> 377
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(377)
<223> n = A,T,C or G

<400> 65
acaacaanaa ntcccttctt taggccactg atggaaacct ggaaccccct tttgatggca      60
gcatggcgtc ctaggccttg acacagcggc tggggtttgg gctntcccaa accgcacacc     120
ccaaccctgg tctacccaca nttctggcta tgggctgtct ctgccactga acatcagggt     180
tcggtcataa natgaaatcc caanggggac agaggtcagt agaggaagct caatgagaaa     240
ggtgctgttt gctcagccag aaaacagctg cctggcattc gccgctgaac tatgaacccg     300
tggggtgaa ctacccccan gaggaatcat gcctgggcga tgcaanggtg ccaacaggag      360
gggcgggagg agcatgt                                                     377

<210> 66
<211> 305
<212> DNA
<213> Homo sapien

<400> 66
acgcctttcc ctcagaattc agggaagaga ctgtcgcctg ccttcctccg ttgttgcgtg      60
agaacccgtg tgcccctcc caccatatcc accctcgctc catctttgaa ctcaaacacg      120
aggaactaac tgcaccctgg tcctctcccc agtccccagt tcaccctcca tccctcacct     180
tcctccactc taagggatat caacactgcc cagcacaggg gccctgaatt tatgtggttt     240
ttatatattt tttaataaga tgcactttat gtcatttttt aataaagtct gaagaattac     300
tgttt                                                                  305

<210> 67
<211> 385
<212> DNA
<213> Homo sapien

<400> 67
actacacaca ctccacttgc ccttgtgaga cactttgtcc cagcacttta ggaatgctga      60
ggtcggacca gccacatctc atgtgcaaga ttgcccagca gacatcaggt ctgagagttc     120
ccctttaaa aaagggggact tgcttaaaaa agaagtctag ccacgattgt gtagagcagc     180
tgtgctgtgc tggagattca cttttgagag agttctcctc tgagacctga tctttagagg     240
ctgggcagtc ttgcacatga gatggggctg gtctgatctc agcactcctt agtctgcttg     300
cctctcccag ggccccagcc tggccacacc tgcttacagg gcactctcag atgcccatac     360
catagtttct gtgctagtgg accgt                                            385

<210> 68
<211> 73
<212> DNA
<213> Homo sapien

<400> 68
acttaaccag atatattttt accccagatg gggatattct ttgtaaaaaa tgaaaataaa      60
gttttttaa tgg                                                          73

<210> 69
<211> 536
<212> DNA
```

26

```
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(536)
<223> n = A,T,C or G

    <400> 69
actagtccag tgtggtggaa ttccattgtg ttgggggctc tcaccctcct ctcctgcagc      60
tccagctttg tgctctgcct ctgaggagac catggcccag catctgagta ccctgctgct     120
cctgctggcc accctagctg tggccctggc ctggagcccc aaggaggagg ataggataat     180
cccgggtggc atctataacg cagacctcaa tgatgagtgg gtacagcgtg cccttcactt     240
cgccatcagc gagtataaca aggccaccaa agatgactac tacagacgtc cgctgcgggt     300
actaagagcc aggcaacaga ccgttggggg ggtgaattac ttcttcgacg tagaggtggg     360
ccgaaccata tgtaccaagt cccagcccaa cttggacacc tgtgccttcc atgaacagcc     420
agaactgcag aagaaacagt tgtgctcttt cgagatctac gaagttccct ggggagaaca     480
gaangtccct gggtgaaatc caggtgtcaa gaaatcctan ggatctgttg ccaggc         536

    <210> 70
    <211> 477
    <212> DNA
    <213> Homo sapien

    <400> 70
atgacccta acaggggccc tctcagccct cctaatgacc tccggcctag ccatgtgatt      60
tcacttccac tccataacgc tcctcatact aggcctacta accaacacac taaccatata     120
ccaatgatgg cgcgatgtaa cacgagaaag cacataccaa ggccaccaca caccacctgt     180
ccaaaaaggc cttcgatacg ggataatcct atttattacc tcagaagttt ttttcttcgc     240
agggattttt ctgagccttt taccactcca gcctagcccc taccccccaa ctaggagggc     300
actggccccc aacaggcatc accccgctaa atcccctaga agtcccactc ctaaacacat     360
ccgtattact cgcatcagga gtatcaatca cctgagctca ccatagtcta atagaaaaca     420
accgaaacca aattattcaa agcactgctt attacaattt tactgggtct ctatttt        477

    <210> 71
    <211> 533
    <212> DNA
    <213> Homo sapien

    <220>
    <221> misc_feature
    <222> (1)...(533)
    <223> n = A,T,C or G

    <400> 71
agagctatag gtacagtgtg atctcagctt tgcaaacaca ttttctacat agatagtact      60
aggtattaat agatatgtaa agaaagaaat cacaccatta ataatggtaa gattggttta     120
tgtgattttta gtggtatttt tggcacccctt atatatgttt tccaaacttt cagcagtgat     180
attatttcca taacttaaaa agtgagtttg aaaaagaaaa tctccagcaa gcatctcatt     240
taaataaagg tttgtcatct ttaaaaatac agcaatatgt gacttttttaa aaaagctgtc     300
aaataggtgt gaccctacta ataattatta gaaatacatt taaaaacatc gagtacctca     360
agtcagtttg ccttgaaaaa tatcaaatat aactcttaga gaaatgtaca taaaagaatg     420
cttcgtaatt ttggagtang aggttccctc ctcaatttttg tatttttaaa aagtacatgg     480
taaaaaaaaa aattcacaac agtatataag gctgtaaaat gaagaattct gcc             533

    <210> 72
    <211> 511
    <212> DNA
    <213> Homo sapien
```

27

```
        <220>
        <221> misc_feature
        <222> (1)...(511)
        <223> n = A,T,C or G

        <400> 72
tattacggaa aaacacacca cataattcaa ctancaaaga anactgcttc agggcgtgta      60
aaatgaaagg cttccaggca gttatctgat taaagaacac taaaagaggg acaaggctaa     120
aagccgcagg atgtctacac tatancaggc gctatttggg ttggctggag gagctgtgga     180
aaacatggan agattggtgc tgganatcgc cgtggctatt cctcattgtt attacanagt     240
gaggttctct gtgtgcccac tggtttgaaa accgttctnc aataatgata gaatagtaca     300
cacatgagaa ctgaaatggc ccaaacccag aaagaaagcc caactagatc ctcagaanac     360
gcttctaggg acaataaccg atgaagaaaa gatggcctcc ttgtgccccc gtctgttatg     420
atttctctcc attgcagcna naaacccgtt cttctaagca aacncaggtg atgatggcna     480
aaatacaccc cctcttgaag naccnggagg a                                    511

        <210> 73
        <211> 499
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(499)
        <223> n = A,T,C or G

        <400> 73
cagtgccagc actggtgcca gtaccagtac caataacagt gccagtgcca gtgccagcac      60
cagtggtggc ttcagtgctg gtgccagcct gaccgccact ctcacatttg ggctcttcgc     120
tggccttggt ggagctggtg ccagcaccag tggcagctct ggtgcctgtg gtttctccta     180
caagtgagat tttagatatt gttaatcctg ccagtctttc tcttcaagcc agggtgcatc     240
ctcagaaacc tactcaacac agcactctag gcagccacta tcaatcaatt gaagttgaca     300
ctctgcatta aatctatttg ccatttctga aaaaaaaaa aaaaaaaggg cggccgctcg     360
antctagagg gcccgtttaa acccgctgat cagcctcgac tgtgccttct anttgccagc     420
catctgttgt ttgcccctcc cccgntgcct tccttgaccc tggaaagtgc cactcccact     480
gtcctttcct aantaaaat                                                  499

        <210> 74
        <211> 537
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(537)
        <223> n = A,T,C or G

        <400> 74
tttcatagga gaacacactg aggagatact tgaagaattt ggattcagcc gcgaagagat      60
ttatcagctt aactcagata aaatcattga aagtaataag gtaaaagcta gtctctaact     120
tccaggccca cggctcaagt gaatttgaat actgcattta cagtgtagag taacacataa     180
cattgtatgc atggaaacat ggaggaacag tattacagtc tcctaccact ctaatcaaga     240
aaagaattac agactctgat tctacagtga tgattgaatt ctaaaaatgg taatcattag     300
ggcttttgat ttataanact ttgggtactt atactaaatt atggtagtta tactgccttc     360
cagtttgctt gatatatttg ttgatattaa gattcttgac ttatattttg aatgggttct     420
actgaaaaan gaatgatata ttcttgaaga catcgatata catttattta cactcttgat     480
tctacaatgt agaaaatgaa ggaaatgccc caaattgtat ggtgataaaa gtcccgt        537
```

28

```
        <210> 75
        <211> 467
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(467)
        <223> n = A,T,C or G

        <400> 75
caaanacaat tgttcaaaag atgcaaatga tacactactg ctgcagctca caaacacctc         60
tgcatattac acgtacctcc tcctgctcct caagtagtgt ggtctatttt gccatcatca        120
cctgctgtct gcttagaaga acggctttct gctgcaangg agagaaatca taacagacgg        180
tggcacaagg aggccatctt ttcctcatcg gttattgtcc ctagaagcgt cttctgagga        240
tctagttggg ctttctttct gggtttgggc catttcantt ctcatgtgtg tactattcta        300
tcattattgt ataacggttt tcaaaccngt gggcacncag agaacctcac tctgtaataa        360
caatgaggaa tagccacggt gatctccagc accaaatctc tccatgttnt tccagagctc        420
ctccagccaa cccaaatagc cgctgctatn gtgtagaaca tccctgn                      467

        <210> 76
        <211> 400
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(400)
        <223> n = A,T,C or G

        <400> 76
aagctgacag cattcgggcc gagatgtctc gctccgtggc cttagctgtg ctcgcgctac         60
tctctctttc tggcctggag gctatccagc gtactccaaa gattcaggtt tactcacgtc        120
atccagcaga gaatggaaag tcaaatttcc tgaattgcta tgtgtctggg tttcatccat        180
ccgacattga agttgactta ctgaagaatg gagagagaat tgaaaagtg gagcattcag         240
acttgtcttt cagcaaggac tggtctttct atctcttgta ctacactgaa ttcacccca         300
ctgaaaaaga tgagtatgcc tgccgtgtga accatgtgac tttgtcacag cccaagatng        360
ttnagtggga tcganacatg taagcagcan catgggaggt                              400

        <210> 77
        <211> 248
        <212> DNA
        <213> Homo sapien

        <400> 77
ctggagtgcc ttggtgtttc aagcccctgc aggaagcaga atgcaccttc tgaggcacct         60
ccagctgccc cggcggggga tgcgaggctc ggagcaccct tgcccggctg tgattgctgc        120
caggcactgt tcatctcagc ttttctgtcc ctttgctccc ggcaagcgct tctgctgaaa        180
gttcatatct ggagcctgat gtcttaacga ataaaggtcc catgctccac ccgaaaaaaa        240
aaaaaaaa                                                                 248

        <210> 78
        <211> 201
        <212> DNA
        <213> Homo sapien

        <400> 78
```

29

```
actagtccag tgtggtggaa ttccattgtg ttgggcccaa cacaatggct acctttaaca    60
tcacccagac cccgccctgc ccgtgcccca cgctgctgct aacgacagta tgatgcttac   120
tctgctactc ggaaactatt tttatgtaat taatgtatgc tttcttgttt ataaatgcct   180
gatttaaaaa aaaaaaaaaa a                                              201
```

```
        <210> 79
        <211> 552
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(552)
        <223> n = A,T,C or G

        <400> 79
tccttttgtt aggtttttga gacaacccta gacctaaact gtgtcacaga cttctgaatg    60
tttaggcagt gctagtaatt tcctcgtaat gattctgtta ttactttcct attctttatt   120
cctctttctt ctgaagatta atgaagttga aaattgaggt ggataaatac aaaaaggtag   180
tgtgatagta taagtatcta agtgcagatg aaagtgtgtt atatatatcc attcaaaatt   240
atgcaagtta gtaattactc agggttaact aaaattacttt aatatgctgt tgaacctact   300
ctgttccttg gctagaaaaa attataaaca ggactttgtt agtttgggaa gccaaattga   360
taatattcta tgttctaaaa gttgggctat acataaanta tnaagaaata tggaatttta   420
ttcccaggaa tatggggttc atttatgaat antacccggg anagaagttt tgantnaaac   480
cngttttggt taatacgtta atatgtcctn aatnaacaag gcntgactta tttccaaaaa   540
aaaaaaaaaa aa                                                        552
```

```
        <210> 80
        <211> 476
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(476)
        <223> n = A,T,C or G

        <400> 80
acagggattt gagatgctaa ggccccagag atcgtttgat ccaaccctct tattttcaga    60
ggggaaaatg gggcctagaa gttacagagc atctagctgg tgcgctggca cccctggcct   120
cacacagact cccgagtagc tgggactaca ggcacacagt cactgaagca ggccctgttt   180
gcaattcacg ttgccacctc caacttaaac attcttcata tgtgatgtcc ttagtcacta   240
aggttaaact ttcccaccca gaaaaggcaa cttagataaa atcttagagt actttcatac   300
tcttctaagt cctcttccag cctcactttg agtcctcctt gggggttgat aggaantntc   360
tcttggcttt ctcaataaaa tctctatcca tctcatgttt aatttggtac gcntaaaaat   420
gctgaaaaaa ttaaatgtt ctggtttcnc tttaaaaaaa aaaaaaaaa aaaaaa         476
```

```
        <210> 81
        <211> 232
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(232)
        <223> n = A,T,C or G

        <400> 81
```

30

```
tttttttttg tatgccntcn ctgtggngtt attgttgctg ccaccctgga ggagcccagt          60
ttcttctgta tctttctttt ctgggggatc ttcctggctc tgccctcca ttcccagcct          120
ctcatcccca tcttgcactt ttgctagggt tggaggcgct ttcctggtag cccctcagag         180
actcagtcag cgggaataag tcctaggggt gggggtgtg gcaagccggc ct                  232
```

```
        <210> 82
        <211> 383
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(383)
        <223> n = A,T,C or G

        <400> 82
aggcgggagc agaagctaaa gccaaagccc aagaagagtg gcagtgccag cactggtgcc          60
agtaccagta ccataacat gccagtgcca gtgccagcac cagtggtggc ttcagtgctg          120
gtgccagcct gaccgccact ctcacatttg ggctcttcgc tggccttggt ggagctggtg         180
ccagcaccag tggcagctct ggtgcctgtg gtttctccta caagtgagat tttagatatt          240
gttaatcctg ccagtctttc tcttcaagcc agggtgcatc ctcagaaacc tactcaacac          300
agcactctng gcagccacta tcaatcaatt gaagttgaca ctctgcatta aatctatttg         360
ccatttcaaa aaaaaaaaaa aaa                                                   383
```

```
        <210> 83
        <211> 494
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(494)
        <223> n = A,T,C or G

        <400> 83
accgaattgg gaccgctggc ttataagcga tcatgtcctc cagtattacc tcaacgagca          60
gggagatcga gtctatacgc tgaagaaatt tgacccgatg ggacaacaga cctgctcagc          120
ccatcctgct cggttctccc cagatgacaa atactctcga caccgaatca ccatcaagaa         180
acgcttcaag gtgctcatga cccagcaacc gcgccctgtc ctctgagggt ccttaaactg          240
atgtctttc tgccacctgt taccctcgg agactccgta accaaactct tcggactgtg           300
agccctgatg cctttttgcc agccatactc tttggcntcc agtctctcgt ggcgattgat         360
tatgcttgtg tgaggcaatc atggtggcat cacccataaa gggaacacat ttganttttt         420
tttcncatat tttaaattac naccagaata nttcagaata aatgaattga aaaactctta         480
aaaaaaaaaa aaaa                                                            494
```

```
        <210> 84
        <211> 380
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(380)
        <223> n = A,T,C or G

        <400> 84
gctggtagcc tatggcgtgg ccacggangg gctcctgagg cacgggacag tgacttccca          60
agtatcctgc gccgcgtctt ctaccgtccc tacctgcaga tcttcgggca gattccccag         120
```

31

```
gaggacatgg acgtggccct catggagcac agcaactgct cgtcggagcc cggcttctgg     180
gcacaccctc ctggggccca ggcgggcacc tgcgtctccc agtatgccaa ctggctggtg     240
gtgctgctcc tcgtcatctt cctgctcgtg gccaacatcc tgctggtcac ttgctcattg     300
ccatgttcag ttacacattc ggcaaagtac agggcaacag cnatctctac tgggaaggcc     360
agcgttnccg cctcatccgg                                                380
```

        <210> 85
        <211> 481
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(481)
        <223> n = A,T,C or G

        <400> 85
```
gagttagctc ctccacaacc ttgatgaggt cgtctgcagt ggcctctcgc ttcataccgc     60
tnccatcgtc atactgtagg tttgccacca cctcctgcat cttggggcgg ctaatatcca     120
ggaaactctc aatcaagtca ccgtcnatna aacctgtggc tggttctgtc ttccgctcgg     180
tgtgaaagga tctccagaag gagtgctcga tcttccccac acttttgatg actttattga     240
gtcgattctg catgtccagc aggaggttgt accagctctc tgacagtgag gtcaccagcc     300
ctatcatgcc nttgaacgtg ccgaagaaca ccgagccttg tgtggggggt gnagtctcac     360
ccagattctg cattaccaga nagccgtggc aaaaganatt gacaactcgc ccaggnngaa     420
aaagaacacc tcctggaagt gctngccgct cctcgtccnt tggtggnngc gcntnccttt     480
t                                                                    481
```

        <210> 86
        <211> 472
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(472)
        <223> n = A,T,C or G

        <400> 86
```
aacatcttcc tgtataatgc tgtgtaatat cgatccgatn ttgtctgctg agaattcatt     60
acttggaaaa gcaacttnaa gcctggacac tggtattaaa attcacaata tgcaacactt     120
taaacagtgt gtcaatctgc tcccttactt tgtcatcacc agtctgggaa taagggtatg     180
ccctattcac acctgttaaa agggcgctaa gcattttga ttcaacatct ttttttttga     240
cacaagtccg aaaaaagcaa aagtaaacag ttnttaattt gttagccaat tcactttctt     300
catgggacag agccatttga tttaaaaagc aaattgcata atattgagct ttgggagctg     360
atatntgagc ggaagantag cctttctact tcaccagaca caactccttt catattggga     420
tgttnacnaa agttatgtct cttacagatg ggatgctttt gtggcaattc tg             472
```

        <210> 87
        <211> 413
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(413)
        <223> n = A,T,C or G

        <400> 87

32

```
agaaaccagt atctctnaaa acaacctctc ataccttgtg gacctaattt tgtgtgcgtg        60
tgtgtgtgcg cgcatattat atagacaggc acatcttttt tacttttgta aaagcttatg       120
cctctttggt atctatatct gtgaaagttt taatgatctg ccataatgtc ttggggacct       180
ttgtcttctg tgtaaatggt actagagaaa acacctatnt tatgagtcaa tctagttngt       240
tttattcgac atgaaggaaa tttccagatn acaacactna caaactctcc cttgactagg       300
ggggacaaag aaaagcanaa ctgaacatna gaaacaattn cctggtgaga aattncataa       360
acagaaattg ggtngtatat tgaaananng catcattnaa acgttttttt ttt            413
```

        <210> 88
        <211> 448
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(448)
        <223> n = A,T,C or G

        <400> 88
```
cgcagcgggt cctctctatc tagctccagc ctctcgcctg ccccactccc cgcgtcccgc        60
gtcctagccn accatggccg ggcccctgcg cgccccgctg ctcctgctgg ccatcctggc       120
cgtggccctg gccgtgagcc ccgcggccgg ctccagtccc ggcaagccgc cgcgcctggt       180
gggaggccca tggaccccgc gtggaagaag aaggtgtgcg gcgtgcactg gactttgccg       240
tcggcnanta caacaaaccc gcaacnactt ttaccnagcn cgcgctgcag gttgtgccgc       300
cccaancaaa ttgttactng gggtaantaa ttcttggaag ttgaacctgg gccaaacnng       360
tttaccagaa ccnagccaat tngaacaatt nccctccat aacagcccct tttaaaaagg       420
gaancantcc tgntcttttc caaatttt                                        448
```

        <210> 89
        <211> 463
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(463)
        <223> n = A,T,C or G

        <400> 89
```
gaattttgtg cactggccac tgtgatggaa ccattgggcc aggatgcttt gagtttatca        60
gtagtgattc tgccaaagtt ggtgttgtaa catgagtatg taaaatgtca aaaaattagc       120
agaggtctag gtctgcatat cagcagacag tttgtccgtg tattttgtag ccttgaagtt       180
ctcagtgaca agttnnttct gatgcgaagt tctnattcca gtgtttaagt cctttgcatc       240
tttnatgttn agacttgcct ctntnaaatt gcttttgtnt tctgcaggta ctatctgtgg       300
tttaacaaaa tagaannact tctctgcttn gaanatttga atatcttaca tctnaaaatn       360
aattctctcc ccatannaaa acccangccc ttggganaat ttgaaaaang gntccttcnn       420
aattcnnana anttcagntn tcatacaaca naacngganc ccc                      463
```

        <210> 90
        <211> 400
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(400)
        <223> n = A,T,C or G

33

```
<400> 90
agggattgaa ggtctnttnt actgtcggac tgttcancca ccaactctac aagttgctgt        60
cttccactca ctgtctgtaa gcntnttaac ccagactgta tcttcataaa tagaacaaat       120
tcttcaccag tcacatcttc taggaccttt ttggattcag ttagtataag ctcttccact       180
tcctttgtta agacttcatc tggtaaagtc ttaagttttg tagaaaggaa tttaattgct       240
cgttctctaa caatgtcctc tccttgaagt atttggctga acaacccacc tnaagtccct       300
ttgtgcatcc attttaaata tacttaatag ggcattggtn cactaggtta aattctgcaa       360
gagtcatctg tctgcaaaag ttgcgttagt atatctgcca                            400
```

```
        <210> 91
        <211> 480
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(480)
        <223> n = A,T,C or G
```

```
        <400> 91
gagctcggat ccaataatct ttgtctgagg gcagcacaca tatncagtgc catggnaact        60
ggtctacccc acatgggagc agcatgccgt agntatataa ggtcattccc tgagtcagac       120
atgcctcttt gactaccgtg tgccagtgct ggtgattctc acacacctcc nnccgctctt       180
tgtggaaaaa ctggcacttg nctggaacta gcaagacatc acttacaaat tcacccacga       240
gacacttgaa aggtgtaaca aagcgactct tgcattgctt tttgtccctc cggcaccagt       300
tgtcaatact aacccgctgg tttgcctcca tcacatttgt gatctgtagc tctggataca       360
tctcctgaca gtactgaaga acttcttctt ttgtttcaaa agcaactctt ggtgcctgtt       420
ngatcaggtt cccatttccc agtccgaatg ttcacatggc atatnttact tcccacaaaa       480
```

```
        <210> 92
        <211> 477
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(477)
        <223> n = A,T,C or G
```

```
        <400> 92
atacagccca natcccacca cgaagatgcg cttgttgact gagaacctga tgcggtcact        60
ggtcccgctg tagccccagc gactctccac ctgctggaag cggttgatgc tgcactcctt       120
cccacgcagg cagcagcggg gccggtcaat gaactccact cgtggcttgg ggttgacggt       180
taantgcagg aagaggctga ccacctcgcg gtccaccagg atgcccgact gtgcgggacc       240
tgcagcgaaa ctcctcgatg gtcatgagcg ggaagcgaat gangcccagg gccttgccca       300
gaaccttccg cctgttctct ggcgtcacct gcagctgctg ccgctnacac tcggcctcgg       360
accagcggac aaacggcgtt gaacagccgc acctcacgga tgcccantgt gtcgcgctcc       420
aggaacggcn ccagcgtgtc caggtcaatg tcggtgaanc ctccgcgggt aatggcg         477
```

```
        <210> 93
        <211> 377
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(377)
        <223> n = A,T,C or G
```

34

```
     <400> 93
gaacggctgg accttgcctc gcattgtgct gctggcagga ataccttggc aagcagctcc    60
agtccgagca gccccagacc gctgccgccc gaagctaagc ctgcctctgg ccttcccctc   120
cgcctcaatg cagaaccant agtgggagca ctgtgtttag agttaagagt gaacactgtn   180
tgattttact tgggaatttc ctctgttata tagcttttcc caatgctaat ttccaaacaa   240
caacaacaaa ataacatgtt tgcctgttna gttgtataaa agtangtgat tctgtatnta   300
aagaaaatat tactgttaca tatactgctt gcaanttctg tatttattgg tnctctggaa   360
ataaatatat tattaaa                                                  377

     <210> 94
     <211> 495
     <212> DNA
     <213> Homo sapien

     <220>
     <221> misc_feature
     <222> (1)...(495)
     <223> n = A,T,C or G

     <400> 94
ccctttgagg ggttagggtc cagttcccag tggaagaaac aggccaggag aantgcgtgc    60
cgagctgang cagatttccc acagtgaccc cagagccctg ggctatagtc tctgacccct   120
ccaaggaaag accaccttct ggggacatgg gctggagggc aggacctaga ggcaccaagg   180
gaaggcccca ttccgggggct gttccccgag gaggaaggga aggggctctg tgtgcccccc   240
acgaggaana ggccctgant cctgggatca nacacccctt cacgtgtatc cccacacaaa   300
tgcaagctca ccaaggtccc ctctcagtcc cttccctaca ccctgaacgg ncactggccc   360
acacccaccc agancancca cccgccatgg ggaatgtnct caaggaatcg cngggcaacg   420
tggactctng tcccnnaagg gggcagaatc tccaatagan ggannngaacc cttgctnana   480
aaaaaaaana aaaaa                                                    495

     <210> 95
     <211> 472
     <212> DNA
     <213> Homo sapien

     <220>
     <221> misc_feature
     <222> (1)...(472)
     <223> n = A,T,C or G

     <400> 95
ggttacttgg tttcattgcc accacttagt ggatgtcatt tagaaccatt ttgtctgctc    60
cctctggaag ccttgcgcag agcggacttt gtaattgttg gagaataact gctgaatttt   120
tagctgtttt gagttgattc gcaccactgc accacaactc aatatgaaaa ctatttnact   180
tatttattat cttgtgaaaa gtatacaatg aaaatttgt tcatactgta tttatcaagt   240
atgatgaaaa gcaatagata tatattctttt tattatgttn aattatgatt gccattatta   300
atcggcaaaa tgtggagtgt atgttctttt cacagtaata tatgcctttt gtaacttcac   360
ttggttattt tattgtaaat gaattacaaa attcttaatt taagaaaatg gtangttata   420
tttanttcan taatttcttt ccttgtttac gttaattttg aaaagaatgc at          472

     <210> 96
     <211> 476
     <212> DNA
     <213> Homo sapien

     <220>
     <221> misc_feature
```

35

<222> (1)...(476)
<223> n = A,T,C or G

<400> 96
ctgaagcatt tcttcaaact tntctacttt tgtcattgat acctgtagta agttgacaat   60
gtggtgaaat ttcaaaatta tatgtaactt ctactagttt tactttctcc cccaagtctt   120
ttttaactca tgatttttac acacacaatc cagaacttat tatatagcct ctaagtcttt   180
attcttcaca gtagatgatg aaagagtcct ccagtgtctt gngcanaatg ttctagntat   240
agctggatac atacngtggg agttctataa actcatacct cagtgggact naaccaaaat   300
tgtgttagtc tcaattccta ccacactgag ggagcctccc aaatcactat attcttatct   360
gcaggtactc ctccagaaaa acngacaggg caggcttgca tgaaaaagtn acatctgcgt   420
tacaaagtct atcttcctca nangtctgtn aaggaacaat ttaatcttct agcttt   476

<210> 97
<211> 479
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(479)
<223> n = A,T,C or G

<400> 97
actctttcta atgctgatat gatcttgagt ataagaatgc atatgtcact agaatggata   60
aaataatgct gcaaacttaa tgttcttatg caaaatggaa cgctaatgaa acacagctta   120
caatcgcaaa tcaaaactca caagtgctca tctgttgtag atttagtgta ataagactta   180
gattgtgctc cttcggatat gattgtttct canatcttgg gcaatnttcc ttagtcaaat   240
caggctacta gaattctgtt attggatatn tgagagcatg aaatttttaa naatacactt   300
gtgattatna aattaatcac aaatttcact tatacctgct atcagcagct agaaaaacat   360
ntnnttttta natcaaagta ttttgtgttt ggaantgtnn aaatgaaatc tgaatgtggg   420
ttcnatctta ttttttcccn gacnactant tncttttta gggnctattc tganccatc   479

<210> 98
<211> 461
<212> DNA
<213> Homo sapien

<400> 98
agtgacttgt cctccaacaa aacccctga tcaagtttgt ggcactgaca atcagaccta   60
tgctagttcc tgtcatctat tcgctactaa atgcagactg gaggggacca aaaagggca   120
tcaactccag ctggattatt ttggagcctg caaatctatt cctacttgta cggactttga   180
agtgattcag tttcctctac ggatgagaga ctggctcaag aatatcctca tgcagcttta   240
tgaagccact ctgaacacgc tggttatcta gatgagaaca gagaaataaa gtcagaaaat   300
ttacctggag aaaagaggct ttggctgggg accatcccat tgaaccttct cttaaggact   360
ttaagaaaaa ctaccacatg ttgtgtatcc tggtgccggc cgtttatgaa ctgaccaccc   420
tttggaataa tcttgacgct cctgaacttg ctcctctgcg a   461

<210> 99
<211> 171
<212> DNA
<213> Homo sapien

<400> 99
gtggccgcgc gcaggtgttt cctcgtaccg cagggccccc tcccttcccc aggcgtccct   60
cggcgcctct gcgggcccga ggaggagcgg ctggcgggtg gggggagtgt gacccaccct   120
cggtgagaaa agccttctct agcgatctga gaggcgtgcc ttggggggtac c   171

36

```
        <210> 100
        <211> 269
        <212> DNA
        <213> Homo sapien

        <400> 100
cggccgcaag tgcaactcca gctggggccg tgcggacgaa gattctgcca gcagttggtc      60
cgactgcgac gacggcggcg gcgacagtcg caggtgcagc gcgggcgcct ggggtcttgc     120
aaggctgagc tgacgccgca gaggtcgtgt cacgtcccac gaccttgacg ccgtcgggga     180
cagccggaac agagcccggt gaagcgggag gcctcgggga gcccctcggg aagggcggcc     240
cgagagatac gcaggtgcag gtggccgcc                                      269

        <210> 101
        <211> 405
        <212> DNA
        <213> Homo sapien

        <400> 101
tttttttttt ttttggaatc tactgcgagc acagcaggtc agcaacaagt ttattttgca      60
gctagcaagg taacagggta gggcatggtt acatgttcag gtcaacttcc tttgtcgtgg     120
ttgattggtt tgtctttatg ggggcggggt ggggtagggg aaacgaagca aataacatgg     180
agtgggtgca ccctccctgt agaacctggt tacaaagctt ggggcagttc acctggtctg     240
tgaccgtcat tttcttgaca tcaatgttat tagaagtcag gatatctttt agagagtcca     300
ctgttctgga gggagattag ggtttcttgc caaatccaac aaaatccact gaaaaagttg     360
gatgatcagt acgaataccg aggcatattc tcatatcggt ggcca                    405

        <210> 102
        <211> 470
        <212> DNA
        <213> Homo sapien

        <400> 102
tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt      60
ggcacttaat ccatttttat ttcaaaatgt ctacaaattt aatcccatta tacggtattt     120
tcaaaatcta aattattcaa attagccaaa tccttaccaa ataataccca aaaatcaaaa     180
atatacttct ttcagcaaac ttgttacata aattaaaaaa atatatacgg ctggtgtttt     240
caaagtacaa ttatcttaac actgcaaaca ttttaaggaa ctaaaataaa aaaaaacact     300
ccgcaaaggt taaagggaac aacaaattct tttacaacac cattataaaa atcatatctc     360
aaatcttagg ggaatatata cttcacacgg gatcttaact tttactcact ttgtttattt     420
ttttaaacca ttgtttgggc ccaacacaat ggaatccccc ctggactagt               470

        <210> 103
        <211> 581
        <212> DNA
        <213> Homo sapien

        <400> 103
tttttttttt ttttttttga cccccctctt ataaaaaaca agttaccatt ttattttact      60
tacacatatt tattttataa ttggtattag atattcaaaa ggcagctttt aaaatcaaac     120
taaatggaaa ctgccttaga tacataattc ttaggaatta gcttaaaatc tgcctaaagt     180
gaaaatcttc tctagctctt ttgactgtaa attttttgact cttgtaaaac atccaaattc     240
attttttcttg tctttaaaat tatctaatct ttccattttt tccctattcc aagtcaattt     300
gcttctctag cctcatttcc tagctcttat ctactattag taagtggctt ttttcctaaa     360
agggaaaaca ggaagagaaa tggcacacaa aacaaacatt ttatattcat atttctacct     420
acgttaataa aatagcattt tgtgaagcca gctcaaaaga aggcttagat cctttatgt      480
ccattttagt cactaaacga tatcaaagtg ccagaatgca aaaggtttgt gaacatttat     540
tcaaaagcta atataagata tttcacatac tcatctttct g                        581
```

```
        <210> 104
        <211> 578
        <212> DNA
        <213> Homo sapien

        <400> 104
tttttttttt tttttttttt tttttctctt cttttttttt gaaatgagga tcgagttttt        60
cactctctag atagggcatg aagaaaactc atctttccag ctttaaaata acaatcaaat       120
ctcttatgct atatcatatt ttaagttaaa ctaatgagtc actggcttat cttctcctga       180
aggaaatctg ttcattcttc tcattcatat agttatatca agtactacct tgcatattga       240
gaggtttttc ttctctattt acacatatat ttccatgtga atttgtatca aacctttatt       300
ttcatgcaaa ctagaaaata atgtttcttt tgcataagag aagagaacaa tatagcatta       360
caaaactgct caaattgttt gttaagttat ccattataat tagttggcag gagctaatac       420
aaatcacatt tacgacagca ataataaaac tgaagtacca gttaaatatc caaaataatt       480
aaaggaacat ttttagcctg ggtataatta gctaattcac tttacaagca tttattagaa       540
tgaattcaca tgttattatt cctagcccaa cacaatgg                               578

        <210> 105
        <211> 538
        <212> DNA
        <213> Homo sapien

        <400> 105
tttttttttt tttttcagta ataatcagaa caatatttat ttttatattt aaaattcata        60
gaaaagtgcc ttacatttaa taaaagtttg tttctcaaag tgatcagagg aattagatat       120
gtcttgaaca ccaatattaa tttgaggaaa atacaccaaa atacattaag taaattattt       180
aagatcatag agcttgtaag tgaaaagata aaatttgacc tcagaaactc tgagcattaa       240
aaatccacta ttagcaaata aattactatg gacttcttgc tttaattttg tgatgaatat       300
ggggtgtcac tggtaaacca acacattctg aaggatacat tacttagtga tagattctta       360
tgtactttgc taatacgtgg atatgagttg acaagtttct ctttcttcaa tcttttaagg       420
ggcgagaaat gaggaagaaa agaaaaggat tacgcatact gttctttcta tggaaggatt       480
agatatgttt cctttgccaa tattaaaaaa ataataatgt ttactactag tgaaaccc        538

        <210> 106
        <211> 473
        <212> DNA
        <213> Homo sapien

        <400> 106
tttttttttt tttttagtc aagtttctat ttttattata attaaagtct tggtcatttc        60
atttattagc tctgcaactt acatatttaa attaaagaaa cgtttagac aactgtacaa       120
tttataaatg taaggtgcca ttattgagta atatattcct ccaagagtgg atgtgtccct       180
tctcccacca actaatgaac agcaacatta gtttaatttt attagtagat atacactgct       240
gcaaacgcta attctcttct ccatccccat gtgatattgt gtatatgtgt gagttggtag       300
aatgcatcac aatctacaat caacagcaag atgaagctag gctgggcttt cggtgaaaat       360
agactgtgtc tgtctgaatc aaatgatctg acctatcctc ggtggcaaga actcttcgaa       420
ccgcttcctc aaaggcgctg ccacatttgt ggctctttgc acttgtttca aaa             473

        <210> 107
        <211> 1621
        <212> DNA
        <213> Homo sapien

        <400> 107
cgccatggca ctgcagggca tctcggtcat ggagctgtcc ggcctggccc cgggcccgtt        60
ctgtgctatg gtcctggctg acttcggggc gcgtgtggta cgcgtggacc ggcccggctc       120
ccgctacgac gtgagccgct ggggccgggg caagcgctcg ctagtgctgg acctgaagca       180
gccgcgggga gccgccgtgc tgcggcgtct gtgcaagcgg tcggatgtgc tgctggagcc       240
```

```
cttccgccgc ggtgtcatgg agaaactcca gctgggccca gagattctgc agcgggaaaa      300
tccaaggctt atttatgcca ggctgagtgg atttggccag tcaggaagct tctgccggtt      360
agctggccac gatatcaact atttggcttt gtcaggtgtt ctctcaaaaa ttggcagaag      420
tggtgagaat ccgtatgccc cgctgaatct cctggctgac tttgctggtg gtggccttat      480
gtgtgcactg ggcattataa tggctctttt tgaccgcaca cgcactgaca agggtcaggt      540
cattgatgca aatatggtgg aaggaacagc atatttaagt tcttttctgt ggaaaactca      600
gaaatcgagt ctgtgggaag cacctcgagg acagaacatg ttggatggtg gagcaccttt      660
ctatacgact tacaggacag cagatgggga attcatggct gttggagcaa tagaacccca      720
gttctacgag ctgctgatca aaggacttgg actaaagtct gatgaacttc ccaatcagat      780
gagcatggat gattggccag aaatgaagaa gaagtttgca gatgtatttg caaagaagac      840
gaaggcagag tggtgtcaaa tctttgacgg cacagatgcc tgtgtgactc cggttctgac      900
ttttgaggag gttgttcatc atgatcacaa caaggaacgg ggctcgttta tcaccagtga      960
ggagcaggac gtgagcccc gccctgcacc tctgctgtta aacaccccag ccatcccttc      1020
tttcaaaagg gatcctttca taggagaaca cactgaggag atacttgaag aatttggatt      1080
cagccgcgaa gagatttatc agcttaactc agataaaatc attgaaagta ataaggtaaa      1140
agctagtctc taacttccag gcccacggct caagtgaatt tgaatactgc atttacagtg      1200
tagagtaaca cataacattg tatgcatgga aacatggagg aacagtatta cagtgtccta      1260
ccactctaat caagaaaaga attacagact ctgattctac agtgatgatt gaattctaaa      1320
aatggttatc attagggctt ttgatttata aaactttggg tacttatact aaaattatggt      1380
agttattctg ccttccagtt tgcttgatat atttgttgat attaagattc ttgacttata      1440
ttttgaatgg gttctagtga aaaaggaatg atatattctt gaagacatcg atatacattt      1500
atttacactc ttgattctac aatgtagaaa atgaggaaat gccacaaatt gtatggtgat      1560
aaaagtcacg tgaaacaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa      1620
a                                                                      1621
```

```
        <210> 108
        <211> 382
        <212> PRT
        <213> Homo sapien

        <400> 108
Met Ala Leu Gln Gly Ile Ser Val Met Glu Leu Ser Gly Leu Ala Pro
1               5                  10                  15
Gly Pro Phe Cys Ala Met Val Leu Ala Asp Phe Gly Ala Arg Val Val
        20                  25                  30
Arg Val Asp Arg Pro Gly Ser Arg Tyr Asp Val Ser Arg Leu Gly Arg
        35                  40                  45
Gly Lys Arg Ser Leu Val Leu Asp Leu Lys Gln Pro Arg Gly Ala Ala
        50                  55                  60
Val Leu Arg Arg Leu Cys Lys Arg Ser Asp Val Leu Leu Glu Pro Phe
65                  70                  75                  80
Arg Arg Gly Val Met Glu Lys Leu Gln Leu Gly Pro Glu Ile Leu Gln
                85                  90                  95
Arg Glu Asn Pro Arg Leu Ile Tyr Ala Arg Leu Ser Gly Phe Gly Gln
            100                 105                 110
Ser Gly Ser Phe Cys Arg Leu Ala Gly His Asp Ile Asn Tyr Leu Ala
        115                 120                 125
Leu Ser Gly Val Leu Ser Lys Ile Gly Arg Ser Gly Glu Asn Pro Tyr
    130                 135                 140
Ala Pro Leu Asn Leu Leu Ala Asp Phe Ala Gly Gly Gly Leu Met Cys
145                 150                 155                 160
Ala Leu Gly Ile Ile Met Ala Leu Phe Asp Arg Thr Arg Thr Asp Lys
                165                 170                 175
Gly Gln Val Ile Asp Ala Asn Met Val Glu Gly Thr Ala Tyr Leu Ser
            180                 185                 190
Ser Phe Leu Trp Lys Thr Gln Lys Ser Ser Leu Trp Glu Ala Pro Arg
        195                 200                 205
Gly Gln Asn Met Leu Asp Gly Gly Ala Pro Phe Tyr Thr Thr Tyr Arg
```

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        210                 215                 220
Thr Ala Asp Gly Glu Phe Met Ala Val Gly Ala Ile Glu Pro Gln Phe
225                 230                 235                 240
Tyr Glu Leu Leu Ile Lys Gly Leu Gly Leu Lys Ser Asp Glu Leu Pro
                245                 250                 255
Asn Gln Met Ser Met Asp Asp Trp Pro Glu Met Lys Lys Lys Phe Ala
            260                 265                 270
Asp Val Phe Ala Lys Lys Thr Lys Ala Glu Trp Cys Gln Ile Phe Asp
        275                 280                 285
Gly Thr Asp Ala Cys Val Thr Pro Val Leu Thr Phe Glu Glu Val Val
    290                 295                 300
His His Asp His Asn Lys Glu Arg Gly Ser Phe Ile Thr Ser Glu Glu
305                 310                 315                 320
Gln Asp Val Ser Pro Arg Pro Ala Pro Leu Leu Leu Asn Thr Pro Ala
                325                 330                 335
Ile Pro Ser Phe Lys Arg Asp Pro Phe Ile Gly Glu His Thr Glu Glu
            340                 345                 350
Ile Leu Glu Glu Phe Gly Phe Ser Arg Glu Glu Ile Tyr Gln Leu Asn
        355                 360                 365
Ser Asp Lys Ile Ile Glu Ser Asn Lys Val Lys Ala Ser Leu
    370                 375                 380
```

```
        <210> 109
        <211> 1524
        <212> DNA
        <213> Homo sapien

        <400> 109
ggcacgaggc tgcgccaggg cctgagcgga ggcggggggca gcctcgccag cgggggcccc        60
gggcctggcc atgcctcact gagccagcgc ctgcgcctct acctcgccga cagctggaac       120
cagtgcgacc tagtggctct cacctgcttc ctcctgggcg tgggctgccg gctgaccccg       180
ggtttgtacc acctgggccg cactgtcctc tgcatcgact tcatggtttt cacggtgcgg       240
ctgcttcaca tcttcacggt caacaaacag ctggggccca agatcgtcat cgtgagcaag       300
atgatgaagg acgtgttctt cttcctcttc ttcctcggcg tgtggctggt agcctatggc       360
gtggccacgg aggggctcct gaggccacgg gacagtgact tcccaagtat cctgcgccgc       420
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gcccaggcgg gcacctgcgt ctcccagtat gccaactggc tggtggtgct gctcctcgtc       600
atcttcctgc tcgtggccaa catcctgctg gtcaacttgc tcattgccat gttcagttac       660
acattcggca aagtacaggg caacagcgat ctctactgga aggcgcagcg ttaccgcctc       720
atccgggaat tccactctcg gcccgcgctg gccccgccct ttatcgtcat ctcccacttg       780
cgcctcctgc tcaggcaatt gtgcaggcga ccccggagcc cccagccgtc ctccccggcc       840
ctcgagcatt tccgggttta cctttctaag gaagccgagc ggaagctgct aacgtgggaa       900
tcggtgcata aggagaactt tctgctggca cgcgctaggg acaagcggga gagcgactcc       960
gagcgtctga agcgcacgtc ccagaaggtg gacttggcac tgaaacagct gggacacatc      1020
cgcgagtacg aacagcgcct gaaagtgctg gagcggggagg tccagcagtg tagccgcgtc      1080
ctggggtggg tggccgaggc cctgagccgc tctgccttgc tgcccccagg tgggccgcca      1140
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ccacagggga ttttgctcct agagtaaggc tcatctgggc ctcggccccc gcacctggtg      1260
gccttgtcct tgaggtgagc cccatgtcca tctgggccac tgtcaggacc acctttggga      1320
gtgtcatcct tacaaaccac agcatgcccg gctcctccca gaaccagtcc cagcctggga      1380
ggatcaaggc ctggatcccg ggccgttatc catctggagg ctgcagggtc cttggggtaa      1440
cagggaccac agaccccctca ccactcacag attcctcaca ctggggaaat aaagccattt     1500
cagaggaaaa aaaaaaaaaa aaaa                                             1524

        <210> 110
        <211> 3410
        <212> DNA
```

40

<213> Homo sapien

<400> 110

```
gggaaccagc ctgcacgcgc tggctccggg tgacagccgc gcgcctcggc caggatctga    60
gtgatgagac gtgtccccac tgaggtgccc cacagcagca ggtgttgagc atgggctgag   120
aagctggacc ggcaccaaag ggctggcaga aatgggcgcc tggctgattc ctaggcagtt   180
ggcggcagca aggaggagag gccgcagctt ctggagcaga gccgagacga agcagttctg   240
gagtgcctga acggcccct gagccctacc cgcctggccc actatggtcc agaggctgtg   300
ggtgagccgc ctgctgcggc accggaaagc ccagctcttg ctggtcaacc tgctaacctt   360
tggcctggag gtgtgtttgg ccgcaggcat cacctatgtg ccgcctctgc tgctggaagt   420
gggggtagag gagaagttca tgaccatggt gctgggcatt ggtccagtgc tgggcctggt   480
ctgtgtcccg ctcctaggct cagccagtga ccactggcgt ggacgctatg gccgccgccg   540
gcccttcatc tgggcactgt ccttgggcat cctgctgagc ctctttctca tcccaagggc   600
cggctggcta gcagggctgc tgtgcccgga tcccaggccc ctggagctgg cactgctcat   660
cctgggcgtg gggctgctgg acttctgtgg ccaggtgtgc ttcactccac tggaggccct   720
gctctctgac ctcttccggg acccggacca ctgtcgccag gcctactctg tctatgcctt   780
catgatcagt cttgggggct gcctgggcta cctcctgcct gccattgact gggacaccag   840
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cgagccagca gaagggctgt cggcccccctc cttgtcgccc cactgctgtc catgccgggc  1020
ccgcttggct ttccggaacc tgggcgccct gcttccccgg ctgcaccagc tgtgctgccg  1080
catgcccgc accctgcgcc ggctcttcgt ggctgagctg tgcagctgga tggcactcat  1140
gaccttcacg ctgtttttaca cggatttcgt ggggcgaggg ctgtaccagg gcgtgcccag  1200
agctgagccg ggcaccgagg cccggagaca ctatgatgaa ggcgttcgga tgggcagcct  1260
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gcagcgattc ggcactcgag cagtctattt ggccagtgtg gcagcttcc ctgtggctgc  1380
cggtgccaca tgcctgtccc acagtgtggc cgtggtgaca gcttcagccg ccctcaccgg  1440
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gaagcaggtg ttcctgccca aataccgagg ggacactgga ggtgctagca gtgaggacag  1560
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gtcctgaggg gcaacacaca agaaccaggt ccctcagcc cacagcactg tctttttgct  2520
gatccacccc cctcttacct tttatcagga tgtggcctgt tggtccttct gttgccatca  2580
cagagacaca ggcatttaaa tatttaactt atttatttaa caaagtagaa gggaatccat  2640
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ctggcccccc aaaatgccta acccaggacc ttggaaattc tactcatccc aaatgataat  2820
tccaaatgct gttacccaag gttagggtgt tgaaggaagg tagagggtgg ggcttcaggt  2880
ctcaacggct tccctaacca cccctcttct cttgcccag cctggttccc cccacttcca  2940
ctcccctcta ctctctctag gactgggctg atgaaggcac tgcccaaaat ttcccctacc  3000
cccaactttc ccctacccccc aactttcccc accagctcca caaccctgtt tggagctact  3060
gcaggaccag aagcacaaag tgcggtttcc caagcctttg tccatctcag ccccagagt  3120
atatctgtgc ttggggaatc tcacacagaa actcaggagc acccctgcc tgagctaagg  3180
gaggtcttat ctctcagggg gggtttaagt gccgtttgca ataatgtcgt cttatttatt  3240
tagcggggtg aatattttat actgtaagtg agcaatcaga gtataatgtt tatggtgaca  3300
```

41

```
aaattaaagg ctttcttata tgtttaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa     3360
aaaaaaaara aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaataa aaaaaaaaaa      3410
```

```
        <210> 111
        <211> 1289
        <212> DNA
        <213> Homo sapien
```

```
        <400> 111
agccaggcgt ccctctgcct gcccactcag tggcaacacc cgggagctgt tttgtccttt      60
gtggagcctc agcagttccc tctttcagaa ctcactgcca agagccctga acaggagcca     120
ccatgcagtg cttcagcttc attaagacca tgatgatcct cttcaatttg ctcatctttc     180
tgtgtggtgc agccctgttg gcagtgggca tctgggtgtc aatcgatggg gcatcctttc     240
tgaagatctt cgggccactg tcgtccagtg ccatgcagtt tgtcaacgtg ggctacttcc     300
tcatcgcagc cggcgttgtg gtctttgctc ttggtttcct gggctgctat ggtgctaaga     360
ctgagagcaa gtgtgccctc gtgacgttct tcttcatcct cctcctcatc ttcattgctg     420
aggttgcagc tgctgtgggtc gccttggtgt acaccacaat ggctgagcac ttcctgacgt     480
tgctggtagt gcctgccatc aagaaagatt atggttccca ggaagacttc actcaagtgt     540
ggaacaccac catgaaaggg ctcaagtgct gtggcttcac caactatacg gattttgagg     600
actcacccta cttcaaagag aacagtgcct ttcccccatt ctgttgcaat gacaacgtca     660
ccaacacagc caatgaaacc tgcaccaagc aaaaggctca cgaccaaaaa gtagagggtt     720
gcttcaatca gctttttgtat gacatccgaa ctaatgcagt caccgtgggt ggtgtggcag     780
ctggaattgg gggcctcgag ctggctgcca tgattgtgtc catgtatctg tactgcaatc     840
tacaataagt ccacttctgc ctctgccact actgctgcca catgggaact gtgaagaggc     900
accctggcaa gcagcagtga ttgggggagg ggacaggatc taacaatgtc acttgggcca     960
gaatggacct gcccttctg tccagactt ggggctagat agggaccact cctttttagcg    1020
atgcctgact ttccttccat tggtgggtgg atgggtgggg ggcattccag agcctctaag    1080
gtagccagtt ctgttgccca ttcccccagt ctattaaacc cttgatatgc ccctaggcc     1140
tagtggtgat cccagtgctc tactggggga tgagagaaag gcattttata gcctgggcat    1200
aagtgaaatc agcagagcct ctgggtggat gtgtagaagg cacttcaaaa tgcataaacc    1260
tgttacaatg ttaaaaaaaa aaaaaaaaa                                      1289
```

```
        <210> 112
        <211> 315
        <212> PRT
        <213> Homo sapien
```

```
        <400> 112
Met Val Phe Thr Val Arg Leu Leu His Ile Phe Thr Val Asn Lys Gln
1               5                   10                  15
Leu Gly Pro Lys Ile Val Ile Val Ser Lys Met Met Lys Asp Val Phe
            20                  25                  30
Phe Phe Leu Phe Phe Leu Gly Val Trp Leu Val Ala Tyr Gly Val Ala
        35                  40                  45
Thr Glu Gly Leu Leu Arg Pro Arg Asp Ser Asp Phe Pro Ser Ile Leu
    50                  55                  60
Arg Arg Val Phe Tyr Arg Pro Tyr Leu Gln Ile Phe Gly Gln Ile Pro
65                  70                  75                  80
Gln Glu Asp Met Asp Val Ala Leu Met Glu His Ser Asn Cys Ser Ser
                85                  90                  95
Glu Pro Gly Phe Trp Ala His Pro Pro Gly Ala Gln Ala Gly Thr Cys
            100                 105                 110
Val Ser Gln Tyr Ala Asn Trp Leu Val Val Leu Leu Leu Val Ile Phe
        115                 120                 125
Leu Leu Val Ala Asn Ile Leu Leu Val Asn Leu Leu Ile Ala Met Phe
    130                 135                 140
Ser Tyr Thr Phe Gly Lys Val Gln Gly Asn Ser Asp Leu Tyr Trp Lys
145                 150                 155                 160
```

42

```
Ala Gln Arg Tyr Arg Leu Ile Arg Glu Phe His Ser Arg Pro Ala Leu
            165                     170                 175
Ala Pro Pro Phe Ile Val Ile Ser His Leu Arg Leu Leu Leu Arg Gln
            180                     185                 190
Leu Cys Arg Arg Pro Arg Ser Pro Gln Pro Ser Ser Pro Ala Leu Glu
        195                     200                 205
His Phe Arg Val Tyr Leu Ser Lys Glu Ala Glu Arg Lys Leu Leu Thr
    210                     215         .           220
Trp Glu Ser Val His Lys Glu Asn Phe Leu Leu Ala Arg Ala Arg Asp
225                     230                     235                 240
Lys Arg Glu Ser Asp Ser Glu Arg Leu Lys Arg Thr Ser Gln Lys Val
            245                     250                 255
Asp Leu Ala Leu Lys Gln Leu Gly His Ile Arg Glu Tyr Glu Gln Arg
            260                     265                 270
Leu Lys Val Leu Glu Arg Glu Val Gln Gln Cys Ser Arg Val Leu Gly
        275                     280                 285
Trp Val Ala Glu Ala Leu Ser Arg Ser Ala Leu Leu Pro Pro Gly Gly
    290  .                 295                 300
Pro Pro Pro Pro Asp Leu Pro Gly Ser Lys Asp
305                 310                 315
```

```
        <210> 113
        <211> 553
        <212> PRT
        <213> Homo sapien

        <400> 113
Met Val Gln Arg Leu Trp Val Ser Arg Leu Leu Arg His Arg Lys Ala
 1               5       .           10              15
Gln Leu Leu Leu Val Asn Leu Leu Thr Phe Gly Leu Glu Val Cys Leu
            20  .                25                  30
Ala Ala Gly Ile Thr Tyr Val Pro Pro Leu Leu Leu Glu Val Gly Val
        35                      40                  45
Glu Glu Lys Phe Met Thr Met Val Leu Gly Ile Gly Pro Val Leu Gly
    50                      55                  60
Leu Val Cys Val Pro Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly
65                  70                  75                  80
Arg Tyr Gly Arg Arg Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile
                85                  90                  95
Leu Leu Ser Leu Phe Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu
            100                     105                 110  ·
Leu Cys Pro Asp Pro Arg Pro Leu Glu Leu Ala Leu Leu Ile Leu Gly
        115                     120                 125
Val Gly Leu Leu Asp Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu
    130                     135                 140
Ala Leu Leu Ser Asp Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala
145                     150                     155                 160
Tyr Ser Val Tyr Ala Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr
                165                     170                 175
Leu Leu Pro Ala Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu
            180                     185                 190
Gly Thr Gln Glu Glu Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu
    ·       195         ·           200                 205
Thr Cys Val Ala Ala Thr Leu Leu Val Ala Glu Glu Ala Ala Leu Gly
    210     ·               215                 220
Pro Thr Glu Pro Ala Glu Gly Leu Ser Ala Pro Ser Leu Ser Pro His
225                     230                     235                 240
Cys Cys Pro Cys Arg Ala Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu
```

43

```
                    245                    250                    255
Leu Pro Arg Leu His Gln Leu Cys Cys Arg Met Pro Arg Thr Leu Arg
            260                    265                    270
Arg Leu Phe Val Ala Glu Leu Cys Ser Trp Met Ala Leu Met Thr Phe
        275                    280                    285
Thr Leu Phe Tyr Thr Asp Phe Val Gly Glu Gly Leu Tyr Gln Gly Val
    290                    295                    300
Pro Arg Ala Glu Pro Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly
305                    310                    315                    320
Val Arg Met Gly Ser Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu
                325                    330                    335
Val Phe Ser Leu Val Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg
            340                    345                    350
Ala Val Tyr Leu Ala Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala
        355                    360                    365
Thr Cys Leu Ser His Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu
    370                    375                    380
Thr Gly Phe Thr Phe Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala
385                    390                    395                    400
Ser Leu Tyr His Arg Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly
                405                    410                    415
Asp Thr Gly Gly Ala Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu
            420                    425                    430
Pro Gly Pro Lys Pro Gly Ala Pro Phe Pro Asn Gly His Val Gly Ala
        435                    440                    445
Gly Gly Ser Gly Leu Leu Pro Pro Pro Ala Leu Cys Gly Ala Ser
    450                    455                    460
Ala Cys Asp Val Ser Val Arg Val Val Val Gly Glu Pro Thr Glu Ala
465                    470                    475                    480
Arg Val Val Pro Gly Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp
            485                    490                    495
Ser Ala Phe Leu Leu Ser Gln Val Ala Pro Ser Leu Phe Met Gly Ser
        500                    505                    510
Ile Val Gln Leu Ser Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala
    515                    520                    525
Gly Leu Gly Leu Val Ala Ile Tyr Phe Ala Thr Gln Val Val Phe Asp
    530                    535                    540
Lys Ser Asp Leu Ala Lys Tyr Ser Ala
545                    550
```

```
        <210> 114
        <211> 241
        <212> PRT
        <213> Homo sapien

        <400> 114
Met Gln Cys Phe Ser Phe Ile Lys Thr Met Met Ile Leu Phe Asn Leu
1                   5                   10                  15
Leu Ile Phe Leu Cys Gly Ala Ala Leu Leu Ala Val Gly Ile Trp Val
            20                  25                  30
Ser Ile Asp Gly Ala Ser Phe Leu Lys Ile Phe Gly Pro Leu Ser Ser
        35                  40                  45
Ser Ala Met Gln Phe Val Asn Val Gly Tyr Phe Leu Ile Ala Ala Gly
    50                  55                  60
Val Val Val Phe Ala Leu Gly Phe Leu Gly Cys Tyr Gly Ala Lys Thr
65                  70                  75                  80
Glu Ser Lys Cys Ala Leu Val Thr Phe Phe Phe Ile Leu Leu Leu Ile
            85                  90                  95
```

44

```
Phe Ile Ala Glu Val Ala Ala Ala Val Val Ala Leu Val Tyr Thr Thr
          100                 105                 110
Met Ala Glu His Phe Leu Thr Leu Leu Val Val Pro Ala Ile Lys Lys
          115                 120                 125
Asp Tyr Gly Ser Gln Glu Asp Phe Thr Gln Val Trp Asn Thr Thr Met
          130                 135                 140
Lys Gly Leu Lys Cys Cys Gly Phe Thr Asn Tyr Thr Asp Phe Glu Asp
145                 150                 155                 160
Ser Pro Tyr Phe Lys Glu Asn Ser Ala Phe Pro Pro Phe Cys Cys Asn
              165                 170                 175
Asp Asn Val Thr Asn Thr Ala Asn Glu Thr Cys Thr Lys Gln Lys Ala
              180                 185                 190
His Asp Gln Lys Val Glu Gly Cys Phe Asn Gln Leu Leu Tyr Asp Ile
          195                 200                 205
Arg Thr Asn Ala Val Thr Val Gly Gly Val Ala Ala Gly Ile Gly Gly
          210                 215                 220
Leu Glu Leu Ala Ala Met Ile Val Ser Met Tyr Leu Tyr Cys Asn Leu
225                 230                 235                 240
Gln
```

```
        <210> 115
        <211> 366
        <212> DNA
        <213> Homo sapien

        <400> 115
gctctttctc tcccctcctc tgaatttaat tctttcaact tgcaatttgc aaggattaca      60
catttcactg tgatgtatat tgtgttgcaa aaaaaaaaa gtgtctttgt ttaaaattac     120
ttggtttgtg aatccatctt gcttttccc cattggaact agtcattaac ccatctctga     180
actggtagaa aaacatctga agagctagtc tatcagcatc tgacaggtga attggatggt     240
tctcagaacc atttcaccca gacagcctgt ttctatcctg tttaataaat tagtttgggt     300
tctctacatg cataacaaac cctgctccaa tctgtcacat aaaagtctgt gacttgaagt     360
ttagtc                                                                366
```

```
        <210> 116
        <211> 282
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(282)
        <223> n = A,T,C or G

        <400> 116
acaaagatga accatttcct atattatagc aaaattaaaa tctacccgta ttctaatatt      60
gagaaatgag atnaaacaca atnttataaa gtctacttag agaagatcaa gtgacctcaa     120
agactttact attttcatat tttaagacac atgatttatc ctattttagt aacctggttc     180
atacgttaaa caaaggataa tgtgaacagc agagaggatt tgttggcaga aaatctatgt     240
tcaatctnga actatctana tcacagacat ttctattcct tt                       282
```

```
        <210> 117
        <211> 305
        <212> DNA
        <213> Homo sapien

        <220>
```

45

```
          <221> misc_feature
          <222> (1)...(305)
          <223> n = A,T,C or G

          <400> 117
acacatgtcg cttcactgcc ttcttagatg cttctggtca acatanagga acagggacca         60
tatttatcct ccctcctgaa acaattgcaa aataanacaa aatatatgaa acaattgcaa        120
aataaggcaa aatatatgaa acaacaggtc tcgagatatt ggaaatcagt caatgaagga        180
tactgatccc tgatcactgt cctaatgcag gatgtgggaa acagatgagg tcacctctgt        240
gactgcccca gcttactgcc tgtagagagt ttctangctg cagttcagac agggagaaat        300
tgggt                                                                      305

          <210> 118
          <211> 71
          <212> DNA
          <213> Homo sapien

          <220>
          <221> misc_feature
          <222> (1)...(71)
          <223> n = A,T,C or G

          <400> 118
accaaggtgt ntgaatctct gacgtgggga tctctgattc ccgcacaatc tgagtggaaa         60
aantcctggg t                                                               71

          <210> 119
          <211> 212
          <212> DNA
          <213> Homo sapien

          <220>
          <221> misc_feature
          <222> (1)...(212)
          <223> n = A,T,C or G

          <400> 119
actccggttg gtgtcagcag cacgtggcat tgaacatngc aatgtggagc ccaaaccaca         60
gaaatggggg tgaaattggc caactttcta tnaacttatg ttggcaantt tgccaccaac        120
agtaagctgg cccttctaat aaaagaaaat tgaaaggttt ctcactaanc ggaattaant        180
aatggantca aganactccc aggcctcagc gt                                        212

          <210> 120
          <211> 90
          <212> DNA
          <213> Homo sapien

          <220>
          <221> misc_feature
          <222> (1)...(90)
          <223> n = A,T,C or G

          <400> 120
actcgttgca natcaggggc cccccagagt caccgttgca ggagtccttc tggtcttgcc         60
ctccgccggc gcagaacatg ctggggtggt                                           90

          <210> 121
          <211> 218
```

46

```
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(218)
<223> n = A,T,C or G

<400> 121
tgtancgtga anacgacaga nagggttgtc aaaaatggag aanccttgaa gtcattttga      60
gaataagatt tgctaaaaga tttggggcta aaacatggtt attgggagac atttctgaag     120
atatncangt aaattangga atgaattcat ggttcttttg ggaattcctt tacgatngcc     180
agcatanact tcatgtgggg atancagcta cccttgta                             218

<210> 122
<211> 171
<212> DNA
<213> Homo sapien

<400> 122
tagggtgta tgcaactgta aggacaaaaa ttgagactca actggcttaa ccaataaagg       60
catttgttag ctcatggaac aggaagtcgg atggtggggc atcttcagtg ctgcatgagt     120
caccaccccg gcggggtcat ctgtgccaca ggtccctgtt gacagtgcgg t             171

<210> 123
<211> 76
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(76)
<223> n = A,T,C or G

<400> 123
tgtagcgtga agacnacaga atggtgtgtg ctgtgctatc caggaacaca tttattatca      60
ttatcaanta ttgtgt                                                     76

<210> 124
<211> 131
<212> DNA
<213> Homo sapien

<400> 124
acctttcccc aaggccaatg tcctgtgtgc taactggccg gctgcaggac agctgcaatt      60
caatgtgctg ggtcatatgg aggggaggag actctaaaat agccaatttt attctcttgg     120
ttaagatttg t                                                         131

<210> 125
<211> 432
<212> DNA
<213> Homo sapien

<400> 125
actttatcta ctggctatga aatagatggt ggaaaattgc gttaccaact ataccactgg      60
cttgaaaaag aggtgatagc tcttcagagg acttgtgact tttgctcaga tgctgaagaa     120
ctacagtctg catttggcag aaatgaagat gaatttggat taaatgagga tgctgaagat     180
ttgcctcacc aaacaaaagt gaaacaactg agagaaaatt ttcaggaaaa aagacagtgg     240
```

47

```
ctcttgaagt atcagtcact tttgagaatg tttcttagtt actgcatact tcatggatcc        300
catggtgggg gtcttgcatc tgtaagaatg gaattgattt tgcttttgca agaatctcag        360
caggaaacat cagaaccact attttctagc cctctgtcag agcaaacctc agtgcctctc        420
ctctttgctt gt                                                            432
```

```
        <210> 126
        <211> 112
        <212> DNA
        <213> Homo sapien
```

```
        <400> 126
acacaacttg aatagtaaaa tagaaactga gctgaaattt ctaattcact ttctaaccat         60
agtaagaatg atatttcccc ccagggatca ccaaatattt ataaaaattt gt                112
```

```
        <210> 127
        <211> 54
        <212> DNA
        <213> Homo sapien
```

```
        <400> 127
accacgaaac cacaaacaag atggaagcat caatccactt gccaagcaca gcag               54
```

```
        <210> 128
        <211> 323
        <212> DNA
        <213> Homo sapien
```

```
      . <400> 128
acctcattag taattgtttt gttgtttcat ttttttctaa tgtctcccct ctaccagctc         60
acctgagata acagaatgaa aatggaagga cagccagatt tctcctttgc tctctgctca        120
ttctctctga agtctaggtt acccattttg gggacccatt ataggcaata aacacagttc        180
ccaaagcatt tggacagttt cttgttgtgt tttagaatgg ttttcctttt tcttagcctt        240
ttcctgcaaa aggctcactc agtcccttgc ttgctcagtg gactgggctc cccagggcct        300
aggctgcctt cttttccatg tcc                                                323
```

```
        <210> 129
        <211> 192
        <212> DNA
        <213> Homo sapien
```

```
        <220>
        <221> misc_feature
        <222> (1)...(192)
        <223> n = A,T,C or G
```

```
        <400> 129
acatacatgt gtgtatattt ttaaatatca cttttgtatc actctgactt tttagcatac         60
tgaaaacaca ctaacataat ttntgtgaac catgatcaga tacaacccaa atcattcatc        120
tagcacattc atctgtgata naaagatagg tgagtttcat ttccttcacg ttggccaatg        180
gataaacaaa gt                                                            192
```

```
        <210> 130
        <211> 362
        <212> DNA
        <213> Homo sapien
```

```
        <220>
        <221> misc_feature
```

48

```
    <222> (1)...(362)
    <223> n = A,T,C or G

    <400> 130
cccttttttta tggaatgagt agactgtatg tttgaanatt tanccacaac ctctttgaca        60
tataatgacg caacaaaaag gtgctgttta gtcctatggt tcagtttatg cccctgacaa       120
gtttccattg tgttttgccg atcttctggc taatcgtggt atcctccatg ttattagtaa       180
ttctgtattc cattttgtta acgcctggta gatgtaacct gctangaggc taactttata       240
cttatttaaa agctcttatt ttgtggtcat taaaatggca atttatgtgc agcactttat       300
tgcagcagga agcacgtgtg ggttggttgt aaagctcttt gctaatctta aaaagtaatg       360
gg                                                                      362


    <210> 131
    <211> 332
    <212> DNA
    <213> Homo sapien


    <220>
    <221> misc_feature
    <222> (1)...(332)
    <223> n = A,T,C or G


    <400> 131
cttttgaaa gatcgtgtcc actcctgtgg acatcttgtt ttaatggagt ttcccatgca         60
gtangactgg tatggttgca gctgtccaga taaaaacatt tgaagagctc caaaatgaga       120
gttctcccag gttcgccctg ctgctccaag tctcagcagc agcctctttt aggaggcatc       180
ttctgaacta gattaaggca gcttgtaaat ctgatgtgat ttggtttatt atccaactaa       240
cttccatctg ttatcactgg agaaagccca gactccccan gacnggtacg gattgtgggc       300
atanaaggat tgggtgaagc tggcgttgtg gt                                     332


    <210> 132
    <211> 322
    <212> DNA
    <213> Homo sapien


    <220>
    <221> misc_feature
    <222> (1)...(322)
    <223> n = A,T,C or G


    <400> 132
acttttgcca ttttgtatat ataaacaatc ttgggacatt ctcctgaaaa ctaggtgtcc         60
agtggctaag agaactcgat ttcaagcaat tctgaaagga aaaccagcat gacacagaat       120
ctcaaattcc caaacagggg ctctgtggga aaaatgaggg aggacctttg tatctcgggt       180
tttagcaagt taaaatgaan atgacaggaa aggcttattt atcaacaaag agaagagttg       240
ggatgcttct aaaaaaaact ttggtagaga aaataggaat gctnaatcct agggaagcct       300
gtaacaatct acaattggtc ca                                                322


    <210> 133
    <211> 278
    <212> DNA
    <213> Homo sapien


    <220>
    <221> misc_feature
    <222> (1)...(278)
    <223> n = A,T,C or G
```

```
        <400> 133
acaagccttc acaagtttaa ctaaattggg attaatcttt ctgtanttat ctgcataatt      60
cttgtttttc tttccatctg gctcctgggt tgacaatttg tggaaacaac tctattgcta     120
ctatttaaaa aaaatcacaa atctttccct ttaagctatg ttnaattcaa actattcctg     180
ctattcctgt tttgtcaaag aaattatatt tttcaaaata tgtntatttg tttgatgggt     240
cccacgaaac actaataaaa accacagaga ccagcctg                             278


        <210> 134
        <211> 121
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(121)
        <223> n = A,T,C or G


        <400> 134
gtttanaaaa cttgtttagc tccatagagg aaagaatgtt aaactttgta ttttaaaaca      60
tgattctctg aggttaaact tggttttcaa atgttatttt tacttgtatt ttgcttttgg     120
t                                                                     121


        <210> 135
        <211> 350
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(350)
        <223> n = A,T,C or G


        <400> 135
acttanaacc atgcctagca catcagaatc cctcaaagaa catcagtata atcctatacc      60
atancaagtg gtgactggtt aagcgtgcga caaaggtcag ctggcacatt acttgtgtgc     120
aaacttgata cttttgttct aagtaggaac tagtatacag tncctaggan tggtactcca     180
gggtgccccc caactcctgc agccgctcct ctgtgccagn ccctgnaagg aactttcgct     240
ccacctcaat caagccctgg gccatgctac ctgcaattgg ctgaacaaac gtttgctgag     300
ttcccaagga tgcaaagcct ggtgctcaac tcctggggcg tcaactcagt                350


        <210> 136
        <211> 399
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(399)
        <223> n = A,T,C or G


        <400> 136
tgtaccgtga agacgacaga agttgcatgg cagggacagg gcagggccga ggccagggtt      60
gctgtgattg tatccgaata ntcctcgtga gaaaagataa tgagatgacg tgagcagcct     120
gcagacttgt gtctgccttc aanaagccag acaggaaggc cctgcctgcc ttggctctga     180
cctggcggcc agccagccag ccacaggtgg gcttcttcct tttgtggtga caacnccaag     240
aaaactgcag aggcccaggg tcaggtgtna gtgggtangt gaccataaaa caccaggtgc     300
tcccaggaac ccgggcaaag gccatcccca cctacagcca gcatgcccac tggcgtgatg     360
ggtgcagang gatgaagcag ccagntgttc tgctgtggt                            399
```

50

```
        <210> 137
        <211> 165
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(165)
        <223> n = A,T,C or G

        <400> 137
actggtgtgg tnggggggtga tgctggtggt anaagttgan gtgacttcan gatggtgtgt        60
ggaggaagtg tgtgaacgta gggatgtaga ngttttggcc gtgctaaatg agcttcggga        120
ttggctggtc ccactggtgg tcactgtcat tggtgggggtt cctgt        165


        <210> 138
        <211> 338
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(338)
        <223> n = A,T,C or G

        <400> 138
actcactgga atgccacatt cacaacagaa tcagaggtct gtgaaaacat taatggctcc        60
ttaacttctc cagtaagaat cagggacttg aaatggaaac gttaacagcc acatgcccaa        120
tgctgggcag tctcccatgc cttccacagt gaaagggctt gagaaaaatc acatccaatg        180
tcatgtgttt ccagccacac caaaaggtgc ttggggtgga gggctggggg catananggt        240
cangcctcag gaagcctcaa gttccattca gctttgccac tgtacattcc ccatntttaa        300
aaaaactgat gcctttttt tttttttttg taaaattc        338


        <210> 139
        <211> 382
        <212> DNA
        <213> Homo sapien

        <400> 139
gggaatcttg gtttttggca tctggtttgc ctatagccga ggccactttg acagaacaaa        60
gaaagggact tcgagtaaga aggtgattta cagccagcct agtgcccgaa gtgaaggaga        120
attcaaacag acctcgtcat tcctggtgtg agcctggtcg gctcaccgcc tatcatctgc        180
atttgcctta ctcaggtgct accggactct ggccctgat gtctgtagtt tcacaggatg         240
ccttatttgt cttctacacc ccacagggcc ccctacttct tcggatgtgt ttttaataat        300
gtcagctatg tgccccatcc tccttcatgc cctccctccc tttcctacca ctgctgagtg        360
gcctggaact tgtttaaagt gt        382


        <210> 140
        <211> 200
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(200)
        <223> n = A,T,C or G
```

51·

```
        <400> 140
accaaanctt cttttctgttg tgttngattt tactataggg gtttngcttn ttctaaanat      60
actttctcatt taacancttt tgttaagtgt caggctgcac tttgctccat anaattattg      120
ttttcacatt tcaacttgta tgtgtttgtc tcttanagca ttggtgaaat cacatatttt      180
atattcagca taaaggagaa                                                    200


        <210> 141
        <211> 335
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(335)
        <223> n = A,T,C or G

        <400> 141
actttatttt caaaacactc atatgttgca aaaaacacat agaaaaataa agtttggtgg      60
gggtgctgac taaacttcaa gtcacagact tttatgtgac agattggagc agggtttgtt      120
atgcatgtag agaacccaaa ctaatttatt aaacaggata gaaacaggct gtctgggtga      180
aatggttctg agaaccatcc aattcacctg tcagatgctg atanactagc tcttcagatg      240
ttttctacc agttcagaga tnggttaatg actanttcca atggggaaaa agcaagatgg      300
attcacaaac caagtaattt taaacaaaga cactt                                 335


        <210> 142
        <211> 459
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(459)
        <223> n = A,T,C or G

        <400> 142
accaggttaa tattgccaca tatatccttt ccaattgcgg gctaaacaga cgtgtattta      60
gggttgttta aagacaaccc agcttaatat caagagaaat tgtgacctt catggagtat      120
ctgatggaga aaacactgag ttttgacaaa tcttatttta ttcagatagc agtctgatca      180
cacatggtcc aacaacactc aaataataaa tcaaatatna tcagatgtta aagattggtc      240
ttcaaacatc atagccaatg atgcccgct tgcctataat ctctccgaca taaaaccaca       300
tcaacacctc agtggccacc aaaccattca gcacagcttc cttaactgtg agctgtttga      360
agctaccagt ctgagcacta ttgactatnt ttttcangct ctgaatagct ctaggggatct    420
cagcangggt gggaggaacc agctcaacct tggcgtant                             459


        <210> 143
        <211> 140
        <212> DNA
        <213> Homo sapien

        <400> 143
acatttcctt ccaccaagtc aggactcctg gcttctgtgg gagttcttat cacctgaggg     60
aaatccaaac agtctctcct agaaaggaat agtgtcacca accccaccca tctccctgag     120
accatccgac ttccctgtgt                                                  140


        <210> 144
        <211> 164
        <212> DNA
        <213> Homo sapien
```

52

```
        <220>
        <221> misc_feature
        <222> (1)...(164)
        <223> n = A,T,C or G

        <400> 144
acttcagtaa caacatacaa taacaacatt aagtgtatat tgccatcttt gtcattttct        60
atctatacca ctctcccttc tgaaaacaan aatcactanc caatcactta tacaaatttg       120
aggcaattaa tccatatttg ttttcaataa ggaaaaaaag atgt                        164

        <210> 145
        <211> 303
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(303)
        <223> n = A,T,C or G

        <400> 145
acgtagacca tccaactttg tatttgtaat ggcaaacatc cagnagcaat tcctaaacaa        60
actggagggt atttataccc aattatccca ttcattaaca tgccctcctc ctcaggctat       120
gcaggacagc tatcataagt cggcccaggc atccagatac taccatttgt ataaacttca       180
gtaggggagt ccatccaagt gacaggtcta atcaaaggag gaaatggaac ataagcccag       240
tagtaaaatn ttgcttagct gaaacagcca caaaagactt accgccgtgg tgattaccat       300
caa                                                                     303

        <210> 146
        <211> 327
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(327)
        <223> n = A,T,C or G

        <400> 146
actgcagctc aattagaagt ggtctctgac tttcatcanc ttctccctgg gctccatgac        60
actggcctgg agtgactcat tgctctggtt ggttgagaga gctcctttgc caacaggcct       120
ccaagtcagg gctgggattt gtttcctttc cacattctag caacaatatg ctggccactt       180
cctgaacagg gagggtggga ggagccagca tggaacaagc tgccactttc taaagtagcc       240
agacttgccc ctgggcctgt cacacctact gatgaccttc tgtgcctgca ggatggaatg       300
taggggtgag ctgtgtgact ctatggt                                           327

        <210> 147
        <211> 173
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(173)
        <223> n = A,T,C or G

        <400> 147
```

53

```
acattgtttt  tttgagataa  agcattgana  gagctctcct  taacgtgaca  caatggaagg        60
actggaacac  atacccacat  ctttgttctg  aggggataatt  ttctgataaa  gtcttgctgt       120
atattcaagc  acatatgtta  tatattattc  agttccatgt  ttatagccta  gtt              173
```

```
        <210> 148
        <211> 477
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(477)
        <223> n = A,T,C or G

        <400> 148
acaaccactt  tatctcatcg  aatttttaac  ccaaactcac  tcactgtgcc  tttctatcct        60
atgggatata  ttatttgatg  ctccatttca  tcacacatat  atgaataata  cactcatact       120
gccctactac  ctgctgcaat  aatcacattc  ccttcctgtc  ctgaccctga  agccattggg       180
gtggtcctag  tggccatcag  tccangcctg  caccttgagc  ccttgagctc  cattgctcac       240
nccancccac  ctcaccgacc  ccatcctctt  acacagctac  ctccttgctc  tctaaccccca       300
tagattatnt  ccaaattcag  tcaattaagt  tactattaac  actctacccg  acatgtccag       360
caccactggt  aagccttctc  cagccaacac  acacacacac  acacncacac  acacacatat       420
ccaggcacag  gctacctcat  cttcacaatc  accccttttaa  ttaccatgct  atggtgg         477
```

```
        <210> 149
        <211> 207
        <212> DNA
        <213> Homo sapien

        <400> 149
acagttgtat  tataatatca  agaaataaac  ttgcaatgag  agcatttaag  agggaagaac        60
taacgtattt  tagagagcca  aggaaggttt  ctgtggggag  tgggatgtaa  ggtggggcct       120
gatgataaat  aagagtcagc  caggtaagtg  ggtggtgtgg  tatgggcaca  gtgaagaaca       180
tttcaggcag  agggaacagc  agtgaaa                                             207
```

```
        <210> 150
        <211> 111
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(111)
        <223> n = A,T,C or G

        <400> 150
accttgattc  cattgctgct  ctgatggaaa  cccaactatc  taatttagct  aaaacatggg        60
cacttaaatg  tggtcagtgt  ttggacttgt  taactantgg  catctttggg  t                111
```

```
        <210> 151
        <211> 196
        <212> DNA
        <213> Homo sapien

        <400> 151
agcgcggcag  gtcatattga  acattccaga  tacctatcat  tactcgatgc  tgttgataac        60
agcaagatgg  ctttgaactc  agggtcacca  ccagctattg  gaccttacta  tgaaaaccat       120
ggataccaac  cggaaaaccc  ctatcccgca  cagcccactg  tggtccccac  tgtctacgag       180
```

54

```
gtgcatccgg ctcagt                                                         196

        <210> 152
        <211> 132
        <212> DNA
        <213> Homo sapien

        <400> 152
acagcacttt cacatgtaag aagggagaaa ttcctaaatg taggagaaag ataacagaac       60
cttccccttt tcatctagtg gtggaaacct gatgctttat gttgacagga atagaaccag       120
gagggagttt gt                                                           132

        <210> 153
        <211> 285
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(285)
        <223> n = A,T,C or G .

        <400> 153
acaanaccca nganaggcca ctggccgtgg tgtcatggcc tccaaacatg aaagtgtcag       60
cttctgctct tatgtcctca tctgacaact ctttaccatt tttatcctcg ctcagcagga       120
gcacatcaat aaagtccaaa gtcttggact tggccttggc ttggaggaag tcatcaacac       180
cctggctagt gagggtgcgg cgccgctcct ggatgacggc atctgtgaag tcgtgcacca       240
gtctgcaggc cctgtggaag cgccgtccac acggagtnag gaatt                       285

        <210> 154
        <211> 333
        <212> DNA
        <213> Homo sapien

        <400> 154
accacagtcc tgttgggcca gggcttcatg accctttctg tgaaaagcca tattatcacc       60
accccaaatt tttccttaaa tatctttaac tgaaggggtc agcctcttga ctgcaaagac       120
cctaagccgg ttacacagct aactcccact ggccctgatt tgtgaaattg ctgctgcctg       180
attggcacag gagtcgaagg tgttcagctc ccctcctccg tggaacgaga ctctgatttg       240
agtttcacaa attctcgggc cacctcgtca ttgctcctct gaaataaaat ccggagaatg       300
gtcaggcctg tctcatccat atggatcttc cgg                                    333

        <210> 155
        <211> 308
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(308)
        <223> n = A,T,C or G

        <400> 155
actggaaata ataaaaccca catcacagtg ttgtgtcaaa gatcatcagg gcatggatgg       60
gaaagtgctt tgggaactgt aaagtgccta acacatgatc gatgattttt gttataatat       120
ttgaatcacg gtgcatacaa actctcctgc ctgctcctcc tgggccccag ccccagcccc       180
atcacagctc actgctctgt tcatccaggc ccagcatgta gtggctgatt cttcttggct       240
gcttttagcc tccanaagtt tctctgaagc caaccaaacc tctangtgta aggcatgctg       300
```

55

```
gccctggt                                                      308

        <210> 156
        <211> 295
        <212> DNA
        <213> Homo sapien

        <400> 156
accttgctcg gtgcttggaa catattagga actcaaaata tgagatgata acagtgccta      60
ttattgatta ctgagagaac tgttagacat ttagttgaag attttctaca caggaactga     120
gaataggaga ttatgtttgg ccctcatatt ctctcctatc ctccttgcct cattctatgt     180
ctaatatatt ctcaatcaaa taaggttagc ataatcagga aatcgaccaa ataccaatat     240
aaaaccagat gtctatcctt aagattttca aatagaaaac aaattaacag actat          295

        <210> 157
        <211> 126
        <212> DNA
        <213> Homo sapien

        <400> 157
acaagtttaa atagtgctgt cactgtgcat gtgctgaaat gtgaaatcca ccacatttct      60
gaagagcaaa acaaattctg tcatgtaatc tctatcttgg gtcgtgggta tatctgtccc     120
cttagt                                                        126

        <210> 158
        <211> 442
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(442)
        <223> n = A,T,C or G

        <400> 158
acccactggt cttggaaaca cccatcctta atacgatgat ttttctgtcg tgtgaaaatg      60
aanccagcag gctgccccta gtcagtcctt ccttccagag aaaaagagat ttgagaaagt     120
gcctgggtaa ttcaccatta atttcctccc ccaaactctc tgagtcttcc cttaatattt     180
ctggtggttc tgaccaaagc aggtcatggt ttgttgagca tttgggatcc cagtgaagta     240
natgtttgta gccttgcata cttagccctt cccacgcaca aacggagtgg cagagtggtg     300
ccaaccctgt tttcccagtc cacgtagaca gattcacagt gcggaattcc ggaagctgga     360
nacagacggg ctctttgcag agccgggact ctgagangga catgagggcc tctgcctctg     420
tgttcattct ctgatgtcct gt                                      442

        <210> 159
        <211> 498
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(498)
        <223> n = A,T,C or G

        <400> 159
acttccaggt aacgttgttg tttccgttga gcctgaactg atgggtgacg ttgtaggttc      60
tccaacaaga actgaggttg cagagcgggt agggaagagt gctgttccag ttgcacctgg     120
gctgctgtgg actgttgttg attcctcact acggcccaag gttgtggaac tggcanaaag     180
```

56

```
gtgtgttgtt gganttgagc tcgggcggct gtggtaggtt gtgggctctt caacaggggc        240
tgctgtggtg ccgggangtg aangtgttgt gtcacttgag cttggccagc tctggaaagt        300
antanattct tcctgaaggc cagcgcttgt ggagctggca ngggtcantg ttgtgtgtaa        360
cgaaccagtg ctgctgtggg tgggtgtana tcctccacaa agcctgaagt tatggtgtcn        420
tcaggtaana atgtggtttc agtgtccctg ggcngctgtg gaaggttgta nattgtcacc        480
aagggaataa gctgtggt                                                       498
```

```
        <210> 160
        <211> 380
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(380)
        <223> n = A,T,C or G

        <400> 160
acctgcatcc agcttccctg ccaaactcac aaggagacat caacctctag acagggaaac         60
agcttcagga tacttccagg agacagagcc accagcagca aaacaaatat tcccatgcct        120
ggagcatggc atagaggaag ctganaaatg tggggtctga ggaagccatt tgagtctggc        180
cactagacat ctcatcagcc acttgtgtga agagatgccc catgacccca gatgcctctc        240
ccaccottac ctccatctca cacacttgag ctttccactc tgtataattc taacatcctg        300
gagaaaaatg gcagtttgac cgaacctgtt cacaacggta gaggctgatt tctaacgaaa        360
cttgtagaat gaagcctgga                                                    380
```

```
        <210> 161
        <211> 114
        <212> DNA
        <213> Homo sapien

        <400> 161
actccacatc ccctctgagc aggcggttgt cgttcaaggt gtatttggcc ttgcctgtca         60
cactgtccac tggccccctta tccacttggt gcttaatccc tcgaaagagc atgt             114
```

```
        <210> 162
        <211> 177
        <212> DNA
        <213> Homo sapien

        <400> 162
actttctgaa tcgaatcaaa tgatacttag tgtagtttta atatcctcat atatatcaaa         60
gttttactac tctgataatt ttgtaaacca ggtaaccaga acatccagtc atacagcttt        120
tggtgatata taacttggca ataacccagt ctggtgatac ataaaactac tcactgt          177
```

```
        <210> 163
        <211> 137
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(137)
        <223> n = A,T,C or G

        <400> 163
catttataca gacaggcgtg aagacattca cgacaaaaac gcgaaattct atcccgtgac         60
canagaaggc agctacggct actcctacat cctggcgtgg gtggccttcg cctgcacctt        120
```

57

```
catcagcggc atgatgt                                                    137

        <210> 164
        <211> 469
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(469)
        <223> n = A,T,C or G

        <400> 164
cttatcacaa tgaatgttct cctgggcagc gttgtgatct ttgccacctt cgtgacttta     60
tgcaatgcat catgctattt catacctaat gagggagttc caggagattc aaccaggaaa    120
tgcatggatc tcaaaggaaa caaacaccca ataaactcgg agtggcagac tgacaactgt    180
gagacatgca cttgctacga aacagaaatt tcatgttgca cccttgtttc tacacctgtg    240
ggttatgaca aagacaactg ccaaagaatc ttcaagaagg aggactgcaa gtatatcgtg    300
gtggagaaga aggacccaaa aaagacctgt tctgtcagtg aatggdataat ctaatgtgct    360
tctagtaggc acagggctcc caggccaggc ctcattctcc tctggcctct aatagtcaat    420
gattgtgtag ccatgcctat cagtaaaaag atntttgagc aaacacttt                469

        <210> 165
        <211> 195
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(195)
        <223> n = A,T,C or G

        <400> 165
acagtttttt atanatatcg acattgccgg cacttgtgtt cagtttcata aagctggtgg     60
atccgctgtc atccactatt ccttggctag agtaaaaatt attcttatag cccatgtccc    120
tgcaggccgc ccgcccgtag ttctcgttcc agtcgtcttg gcacacaggg tgccaggact    180
tcctctgaga tgagt                                                     195

        <210> 166
        <211> 383
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(383)
        <223> n = A,T,C or G

        <400> 166
acatcttagt agtgtggcac atcagggggc catcagggtc acagtcactc atagcctcgc     60
cgaggtcgga gtccacacca ccggtgtagg tgtgctcaat cttgggcttg gcgcccacct    120
ttggagaagg gatatgctgc acacacatgt ccacaaagcc tgtgaactcg ccaaagaatt    180
tttgcagacc agcctgagca aggggcggat gttcagcttc agctcctcct tcgtcaggtg    240
gatgccaacc tcgtctangg tccgtgggaa gctggtgtcc acntcaccta caacctgggc    300
gangatctta taaagaggct ccnagataaa ctccacgaaa cttctctggg agctgctagt    360
ngggggccttt ttggtgaact ttc                                           383

        <210> 167
```

58

```
        <211> 247
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(247)
        <223> n = A,T,C or G

        <400> 167
acagagccag accttggcca taaatgaanc agagattaag actaaacccc aagtcganat      60
tggagcagaa actggagcaa gaagtgggcc tggggctgaa gtagagacca aggccactgc     120
tatanccata cacagagcca actctcaggc caaggcnatg gttggggcag anccagagac     180
tcaatctgan tccaaagtgg tggctggaac actggtcatg acanaggcag tgactctgac     240
tgangtc                                                               247

        <210> 168
        <211> 273
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(273)
        <223> n = A,T,C or G

        <400> 168
acttctaagt tttctagaag tggaaggatt gtantcatcc tgaaaatggg tttacttcaa      60
aatccctcan ccttgttctt cacnactgtc tatactgana gtgtcatgtt tccacaaagg     120
gctgacacct gagcctgnat tttcactcat ccctgagaag ccctttccag tagggtgggc     180
aattcccaac ttccttgcca caagcttccc aggctttctc ccctggaaaa ctccagcttg     240
agtcccagat acactcatgg gctgccctgg gca                                  273

        <210> 169
        <211> 431
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(431)
        <223> n = A,T,C or G

        <400> 169
acagccttgg cttccccaaa ctccacagtc tcagtgcaga aagatcatct tccagcagtc      60
agctcagacc agggtcaaag gatgtgacat caacagtttc tggtttcaga acaggttcta     120
ctactgtcaa atgaccccc atacttcctc aaaggctgtg gtaagttttg cacaggtgag     180
ggcagcagaa aggggtant tactgatgga caccatcttc tctgtatact ccacactgac     240
cttgccatgg gcaaaggccc ctaccacaaa aacaatagga tcactgctgg gcaccagctc     300
acgcacatca ctgacaaccg ggatggaaaa agaantgcca actttcatac atccaactgg     360
aaagtgatct gatactggat tcttaattac cttcaaaagc ttctggggc catcagctgc     420
tcgaacactg a                                                         431

        <210> 170
        <211> 266
        <212> DNA
        <213> Homo sapien
```

59

```
<220>
<221> misc_feature
<222> (1)...(266)
<223> n = A,T,C or G

<400> 170
acctgtgggc tgggctgtta tgcctgtgcc ggctgctgaa agggagttca gaggtggagc        60
tcaaggagct ctgcaggcat tttgccaanc ctctccanag canagggagc aacctacact       120
ccccgctaga aagacaccag attggagtcc tgggagggg agttggggtg ggcatttgat       180
gtatacttgt cacctgaatg aangagccag agaggaanga gacgaanatg anattggcct       240
tcaaagctag gggtctggca ggtgga                                           266


<210> 171
<211> 1248
<212> DNA
<213> Homo sapien


<220>
<221> misc_feature
<222> (1)...(1248)
<223> n = A,T,C or G


<400> 171
ggcagccaaa tcataaacgg cgaggactgc agcccgcact cgcagccctg gcaggcggca        60
ctggtcatgg aaaacgaatt gttctgctcg ggcgtcctgg tgcatccgca gtgggtgctg       120
tcagccgcac actgtttcca gaagtgagtg cagagctcct acaccatcgg gctgggcctg       180
cacagtcttg aggccgacca agagccaggg agccagatgg tggaggccag cctctccgta       240
cggcacccag agtacaacag acccttgctc gctaacgacc tcatgctcat caagttggac       300
gaatccgtgt ccgagtctga caccatccgg agcatcagca ttgcttcgca gtgccctacc       360
gcggggaact cttgcctcgt ttctggctgg ggtctgctgg cgaacggcag aatgcctacc       420
gtgctgcagt gcgtgaacgt gtcggtggtg tctgaggagg tctgcagtaa gctctatgac       480
ccgctgtacc accccagcat gttctgcgcc ggcggagggc aagaccagaa ggactcctgc       540
aacggtgact ctggggggcc cctgatctgc aacgggtact tgcagggcct tgtgtctttc       600
ggaaaagccc cgtgtggcca agttggcgtg ccaggtgtct acaccaacct ctgcaaattc       660
actgagtgga tagagaaaac cgtccaggcc agttaactct ggggactggg aacccatgaa       720
attgaccccc aaatacatcc tgcggaagga attcaggaat atctgttccc agcccctcct       780
ccctcaggcc caggagtcca ggcccccagc ccctcctccc tcaaaccaag ggtacagatc       840
cccagccccct cctccctcag acccaggagt ccagaccccc cagccccctc tccctcagac       900
ccaggagtcc agcccctcct ccctcagacc caggagtcca gacccccag ccccctcctcc       960
ctcagaccca ggggtccagg ccccaaccc ctcctccctc agactcagag gtccaagccc      1020
ccaacccntc attccccaga cccagaggtc caggtcccag ccctcntcc ctcagaccca      1080
gcggtccaat gccacctaga ctntccctgt acacagtgcc cccttgtggc acgttgaccc      1140
aaccttacca gttggttttt catttttngt cccttccccc tagatccaga aataaagttt      1200
aagagaagng caaaaaaaaa aaaaaaaaa aaaaaaaaa aaaaaaaa                     1248


<210> 172
<211> 159
<212> PRT
<213> Homo sapien


<220>
<221> VARIANT
<222> (1)...(159)
<223> Xaa = Any Amino Acid


<400> 172
Met Val Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro
  1               5                  10                  15
```

60

```
Leu Leu Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser
        20                      25                  30
Glu Ser Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr
        35                      40                  45
Ala Gly Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly
    50                      55                  60
Arg Met Pro Thr Val Leu Gln Cys Val Asn Val Ser Val Val Ser Glu
65                      70                  75                  80
Glu Val Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe
                85                  90                  95
Cys Ala Gly Gly Gly Gln Xaa Gln Xaa Asp Ser Cys Asn Gly Asp Ser
            100                 105                 110
Gly Gly Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe
        115                 120                 125
Gly Lys Ala Pro Cys Gly Gln Val Gly Val Pro Gly Val Tyr Thr Asn
    130                 135                 140
Leu Cys Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser
145                 150                 155
```

```
        <210> 173
        <211> 1265
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(1265)
        <223> n = A,T,C or G

        <400> 173
ggcagcccgc actcgcagcc ctggcaggcg gcactggtca tggaaaacga attgttctgc      60
tcgggcgtcc tggtgcatcc gcagtgggtg ctgtcagccg cacactgttt ccagaactcc     120
tacaccatcg ggctgggcct gcacagtctt gaggccgacc aagagccagg gagccagatg     180
gtggaggcca gcctctccgt acggcaccca gagtacaaca gacccttgct cgctaacgac     240
ctcatgctca tcaagttgga cgaatccgtg tccgagtctg acaccatccg gagcatcagc     300
attgcttcgc agtgccctac cgcgggggaac tcttgcctcg tttctggctg gggtctgctg     360
gcgaacggtg agctcacggg tgtgtgtctg ccctcttcaa ggaggtcctc tgcccagtcg     420
cggggggctga cccagagctc tgcgtcccag gcagaatgcc taccgtgctg cagtgcgtga     480
acgtgtcggt ggtgtctgag gaggtctgca gtaagctcta tgaccgctg taccaccca     540
gcatgttctg cgccggcgga gggcaagacc agaaggactc ctgcaacggt gactctgggg     600
ggcccctgat ctgcaacggg tacttgcagg gccttgtgtc tttcggaaaa gccccgtgtg     660
gccaagttgg cgtgccaggt gtctacacca acctctgcaa attcactgag tggatagaga     720
aaaccgtcca ggccagttaa ctctgggggac tgggaaccca tgaaattgac ccccaaatac     780
atcctgcgga aggaattcag gaatatctgt tcccagcccc tcctccctca ggcccaggag     840
tccaggcccc cagcccctcc tccctcaaac caagggtaca gatccccagc ccctcctccc     900
tcagacccag gagtccagac cccccagccc ctcctccctc agacccagga gtccagcccc     960
tcctccntca gacccaggag tccagacccc ccagcccctc ctccctcaga cccagggggtt    1020
gaggccccca accctcctc cttcagagtc agaggtccaa gcccccaacc cctcgttccc    1080
cagacccaga ggtnnaggtc ccagcccctc ttccntcaga cccagnggtc caatgccacc    1140
tagattttcc ctgnacacag tgccccttg tggnangttg acccaaccttt accagttggt    1200
tttcatttt tngtcccttt ccctagatc cagaaataaa gtttaagaga ngngcaaaaa     1260
aaaaa                                                             1265
```

```
        <210> 174
        <211> 1459
        <212> DNA
        <213> Homo sapien
```

61

```
<400> 174
ggtcagccgc acactgtttc cagaagtgag tgcagagctc ctacaccatc gggctgggcc        60
tgcacagtct tgaggccgac caagagccag ggagccagat ggtggaggcc agcctctccg       120
tacggcaccc agagtacaac agacccttgc tcgctaacga cctcatgctc atcaagttgg       180
acgaatccgt gtccgagtct gacaccatcc ggagcatcag cattgcttcg cagtgcccta       240
ccgcggggaa ctcttgcctc gtttctggct ggggtctgct ggcgaacggt gagctcacgg       300
gtgtgtgtct gccctcttca aggaggtcct ctgcccagtc gcgggggctg acccagagct       360
ctgcgtccca ggcagaatgc ctaccgtgct gcagtgcgtg aacgtgtcgg tggtgtctga       420
ngaggtctgc antaagctct atgaccgct gtaccacccc ancatgttct cgcgcggcgg       480
aggggcaagac cagaaggact cctgcaacgt gagagagggg aaaggggagg gcaggcgact       540
cagggaaggg tggagaaggg gggagacatgag acacacaggg ccgcatggcg agatgcagag       600
atggagagac acacagggag acagtgcacaa ctagagagag aaactgagag aaacagagaa       660
ataaacacag gaataaagag aagcaaagga agagagaaac agaaacagac atggggaggc       720
agaaacacac acacatagaa atgcagttga ccttccaaca gcatggggcc tgagggcggt       780
gacctccacc caatagaaaa tcctcttata acttttgact ccccaaaaac ctgactagaa       840
atagcctact gttgacgggg agccttacca ataacataaa tagtcgattt atgcatacgt       900
tttatgcatt catgatatac ctttgttgga attttttgat atttctaagc tacacagttc       960
gtctgtgaat tttttttaaat tgttgcaact ctcctaaaat ttttctgatg tgtttattga      1020
aaaaatccaa gtataagtgg acttgtgcat tcaaaccagg gttgttcaag ggtcaactgt      1080
gtacccagag ggaaacagtg acacagattc atagaggtga aacacgaaga gaaacaggaa      1140
aaatcaagac tctacaaaga ggctgggcag ggtggctcat gcctgtaatc ccagcacttt      1200
gggaggcgag gcaggcagat cacttgaggt aaggagttca agaccagcct ggccaaaatg      1260
gtgaaatcct gtctgtacta aaaatacaaa agttagctgg atatggtggc aggcgcctgt      1320
aatcccagct acttgggagg ctgaggcagg agaattgctt gaatatggga ggcagaggtt      1380
gaagtgagtt gagatcacac cactatactc cagctggggc aacagagtaa gactctgtct      1440
caaaaaaaaa aaaaaaaaa                                                    1459
```

```
<400> 175
gcgcagccct ggcaggcggc actggtcatg gaaaacgaat tgttctgctc gggcgtcctg        60
gtgcatccgc agtgggtgct gtcagccgca cactgtttcc agaactccta caccatcggg       120
ctgggcctgc acagtcttga ggccgaccaa gagccaggga gccagatggt ggaggccagc       180
ctctccgtac ggcacccaga gtacaacaga ctcttgctcg ctaacgacct catgctcatc       240
aagttggacg aatccgtgtc cgagtctgac accatccgga gcatcagcat tgcttcgcag       300
tgccctaccg cggggaactc ttgcctcgtn tctggctggg gtctgctggc gaacggcaga       360
atgcctaccg tgctgcactg cgtgaacgtg tcggtggtgt ctgaggangt ctgcagtaag       420
ctctatgacc cgctgtacca ccccagcatg ttctgcgccg cgggagggca agaccagaag       480
gactcctgca cggtgactc tggggggccc ctgatctgca acgggtactt gcagggcctt       540
gtgtctttcg aaaagcccc gtgtggccaa cttggcgtgc caggtgtcta caccaacctc       600
tgcaaattca ctgagtggat agagaaaacc gtccagncca gttaactctg gggactggga       660
acccatgaaa ttgaccccca aatacatcct gcggaangaa ttcaggaata tctgttccca       720
gcccctcctc cctcaggccc aggagtccag gccccagcc cctcctccct caaaccaagg       780
gtacagatcc ccagcccctc ctccctcaga cccaggagtc cagacccccc agcccctcnt       840
ccntcagacc caggagtcca gccccctcctc cntcagacgc aggagtccag accccccagc       900
```

62

```
ccntcntccg tcagacccag gggtgcaggc ccccaacccc tcntccntca gagtcagagg      960
tccaagcccc caacccctcg ttccccagac ccagaggtnc aggtcccagc ccctcctccc     1020
tcagacccag cggtccaatg ccacctagan tntccctgta cacagtgccc ccttgtggca     1080
ngttgaccca accttaccag ttggtttttc attttttgtc cctttcccct agatccagaa     1140
ataaagtnta agagaagcgc aaaaaaa                                         1167
```

```
        <210> 176
        <211> 205
        <212> PRT
        <213> Homo sapien

        <220>
        <221> VARIANT
        <222> (1)...(205)
        <223> Xaa = Any Amino Acid

        <400> 176
Met Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln Trp
 1               5                  10                  15
Val Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu
            20                  25                  30
Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val
        35                  40                  45
Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Leu Leu Leu
    50                  55                  60
Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser
65                  70                  75                  80
Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly
                85                  90          -       95
Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly Arg Met
            100                 105                 110
Pro Thr Val Leu His Cys Val Asn Val Ser Val Val Ser Glu Xaa Val
        115                 120                 125
Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe Cys Ala
        130                 135                 140
Gly Gly Gly Gln Asp Gln Lys Asp Ser Cys Asn Gly Asp Ser Gly Gly
145                 150                 155                 160
Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe Gly Lys
                165                 170                 175
Ala Pro Cys Gly Gln Leu Gly Val Pro Gly Val Tyr Thr Asn Leu Cys
            180                 185                 190
Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Xaa Ser
        195                 200                 205
```

```
        <210> 177
        <211> 1119
        <212> DNA
        <213> Homo sapien

        <400> 177
gcgcactcgc agccctggca ggcggcactg gtcatggaaa acgaattgtt ctgctcgggc       60
gtcctggtgc atccgcagtg ggtgctgtca gccgcacact gtttccagaa ctcctacacc      120
atcgggctgg gcctgcacag tcttgaggcc gaccaagagc cagggagcca gatggtggag      180
gccagcctct ccgtacggca cccagagtac aacagaccct tgctcgctaa cgacctcatg      240
ctcatcaagt tggacgaatc cgtgtccgag tctgacacca tccggagcat cagcattgct      300
tcgcagtgcc ctaccgcggg gaactcttgc ctcgtttctg gctggggtct gctggcgaac      360
gatgctgtga ttgccatcca gtcccagact gtgggaggct gggagtgtga gaagctttcc      420
caaccctggc aggttgtac cattcggca acttccagtg caaggacgtc ctgctgcatc      480
```

63

```
ctcactgggt gctcactact gctcactgca tcacccggaa cactgtgatc aactagccag    540
caccatagtt ctccgaagtc agactatcat gattactgtg ttgactgtgc tgtctattgt    600
actaaccatg ccgatgttta ggtgaaatta gcgtcacttg gcctcaacca tcttggtatc    660
cagttatcct cactgaattg agatttcctg cttcagtgtc agccattccc acataatttc    720
tgacctacag aggtgaggga tcatatagct cttcaaggat gctggtactc ccctcacaaa    780
ttcatttctc ctgttgtagt gaaaggtgcg ccctctggag cctcccaggg tgggtgtgca    840
ggtcacaatg atgaatgtat gatcgtgttc ccattaccca aagcctttaa atccctcatg    900
ctcagtacac cagggcaggt ctagcatttc ttcatttagt gtatgctgtc cattcatgca    960
accacctcag gactcctgga ttctctgcct agttgagctc ctgcatgctg cctccttggg   1020
gaggtgaggg agagggccca tggttcaatg ggatcgtgtgc agttgtaaca cattaggtgc   1080
ttaataaaca gaagctgtga tgttaaaaaa aaaaaaaaa                         1119
```

```
         <210> 178
         <211> 164
         <212> PRT
         <213> Homo sapien

         <220>
         <221> VARIANT
         <222> (1)...(164)
         <223> Xaa = Any Amino Acid

         <400> 178
Met Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln Trp
1               5                   10                  15
Val Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu
            20                  25                  30
Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val
        35                  40                  45
Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro Leu Leu
    50                  55                  60
Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser
65                  70                  75                  80
Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly
                85                  90                  95
Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Asp Ala Val
            100                 105                 110
Ile Ala Ile Gln Ser Xaa Thr Val Gly Gly Trp Glu Cys Glu Lys Leu
        115                 120                 125
Ser Gln Pro Trp Gln Gly Cys Thr Ile Ser Ala Thr Ser Ser Ala Arg
    130                 135                 140
Thr Ser Cys Cys Ile Leu Thr Gly Cys Ser Leu Leu Leu Thr Ala Ser
145                 150                 155                 160
Pro Gly Thr Leu
```

```
         <210> 179
         <211> 250
         <212> DNA
         <213> Homo sapien

         <400> 179
ctggagtgcc ttggtgtttc aagcccctgc aggaagcaga atgcaccttc tgaggcacct    60
ccagctgccc ccggccgggg gatgcgaggc tcggagcacc cttgcccggc tgtgattgct   120
gccaggcact gttcatctca gcttttctgt ccctttgctc ccggcaagcg cttctgctga   180
aagttcatat ctggagcctg atgtcttaac gaataaaggt cccatgctcc acccgaaaaa   240
aaaaaaaaaa                                                         250
```

64

```
<210> 180
<211> 202
<212> DNA
<213> Homo sapien

<400> 180
actagtccag tgtggtggaa ttccattgtg ttgggcccaa cacaatggct acctttaaca      60
tcacccagac cccgcccctg cccgtgcccc acgctgctgc taacgacagt atgatgctta     120
ctctgctact cggaaactat ttttatgtaa ttaatgtatg ctttcttgtt tataaatgcc     180
tgatttaaaa aaaaaaaaaa aa                                              202


<210> 181
<211> 558
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(558)
<223> n = A,T,C or G

<400> 181
tccytttgkt naggtttkkg agacamccck agacctwaan ctgtgtcaca gacttcyngg      60
aatgtttagg cagtgctagt aatttcytcg taatgattct gttattactt tcctnattct     120
ttattcctct ttcttctgaa gattaatgaa gttgaaaatt gaggtggata aatacaaaaa     180
ggtagtgtga tagtataagt atctaagtgc agatgaaagt gtgttatata tatccattca     240
aaattatgca agttagtaat tactcagggt taactaaatt actttaatat gctgttgaac     300
ctactctgtt ccttggctag aaaaaattat aaacaggact ttgttagttt gggaagccaa     360
attgataata ttctatgttc taaaagttgg gctatacata aattattaag aaatatggaw     420
ttttattccc aggaatatgg kgttcatttt atgaatatta cscrggatag awgtwtgagt     480
aaaaycagtt ttggtwaata ygtwaatatg tcmtaaataa acaakgcttt gacttatttc     540
caaaaaaaaa aaaaaaaa                                                   558


<210> 182
<211> 479
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(479)
<223> n = A,T,C or G

<400> 182
acagggwttk grggatgcta agsccccrga rwtygtttga tccaaccctg gcttwttttc      60
agaggggaaa atggggccta gaagttacag mscatytagy tggtgcgmtg gcaccccctgg    120
cstcacacag astcccgagt agctgggact acaggcacac agtcactgaa gcaggccctg     180
ttwgcaattc acgttgccac ctccaactta aacattcttc atatgtgatg tccttagtca     240
ctaaggttaa actttcccac ccagaaaagg caacttagat aaaatcttag agtactttca     300
tactmttcta agtcctcttc cagcctcact kkgagtcctm cytgggggtt gataggaant     360
ntctcttggc tttctcaata aartctctat ycatctcatg tttaatttgg tacgcatara     420
awtgstgara aaattaaaat gttctggtty mactttaaaa araaaaaaaa aaaaaaaaa     479


<210> 183
<211> 384
<212> DNA
<213> Homo sapien
```

65

<400> 183
```
aggcgggagc agaagctaaa gccaaagccc aagaagagtg gcagtgccag cactggtgcc      60
agtaccagta ccaataacag tgccagtgcc agtgccagca ccagtggtgg cttcagtgct     120
ggtgccagcc tgaccgccac tctcacattt gggctcttcg ctggccttgg tggagctggt     180
gccagcacca gtggcagctc tggtgcctgt ggtttctcct acaagtgaga ttttagatat     240
tgttaatcct gccagtcttt ctcttcaagc cagggtgcat cctcagaaac ctactcaaca     300
cagcactcta ggcagccact atcaatcaat tgaagttgac actctgcatt aratctattt     360
gccatttcaa aaaaaaaaaa aaaa                                            384
```

<210> 184
<211> 496
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(496)
<223> n = A,T,C or G

<400> 184
```
accgaattgg gaccgctggc ttataagcga tcatgtyynt ccrgtatkac ctcaacgagc      60
agggagatcg agtctatacg ctgaagaaat ttgacccgat gggacaacag acctgctcag     120
cccatcctgc tcggttctcc ccagatgaca aatactctsg acaccgaatc accatcaaga     180
aacgcttcaa ggtgctcatg acccagcaac cgcgccctgt cctctgaggg tcccttaaac     240
tgatgtcttt tctgccacct gttacccctc ggagactccg taaccaaact cttcggactg     300
tgagccctga tgcctttttg ccagccatac tctttggcat ccagtctctc gtggcgattg     360
attatgcttg tgtgaggcaa tcatggtggc atcacccata aagggaacac atttgacttt     420
tttttctcat attttaaatt actacmagaw tattwmagaw waaatgawtt gaaaaactst     480
taaaaaaaaa aaaaaa                                                    496
```

<210> 185
<211> 384
<212> DNA
<213> Homo sapien

<400> 185
```
gctggtagcc tatggcgkgg cccacggagg ggctcctgag gccacggrac agtgacttcc      60
caagtatcyt gcgcsgcgtc ttctaccgtc cctacctgca gatcttcggg cagattcccc     120
aggaggacat ggacgtggcc ctcatggagc acagcaactg ytcgtcggag cccggcttct     180
gggcacaccc tcctgggggcc caggcgggca cctgcgtctc ccagtatgcc aactggctgg     240
tggtgctgct cctcgtcatc ttcctgctcg tggccaacat cctgctggtc aacttgctca     300
ttgccatgtt cagttacaca ttcggcaaag tacagggcaa cagcgatctc tactgggaag     360
gcgcagcgtt accgcctcat ccgg                                           384
```

<210> 186
<211> 577
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(577)
<223> n = A,T,C or G

<400> 186
```
gagttagctc ctccacaacc ttgatgaggt cgtctgcagt ggcctctcgc ttcataccgc      60
tnccatcgtc atactgtagg tttgccacca cytcctggca tcttggggcg gcntaatatt     120
ccaggaaact ctcaatcaag tcaccgtcga tgaaacctgt gggctggttc tgtcttccgc     180
```

```
tcggtgtgaa aggatctccc agaaggagtg ctcgatcttc cccacacttt tgatgacttt    240
attgagtcga ttctgcatgt ccagcaggag gttgtaccag ctctctgaca gtgaggtcac    300
cagccctatc atgccgttga mcgtgccgaa garcaccgag ccttgtgtgg gggkkgaagt    360
ctcacccaga ttctgcatta ccagagagcc gtggcaaaag acattgacaa actcgcccag    420
gtggaaaaag amcamctcct ggargtgctn gccgctcctc gtcmgttggt ggcagcgctw    480
tccttttgac acacaaacaa gttaaaggca ttttcagccc ccagaaantt gtcatcatcc    540
aagatntcgc acagcactna tccagttggg attaaat                             577
```

        <210> 187
        <211> 534
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(534)
        <223> n = A,T,C or G

        <400> 187
```
aacatcttcc tgtataatgc tgtgtaatat cgatccgatn ttgtctgstg agaatycatw     60
actkggaaaa gmaacattaa agcctggaca ctggtattaa aattcacaat atgcaacact    120
ttaaacagtg tgtcaatctg ctcccyynac tttgtcatca ccagtctggg aakaagggta    180
tgccctattc acacctgtta aaagggcgct aagcattttt gattcaacat cttttttttt    240
gacacaagtc cgaaaaaagc aaaagtaaac agttatyaat ttgttagcca attcactttc    300
ttcatgggac agagccatyt gatttaaaaa gcaaattgca taatattgag cttygggagc    360
tgatatttga gcggaagagt agcctttcta cttcaccaga cacaactccc tttcatattg    420
ggatgttnac naaagtwatg tctctwacag atgggatgct tttgtggcaa ttctgttctg    480
aggatctccc agtttattta ccacttgcac aagaaggcgt tttcttcctc aggc          534
```

        <210> 188
        <211> 761
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(761)
        <223> n = A,T,C or G

        <400> 188
```
agaaaccagt atctctnaaa acaacctctc ataccttgtg gacctaattt tgtgtgcgtg     60
tgtgtgtgcg cgcatattat atagacaggc acatcttttt tacttttgta aaagcttatg    120
cctctttggt atctatatct gtgaaagttt taatgatctg ccataatgtc ttggggacct    180
ttgtcttctg tgtaaatggt actagagaaa acacctatnt tatgagtcaa tctagttngt    240
tttattcgac atgaaggaaa tttccagatn acaacactna caaactctcc ctkgackarg    300
ggggacaaag aaaagcaaaa ctgamcataa raaacaatwa cctggtgaga arttgcataa    360
acagaaatwr ggtagtatat tgaarnacag catcattaaa rmgttwtktt wttctccctt    420
gcaaaaaaca tgtacngact tcccgttgag taatgccaag ttgttttttt tatnataaaa    480
cttgcccttc attacatgtt tnaaagtggt gtggtgggcc aaaatattga aatgatggaa    540
ctgactgata aagctgtaca aataagcagt gtgcctaaca agcaacacag taatgttgac    600
atgcttaatt cacaaatgct aatttcatta taaatgtttg ctaaaataca ctttgaacta    660
tttttctgtn ttcccagagc tgagatntta gattttatgt agtatnaagt gaaaaantac    720
gaaataata  acattgaaga aaaananaaa aaanaaaaaa a                        761
```

        <210> 189
        <211> 482
        <212> DNA
        <213> Homo sapien

67

```
<220>
<221> misc_feature
<222> (1)...(482)
<223> n = A,T,C or G

<400> 189
ttttttttttt tttgccgatn ctactatttt attgcaggan gtgggggtgt atgcaccgca      60
caccgggggct atnagaagca agaaggaagg agggagggca cagcccttg ctgagcaaca       120
aagccgcctg ctgccttctc tgtctgtctc ctggtgcagg cacatgggga gaccttcccc       180
aaggcagggg ccaccagtcc aggggtggga atacaggggg tgggangtgt gcataagaag       240
tgataggcac aggccacccg gtacagaccc ctcggctcct gacaggtnga tttcgaccag       300
gtcattgtgc cctgcccagg cacagcgtan atctggaaaa gacagaatgc tttccttttc       360
aaatttggct ngtcatngaa ngggcanttt tccaanttng gctnggtctt ggtacncttg       420
gttcggccca gctccncgtc caaaaantat tcacccnnct ccnaattgct tgcnggnccc       480
cc                                                                       482


<210> 190
<211> 471
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(471)
<223> n = A,T,C or G

<400> 190
ttttttttttt ttttaaaaca gtttttcaca acaaaattta ttagaagaat agtggttttg      60
aaaactctcg catccagtga gaactaccat acaccacatt acagctngga atgtnctcca       120
aatgtctggt caaatgatac aatggaacca ttcaatctta cacatgcacg aaagaacaag       180
cgcttttgac atacaatgca caaaaaaaaa aggggggggg gaccacatgg attaaaattt       240
taagtactca tcacatacat taagacacag ttctagtcca gtcnaaaatc agaactgcnt       300
tgaaaaattt catgtatgca atccaaccaa agaacttnat tggtgatcat gantnctcta       360
ctacatcnac cttgatcatt gccaggaacn aaaagttnaa ancacncgt acaaaaaanaa       420
tctgtaattn anttcaacct ccgtacngaa aaatnttnnt tatacactcc c                471


<210> 191
<211> 402
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(402)
<223> n = A,T,C or G

<400> 191
gagggattga aggtctgttc tastgtcggm ctgttcagcc accaactcta acaagttgct       60
gtcttccact cactgtctgt aagctttta acccagacwg tatcttcata aatagaacaa       120
attcttcacc agtcacatct tctaggacct ttttggattc agttagtata agctcttcca       180
cttcctttgt taagacttca tctggtaaag tcttaagttt tgtagaaagg aattyaattg       240
ctcgttctct aacaatgtcc tctccttgaa gtatttggct gaacaaccca cctaaagtcc       300
ctttgtgcat ccattttaaa tatacttaat agggcattgk tncactaggt taaattctgc       360
aagagtcatc tgtctgcaaa agttgcgtta gtatatctgc ca                          402


<210> 192
<211> 601
```

68

```
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(601)
        <223> n = A,T,C or G

        <400> 192
gagctcggat ccaataatct ttgtctgagg gcagcacaca tatncagtgc catggnaact      60
ggtctacccc acatgggagc agcatgccgt agntatataa ggtcattccc tgagtcagac     120
atgcytyttt gaytaccgtg tgccaagtgc tggtgattct yaacacacyt ccatcccgyt     180
cttttgtgga aaaactggca cttktctgga actagcarga catcacttac aaattcaccc     240
acgagacact tgaaaggtgt aacaaagcga ytcttgcatt gctttttgtc cctccggcac     300
cagttgtcaa tactaacccg ctggtttgcc tccatcacat ttgtgatctg tagctctgga     360
tacatctcct gacagtactg aagaacttct tcttttgttt caaaagcarc tcttggtgcc     420
tgttggatca ggttcccatt tcccagtcyg aatgttcaca tggcatattt wacttcccac     480
aaaacattgc gatttgaggc tcagcaacag caaatcctgt tccggcattg gctgcaagag     540
cctcgatgta gccggccagc gccaaggcag gcgccgtgag ccccaccagc agcagaagca     600
g                                                                     601

        <210> 193
        <211> 608
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(608)
        <223> n = A,T,C or G

        <400> 193
atacagccca natcccacca cgaagatgcg cttgttgact gagaacctga tgcggtcact      60
ggtcccgctg tagccccagc gactctccac ctgctggaag cggttgatgc tgcactcytt     120
cccaacgcag gcagmagcgg gsccggtcaa tgaactccay tcgtggcttg gggtkgacgg     180
tkaagtgcag gaagaggctg accacctcgc ggtccaccag gatgcccgac tgtgcgggac     240
ctgcagcgaa actcctcgat ggtcatgagc gggaagcgaa tgaggcccag ggccttgccc     300
agaaccttcc gcctgttctc tggcgtcacc tgcagctgct gccgctgaca ctcggcctcg     360
gaccagcgga caaacggcrt tgaacagccg cacctcacgg atgcccagtg tgtcgcgctc     420
caggammgsc accagcgtgt ccaggtcaat gtcggtgaag ccctccgcgg gtratggcgt     480
ctgcagtgtt tttgtcgatg ttctccaggc acaggctggc cagctgcggt tcatcgaaga     540
gtcgcgcctg cgtgagcagc atgaaggcgt tgtcggctcg cagttcttct tcaggaactc     600
cacgcaat                                                              608

        <210> 194
        <211> 392
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(392)
        <223> n = A,T,C or G

        <400> 194
gaacggctgg accttgcctc gcattgtgct tgctggcagg gaataccttg gcaagcagyt      60
ccagtccgag cagccccaga ccgctgccgc ccgaagctaa gcctgcctct ggccttcccc     120
tccgcctcaa tgcagaacca gtagtgggag cactgtgttt agagttaaga gtgaacactg     180
```

69

```
tttgatttta cttgggaatt tcctctgtta tatagctttt cccaatgcta atttccaaac      240
aacaacaaca aaataacatg tttgcctgtt aagttgtata aaagtaggtg attctgtatt      300
taaagaaaat attactgtta catatactgc ttgcaatttc tgtatttatt gktnctstgg      360
aaataaatat agttattaaa ggttgtcant cc                                    392
```

```
        <210> 195
        <211> 502
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(502)
        <223> n = A,T,C or G

        <400> 195
ccsttkgagg ggtkaggkyc cagttyccga gtggaagaaa caggccagga gaagtgcgtg      60
ccgagctgag gcagatgttc ccacagtgac ccccagagcc stgggstata gtytctgacc      120
cctcncaagg aaagaccacs ttctgggggac atgggctgga gggcaggacc tagaggcacc      180
aagggaaggc cccattccgg ggstgttccc cgaggaggaa gggaagggggc tctgtgtgcc      240
ccccasgagg aagaggccct gagtcctggg atcagacacc ccttcacgtg tatccccaca      300
caaatgcaag ctcaccaagg tcccctctca gtcccccttcc stacaccctg amcggccact      360
gscscacacc cacccagagc acgccacccg ccatgggar tgtgctcaag gartcgcngg      420
gcarcgtgga catctngtcc cagaagggg cagaatctcc aatagangga ctgarcmstt      480
gctnanaaaa aaaaanaaaa aa                                              502
```

```
        <210> 196
        <211> 665
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(665)
        <223> n = A,T,C or G

        <400> 196
ggttacttgg tttcattgcc accacttagt ggatgtcatt tagaaccatt ttgtctgctc      60
cctctggaag ccttgcgcag agcggacttt gtaattgttg gagaataact gctgaatttt      120
wagctgtttk gagttgatts gcaccactgc acccacaact tcaatatgaa aacyawttga      180
actwatttat tatcttgtga aaagtataac aatgaaaatt ttgttcatac tgtattkatc      240
aagtatgatg aaaagcaawa gatatatatt cttttattat gttaaattat gattgccatt      300
attaatcggc aaaatgtgga gtgtatgttc ttttcacagt aatatatgcc ttttgtaact      360
tcacttggtt attttattgt aaatgartta caaaattctt aatttaagar aatggtatgt      420
watatttatt tcattaatttt ctttcctkgt ttacgtwaat tttgaaaaga wtgcatgatt      480
tcttgacaga aatcgatctt gatgctgtgg aagtagtttg acccacatcc ctatgagttt      540
ttcttagaat gtataaaggt tgtagcccat cnaacttcaa agaaaaaaat gaccacatac      600
tttgcaatca ggctgaaatg tggcatgctn ttctaattcc aactttataa actagcaaan      660
aagtg                                                                 665
```

```
        <210> 197
        <211> 492
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(492)
```

70

<210> n = A,T,C or G

<400> 197
```
ttttnttttt tttttttttgc aggaaggatt ccatttattg tggatgcatt ttcacaatat      60
atgtttattg gagcgatcca ttatcagtga aaagtatcaa gtgtttataa nattttagg       120
aaggcagatt cacagaacat gctngtcngc ttgcagtttt acctcgtana gatnacagag      180
aattatagtc naaccagtaa acnaggaatt tacttttcaa aagattaaat ccaaactgaa      240
caaaattcta ccctgaaact tactccatcc aaatattgga ataanagtca gcagtgatac      300
attctcttct gaactttaga ttttctagaa aaatatgtaa tagtgatcag gaagagctct      360
tgttcaaaag tacaacnaag caatgttccc ttaccatagg ccttaattca aactttgatc      420
catttcactc ccatcacggg agtcaatgct acctgggaca cttgtatttt gttcatnctg      480
ancntggctt aa                                                          492
```

<210> 198
<211> 478
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(478)
<223> n = A,T,C or G

<400> 198
```
tttnttttgn atttcantct gtannaanta ttttcattat gtttattana aaaatatnaa      60
tgtntccacn acaaatcatn ttacntnagt aagaggccan ctacattgta caacatacac      120
tgagtatatt ttgaaaagga caagtttaaa gtanacncat attgccganc atancacatt      180
tatacatggc ttgattgata tttagcacag canaaactga gtgagttacc agaaanaaat      240
natatatgtc aatcngattt aagatacaaa acagatccta tggtacatan catcntgtag      300
gagttgtggc tttatgttta ctgaaagtca atgcagttcc tgtacaaaga gatggccgta      360
agcattctag tacctctact ccatggttaa gaatcgtaca cttatgttta catatgtnca      420
gggtaagaat tgtgttaagt naanttatgg agaggtccan gagaaaaatt tgatncaa       478
```

<210> 199
<211> 482
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(482)
<223> n = A,T,C or G

<400> 199
```
agtgacttgt cctccaacaa aaccccttga tcaagtttgt ggcactgaca atcagaccta      60
tgctagttcc tgtcatctat tcgctactaa atgcagactg gagggggacca aaaagggca    120
tcaactccag ctggattatt ttggagcctg caaatctatt cctacttgta cggactttga     180
agtgattcag tttcctctac ggatgagaga ctggctcaag aatatcctca tgcagcttta     240
tgaagccnac tctgaacacg ctggttatct nagatgagaa ncagagaaat aaagtcnaga     300
aaatttacct ggangaaaag aggctttngg ctggggacca tcccattgaa ccttctctta    360
anggacttta agaanaaact accacatgtn tgtngtatcc tggtgccngg ccgtttantg     420
aacntngacn ncaccccttnt ggaatanant cttgacngcn tcctgaactt gctcctctgc   480
ga                                                                    482
```

<210> 200
<211> 270
<212> DNA
<213> Homo sapien

71

```
      <220>
      <221> misc_feature
      <222> (1)...(270)
      <223> n = A,T,C or G

      <400> 200
cggccgcaag tgcaactcca gctggggccg tgcggacgaa gattctgcca gcagttggtc          60
cgactgcgac gacggcggcg gcgacagtcg caggtgcagc gcgggcgcct ggggtcttgc         120
aaggctgagc tgacgccgca gaggtcgtgt cacgtcccac gaccttgacg ccgtcgggga         180
cagccggaac agagcccggt gaangcggga ggcctcgggg agcccctcgg gaagggcggc         240
ccgagagata cgcaggtgca ggtggccgcc                                          270

      <210> 201
      <211> 419
      <212> DNA
      <213> Homo sapien

      <220>
      <221> misc_feature
      <222> (1)...(419)
      <223> n = A,T,C or G

      <400> 201
tttttttttt ttttggaatc tactgcgagc acagcaggtc agcaacaagt ttattttgca          60
gctagcaagg taacagggta gggcatggtt acatgttcag gtcaacttcc tttgtcgtgg         120
ttgattggtt tgtctttatg ggggcggggt ggggtagggg aaancgaagc anaantaaca         180
tggagtgggt gcaccctccc tgtagaacct ggttacnaaa gcttggggca gttcacctgg         240
tctgtgaccg tcattttctt gacatcaatg ttattagaag tcaggatatc ttttagagag         300
tccactgtnt ctggagggag attagggttt cttgccaana tccaancaaa atccacntga         360
aaaagttgga tgatncangt acngaatacc ganggcatan ttctcatant cggtggcca          419

      <210> 202
      <211> 509
      <212> DNA
      <213> Homo sapien

      <220>
      <221> misc_feature
      <222> (1)...(509)
      <223> n = A,T,C or G

      <400> 202
tttntttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt          60
tggcacttaa tccatttttta tttcaaaatg tctacaaant ttnaatncnc cattatacng         120
gtnattttnc aaaatctaaa nnttattcaa atntnagcca aantccttac ncaaatnnaa         180
tacncncaaa aatcaaaaat atacntntct ttcagcaaac ttngttacat aaattaaaaa         240
aatatatacg gctggtgttt tcaaagtaca attatcttaa cactgcaaac atntttnnaa         300
ggaactaaaa taaaaaaaaa cactnccgca aaggttaaag ggaacaacaa attcnttttta        360
caacancnnc nattataaaa atcatatctc aaatcttagg ggaatatata cttcacacng         420
ggatcttaac ttttactnca ctttgtttat tttttttanaa ccattgtntt gggcccaaca       480
caatggnaat nccnccncnc tggactagt                                           509

      <210> 203
      <211> 583
      <212> DNA
      <213> Homo sapien
```

72

```
<220>
<221> misc_feature
<222> (1)...(583)
<223> n = A,T,C or G


    <400> 203
ttttttttttt tttttttttga cccccctctt ataaaaaaca agttaccatt ttattttact      60
tacacatatt tattttataa ttggtattag atattcaaaa ggcagctttt aaaatcaaac        120
taaatggaaa ctgccttaga tacataattc ttaggaatta gcttaaaatc tgcctaaagt        180
gaaaatcttc tctagctctt ttgactgtaa attttttgact cttgtaaaac atccaaattc       240
attttcttg tctttaaaat tatctaatct ttccattttt tccctattcc aagtcaattt        300
gcttctctag cctcatttcc tagctcttat ctactattag taagtggctt ttttcctaaa       360
agggaaaaca ggaagagana atggcacaca aaacaaacat tttatattca tatttctacc       420
tacgttaata aaatagcatt ttgtgaagcc agctcaaaag aaggcttaga tccttttatg       480
tccatttag tcactaaacg atatcnaaag tgccagaatg caaaaggttt gtgaacattt        540
attcaaaagc taatataaga tatttcacat actcatcttt ctg                        583


    <210> 204
    <211> 589
    <212> DNA
    <213> Homo sapien


    <220>
    <221> misc_feature
    <222> (1)...(589)
    <223> n = A,T,C or G


    <400> 204
ttttttttnt tttttttttt tttttnctc ttctttttttt ttganaatga ggatcgagtt        60
tttcactctc tagatagggc atgaagaaaa ctcatctttc cagctttaaa ataacaatca        120
aatctcttat gctatatcat attttaagtt aaactaatga gtcactggct tatcttctcc       180
tgaaggaaat ctgttcattc ttctcattca tatagttata tcaagtacta ccttgcatat       240
tgagaggttt ttcttctcta tttacacata tatttccatg tgaatttgta tcaaaccttt       300
attttcatgc aaactagaaa ataatgtntt cttttgcata agagaagaga acaatatnag       360
cattacaaaa ctgctcaaat tgtttgttaa gnttatccat tataattagt tnggcaggag       420
ctaatacaaa tcacatttac ngacnagcaa taataaaact gaagtaccag ttaaatatcc       480
aaaataatta aaggaacatt tttagcctgg gtataaattag ctaattcact ttacaagcat      540
ttattnagaa tgaattcaca tgttattatt ccntagccca acacaatgg                  589


    <210> 205
    <211> 545
    <212> DNA
    <213> Homo sapien


    <220>
    <221> misc_feature
    <222> (1)...(545)
    <223> n = A,T,C or G


    <400> 205
ttttttntttt tttttcagt aataatcaga acaatattta ttttttatatt taaaattcat       60
agaaaagtgc cttcatttta ataaaagttt gtttctcaaa gtgatcagag gaattagata        120
tngtcttgaa caccaatatt aatttgagga aaatacacca aaatacatta agtaaattat        180
ttaagatcat agagcttgta agtgaaaaga taaaatttga cctcagaaac tctgagcatt       240
aaaaatccac tattagcaaa taaattacta tggacttctt gctttaattt tgtgatgaat       300
atggggtgtc actggtaaac caacacattc tgaaggatac attacttagt gatagattct        360
tatgtacttt gctanatnac gtggatatga gttgacaagt ttctctttct tcaatctttt       420
aaggggcnga ngaaatgagg aagaaaagaa aaggattacg catactgttc tttctatngg       480
```

73

```
aaggattaga tatgtttcct ttgccaatat taaaaaaata ataatgttta ctactagtga      540
aaccc                                                                  545
```

```
        <210> 206
        <211> 487
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(487)
        <223> n = A,T,C or G

        <400> 206
tttttttttt tttttagtc aagtttctna ttttattat aattaaagtc ttggtcattt        60
catttattag ctctgcaact tacatattta aattaaagaa acgttnttag acaactgtna      120
caatttataa atgtaaggtg ccattattga gtanatatat tcctccaaga gtggatgtgt      180
cccttctccc accaactaat gaancagcaa cattagttta attttattag tagatnatac      240
actgctgcaa acgctaattc tcttctccat ccccatgtng atattgtgta tatgtgtgag      300
ttggtnagaa tgcatcanca atctnacaat caacagcaag atgaagctag gcntgggctt      360
tcggtgaaaa tagactgtgt ctgtctgaat caaatgatct gacctatcct cggtggcaag      420
aactcttcga accgcttcct caaaggcngc tgccacattt gtggcntctn ttgcacttgt      480
ttcaaaa                                                                487
```

```
        <210> 207
        <211> 332
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(332)
        <223> n = A,T,C or G

        <400> 207
tgaattggct aaaagactgc atttttanaa ctagcaactc ttatttcttt cctttaaaaa      60
tacatagcat taaatcccaa atcctattta aagacctgac agcttgagaa ggtcactact      120
gcatttatag gaccttctgg tggttctgct gttacntttg aantctgaca atccttgana      180
atctttgcat gcagaggagg taaaaggtat tggattttca cagaggaana acacagcgca      240
gaaatgaagg ggccaggctt actgagcttg tccactggag ggctcatggg tgggacatgg      300
aaaagaaggc agcctaggcc ctggggagcc ca                                    332
```

```
        <210> 208
        <211> 524
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(524)
        <223> n = A,T,C or G

        <400> 208
agggcgtggt gcggagggcg ttactgtttt gtctcagtaa caataaatac aaaaagactg      60
gttgtgttcc ggccccatcc aaccacgaag ttgatttctc ttgtgtgcag agtgactgat      120
tttaaaggac atggagcttg tcacaatgtc acaatgtcac agtgtgaagg gcacactcac      180
tcccgcgtga ttcacattta gcaaccaaca atagctcatg agtccatact tgtaaatact      240
tttggcagaa tacttnttga aacttgcaga tgataactaa gatccaagat atttcccaaa      300
```

74

```
gtaaatagaa gtgggtcata atattaatta cctgttcaca tcagcttcca tttacaagtc        360
atgagcccag acactgacat caaactaagc ccacttagac tcctcaccac cagtctgtcc        420
tgtcatcaga caggaggctg tcaccttgac caaattctca ccagtcaatc atctatccaa        480
aaaccattac ctgatccact tccggtaatg caccaccttg gtga                        524

        <210> 209
        <211> 159
        <212> DNA
        <213> Homo sapien

        <400> 209
gggtgaggaa atccagagtt gccatggaga aaattccagt gtcagcattc ttgctccttg         60
tggccctctc ctacactctg gccagagata ccacagtcaa acctggagcc aaaaaggaca        120
caaaggactc tcgacccaaa ctgccccaga ccctctcca                              159

        <210> 210
        <211> 256
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(256)
        <223> n = A,T,C or G

        <400> 210
actccctggc agacaaaggc agaggagaga gctctgttag ttctgtgttg ttgaactgcc         60
actgaatttc tttccacttg gactattaca tgccanttga gggactaatg gaaaaacgta        120
tggggagatt ttanccaatt tangtntgta aatggggaga ctggggcagg cgggagagat        180
ttgcaggggtg naaatgggan ggctggtttg ttanatgaac agggacatag gaggtaggca       240
ccaggatgct aaatca                                                       256

        <210> 211
        <211> 264
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(264)
        <223> n = A,T,C or G

        <400> 211
acattgtttt tttgagataa agcattgaga gagctctcct taacgtgaca caatggaagg         60
actggaacac atacccacat ctttgttctg agggataatt ttctgataaa gtcttgctgt        120
atattcaagc acatatgtta tatattattc agttccatgt ttatagccta gttaaggaga        180
ggggagatac attcngaaag aggactgaaa gaaatactca agtnggaaaa cagaaaaaga        240
aaaaaggag caaatgagaa gcct                                               264

        <210> 212
        <211> 328
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(328)
        <223> n = A,T,C or G
```

```
        <400> 212
acccaaaaat ccaatgctga atatttggct tcattattcc canattcttt gattgtcaaa            60
ggatttaatg ttgtctcagc ttgggcactt cagttaggac ctaaggatgc cagccggcag           120
gtttatatat gcagcaacaa tattcaagcg cgacaacagg ttattgaact tgcccgccag           180
ttnaatttca ttcccattga cttgggatcc ttatcatcag ccagagagat tgaaaattta          240
cccctacnac tctttactct ctgganaggg ccagtggtgg tagctataag cttggccaca          300
tttttttttc ctttattcct ttgtcaga                                              328
```

```
        <210> 213
        <211> 250
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(250)
        <223> n = A,T,C or G

        <400> 213
acttatgagc agagcgacat atccnagtgt agactgaata aaactgaatt ctctccagtt            60
taaagcattg ctcactgaag ggatagaagt gactgccagg agggaaagta agccaaggct           120
cattatgcca aagganatat acatttcaat tctccaaact tcttcctcat tccaagagtt          180
ttcaatattt gcatgaacct gctgataanc catgttaana aacaaatatc tctctnacct          240
tctcatcggt                                                                  250
```

```
        <210> 214
        <211> 444
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(444)
        <223> n = A,T,C or G

        <400> 214
acccagaatc caatgctgaa tatttggctt cattattccc agattctttg attgtcaaag            60
gatttaatgt tgtctcagct tgggcacttc agttaggacc taaggatgcc agccggcagg           120
tttatatatg cagcaacaat attcaagcgc gacaacaggt tattgaactt gcccgccagt          180
tgaatttcat tcccattgac ttgggatcct tatcatcagc canagagatt gaaaatttac          240
ccctacgact ctttactctc tggagagggc cagtggtggt agctataagc ttggccacat          300
ttttttttcc tttattcctt tgtcagagat gcgattcatc catatgctan aaaccaacag          360
agtgactttt acaaaattcc tataganatt gtgaataaaa ccttacctat agttgccatt          420
actttgctct ccctaatata cctc                                                  444
```

```
        <210> 215
        <211> 366
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(366)
        <223> n = A,T,C or G

        <400> 215
acttatgagc agagcgacat atccaagtgt anactgaata aaactgaatt ctctccagtt            60
```

76

```
taaagcattg ctcactgaag ggatagaagt gactgccagg agggaaagta agccaaggct      120
cattatgcca aagganatat acatttcaat tctccaaact tcttcctcat tccaagagtt      180
ttcaatattt gcatgaacct gctgataagc catgttgaga aacaaatatc tctctgacct      240
tctcatcggt aagcagaggc tgtaggcaac atggaccata gcgaanaaaa aacttagtaa      300
tccaagctgt tttctacact gtaaccaggt ttccaaccaa ggtggaaatc tcctatactt      360
ggtgcc                                                                 366
```

        <210> 216
        <211> 260
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(260)
        <223> n = A,T,C or G

        <400> 216
```
ctgtataaac agaactccac tgccangaggg agggccgggc caggagaatc tccgcttgtc       60
caagacaggg gcctaaggag ggtctccaca ctgctnntaa gggctnttnc attttttttat      120
taataaaaag tnnaaaaggc ctcttctcaa cttttttccc ttnggctgga aaatttaaaa      180
atcaaaaatt tcctnaagtt ntcaagctat catatatact ntatcctgaa aaagcaacat      240
aattcttcct tccctccttt                                                  260
```

        <210> 217
        <211> 262
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(262)
        <223> n = A,T,C or G

        <400> 217
```
acctacgtgg gtaagtttan aaatgttata atttcaggaa naggaacgca tataattgta       60
tcttgcctat aattttctat tttaataagg aaatagcaaa ttggggtggg gggaatgtag      120
ggcattctac agtttgagca aaatgcaatt aaatgtggaa ggacagcact gaaaaatttt      180
atgaataatc tgtatgatta tatgtctcta gagtagattt ataattagcc acttacccta      240
atatccttca tgcttgtaaa gt                                               262
```

        <210> 218
        <211> 205
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(205)
        <223> n = A,T,C or G

        <400> 218
```
accaaggtgg tgcattaccg gaantggatc aangacacca tcgtggccaa cccctgagca       60
cccctatcaa ctcccttttg tagtaaactt ggaaccttgg aaatgaccag gccaagactc      120
aggcctcccc agttctactg acctttgtcc ttangtntna ngtccagggt tgctaggaaa      180
anaaatcagc agacacaggt gtaaa                                            205
```

        <210> 219

77

```
          <211> 114
          <212> DNA
          <213> Homo sapien

          <400> 219
tactgttttg tctcagtaac aataaataca aaaagactgg ttgtgttccg gccccatcca      60
accacgaagt tgatttctct tgtgtgcaga gtgactgatt ttaaaggaca tgga           114

          <210> 220
          <211> 93
          <212> DNA
          <213> Homo sapien

          <400> 220
actagccagc acaaaaggca gggtagcctg aattgctttc tgctctttac atttctttta      60
aaataagcat ttagtgctca gtccctactg agt                                   93

          <210> 221
          <211> 167
          <212> DNA
          <213> Homo sapien

          <220>
          <221> misc_feature
          <222> (1)...(167)
          <223> n = A,T,C or G

          <400> 221
actangtgca ggtgcgcaca aatatttgtc gatattccct tcatcttgga ttccatgagg      60
tcttttgccc agcctgtggc tctactgtag taagtttctg ctgatgagga gccagnatgc     120
cccccactac cttccctgac gctccccana aatcacccaa cctctgt                   167

          <210> 222
          <211> 351
          <212> DNA
          <213> Homo sapien

          <400> 222
agggcgtggt gcggagggcg gtactgacct cattagtagg aggatgcatt ctggcacccc      60
gttcttcacc tgtcccccaa tccttaaaag gccatactgc ataaagtcaa caacagataa     120
atgtttgctg aattaaagga tggatgaaaa aaattaataa tgaatttttg cataatccaa     180
ttttctcttt tatatttcta gaagaagttt ctttgagcct attagatccc gggaatcttt     240
taggtgagca tgattagaga gcttgtaggt tgctttttaca tatatctggc atatttgagt    300
ctcgtatcaa aacaatagat tggtaaaggt ggtattattg tattgataag t              351

          <210> 223
          <211> 383
          <212> DNA
          <213> Homo sapien

          <220>
          <221> misc_feature
          <222> (1)...(383)
          <223> n = A,T,C or G

          <400> 223
aaaacaaaca aacaaaaaaa acaattcttc attcagaaaa attatcttag ggactgatat      60
tggtaattat ggtcaattta atwrtrttkt ggggcatttc cttacattgt cttgacaaga     120
```

78

```
ttaaaatgtc tgtgccaaaa ttttgtattt tatttggaga cttcttatca aaagtaatgc      180
tgccaaagga agtctaagga attagtagtg ttcccmtcac ttgtttggag tgtgctattc      240
taaaagattt tgatttcctg gaatgacaat tatattttaa ctttggtggg ggaaanagtt      300
ataggaccac agtcttcact tctgatactt gtaaattaat cttttattgc acttgttttg      360
accattaagc tatatgttta aaa                                             383
```

```
        <210> 224
        <211> 320
        <212> DNA
        <213> Homo sapien

        <400> 224
cccctgaagg cttcttgtta gaaaatagta cagttacaac caataggaac aacaaaaga       60
aaaagtttgt gacattgtag tagggagtgt gtaccccta ctccccatca aaaaaaaaat      120
ggatacatgg ttaaaggata raagggcaat attttatcat atgttctaaa agagaaggaa     180
gagaaaatac tactttctcr aaatggaagc ccttaaaggt gctttgatac tgaaggacac     240
aaatgtggcc gtccatcctc ctttaragtt gcatgacttg gacacggtaa ctgttgcagt     300
tttaractcm gcattgtgac                                                 320
```

```
        <210> 225
        <211> 1214
        <212> DNA
        <213> Homo sapien

        <400> 225
gaggactgca gcccgcactc gcagccctgg caggcggcac tggtcatgga aaacgaattg      60
ttctgctcgg gcgtcctggt gcatccgcag tgggtgctgt cagccgcaca ctgtttccag     120
aactcctaca ccatcgggct gggcctgcac agtcttgagg ccgaccaaga gccaggagc      180
cagatggtgg aggccagcct ctccgtacgg cacccagagt acaacagacc cttgctcgct     240
aacgacctca tgctcatcaa gttggacgaa tccgtgtccg agtctgacac catccggagc      300
atcagcattg cttcgcagtg ccctaccgcg gggaactctt gcctcgtttc tggctggggt     360
ctgctggcga acggcagaat gcctaccgtg ctgcagtgcg tgaacgtgtc ggtggtgtct     420
gaggaggtct gcagtaagct ctatgacccg ctgtaccacc ccagcatgtt ctgcgccggc     480
ggagggcaag accagaagga ctcctgcaac ggtgactctg ggggccccct gatctgcaac     540
gggtacttgc agggccttgt gtctttcgga aaagccccgt gtggccaagt tggcgtgcca     600
ggtgtctaca ccaacctctg caaattcact gagtggatag agaaaaccgt ccaggccagt     660
taactctggg gactgggaac ccatgaaatt gacccccaaa tacatcctgc ggaaggaatt     720
caggaatatc tgttcccagc ccctcctccc tcaggcccag gagtccaggc ccccagcccc     780
tcctccctca aaccaagggt acagatcccc agcccctcct ccctcagacc caggagtcca     840
gacccccag ccccctcctcc ctcagaccca ggagtccagc ccctcctccc tcagaccag    900
gagtccagac cccccagccc ctcctccctc agacccaggg gtccaggccc ccaacccctc     960
ctccctcaga ctcagaggtc caagcccca accctccctt ccccagaccc agaggtccag   1020
gtcccagccc ctcctccctc agacccagcg gtccaatgcc acctagactc tccctgtaca    1080
cagtgccccc ttgtggcacg ttgacccaac cttaccagtt ggttttttcat ttttttgtccc   1140
tttcccctag atccagaaat aaagtctaag agaagcgcaa aaaaaaaaa aaaaaaaaa      1200
aaaaaaaaa aaaa                                                      1214
```

```
        <210> 226
        <211> 119
        <212> DNA
        <213> Homo sapien

        <400> 226
acccagtatg tgcagggaga cggaacccca tgtgacagcc cactccacca gggttcccaa       60
agaacctggc ccagtcataa tcattcatcc tgacagtggc aataatcacg ataaccagt      119
```

```
        <210> 227
        <211> 818
```

79

```
<212> DNA
<213> Homo sapien

<400> 227
acaattcata gggacgacca atgaggacag ggaatgaacc cggctctccc ccagccctga      60
tttttgctac atatgggggtc ccttttcatt ctttgcaaaa acactgggtt ttctgagaac     120
acggacggtt cttagcacaa tttgtgaaat ctgtgtaraa ccgggctttg cagggggagat     180
aattttcctc ctctggagga aaggtggtga ttgacaggca gggagacagt gacaaggcta     240
gagaaagcca cgctcggcct tctctgaacc aggatggaac ggcagacccc tgaaaacgaa     300
gcttgtcccc ttccaatcag ccacttctga gaaccccccat ctaacttcct actggaaaag     360
agggcctcct caggagcagt ccaagagttt tcaaagataa cgtgacaact accatctaga     420
ggaaaggggtg cacccctcagc agagaagccg agagcttaac tctggtcgtt tccagagaca     480
acctgctggc tgtcttggga tgcgcccagc ctttgagagg ccactacccc atgaacttct     540
gccatccact ggacatgaag ctgaggacac tgggcttcaa cactgagttg tcatgagagg     600
gacaggctct gccctcaagc cggctgaggg cagcaaccac tctcctcccc tttctcacgc     660
aaagccattc ccacaaatcc agaccatacc atgaagcaac gagacccaaa cagtttggct     720
caagaggata tgaggactgt ctcagcctgg ctttgggctg acaccatgca cacacacaag     780
gtccacttct aggttttcag cctagatggg agtcgtgt                            818

<210> 228
<211> 744
<212> DNA
<213> Homo sapien

<400> 228
actggagaca ctgttgaact tgatcaagac ccagaccacc ccaggtctcc ttcgtgggat      60
gtcatgacgt ttgacatacc tttggaacga gcctcctcct tggaagatgg aagaccgtgt     120
tcgtggccga cctggcctct cctggcctgt ttcttaagat gcggagtcac atttcaatgg     180
taggaaaagt ggcttcgtaa aatagaagag cagtcactgt ggaactacca aatggcgaga     240
tgctcggtgc acattggggt gctttgggat aaaagattta tgagccaact attctctggc     300
accagattct aggccagttt gttccactga agcttttccc acagcagtcc acctctgcag     360
gctggcagct gaatggcttg ccggtggctc tgtggcaaga tcacactgag atcgatgggt     420
gagaaggcta ggatgcttgt ctagtgttct tagctgtcac gttggctcct ccaggttgg     480
ccagacggtg ttggccactc ccttctaaaa cacaggcgcc ctcctggtga cagtgacccg     540
ccgtggtatg ccttggccca ttccagcagt cccagttatg catttcaagt ttggggtttg     600
ttcttttcgt taatgttcct ctgtgttgtc agctgtcttc atttcctggg ctaagcagca     660
ttgggagatg tggaccagag atccactcct taagaaccag tggcgaaaga cactttcttt     720
cttcactctg aagtagctgg tggt                                           744

<210> 229
<211> 300
<212> DNA
<213> Homo sapien

<400> 229
cgagtctggg ttttgtctat aaagtttgat ccctcctttt ctcatccaaa tcatgtgaac      60
cattacacat cgaaataaaa gaaaggtggc agacttgccc aacgccaggc tgacatgtgc     120
tgcaggggttg ttgttttta attattattg ttagaaacgt cacccacagt ccctgttaat     180
ttgtatgtga cagccaactc tgagaaggtc ctattttttcc acctgcagag gatccagtct     240
cactaggctc ctccttgccc tcacactgga gtctccgcca gtgtgggtgc ccactgacat     300

<210> 230
<211> 301
<212> DNA
<213> Homo sapien

<400> 230
cagcagaaca aatacaaata tgaagagtgc aaagatctca taaaatctat gctgaggaat      60
```

80

```
gagcgacagt tcaaggagga gaagcttgca gagcagctca agcaagctga ggagctcagg          120
caatataaag tcctggttca cactcaggaa cgagagctga cccagttaag ggagaagttg          180
cgggaaggga gagatgcctc cctctcattg aatgagcatc tccaggccct cctcactccg          240
gatgaaccgg acaagtccca ggggcaggac ctccaagaaa cagacctcgg ccgcgaccac          300
g                                                                          301
```

```
        <210> 231
        <211> 301
        <212> DNA
        <213> Homo sapien


        <400> 231
gcaagcacgc tggcaaatct ctgtcaggtc agctccagag aagccattag tcattttagc          60
caggaactcc aagtccacat ccttggcaac tggggacttg cgcaggttag ccttgaggat          120
ggcaacacgg gacttctcat caggaagtgg gatgtagatg agctgatcaa gacggccagg          180
tctgaggatg gcaggatcaa tgatgtcagg ccggttggta ccgccaatga tgaacacatt          240
ttttttttgtg gacatgccat ccatttctgt caggatctgg ttgatgactc ggtcagcagc         300
c                                                                          301
```

```
        <210> 232
        <211> 301
        <212> DNA
        <213> Homo sapien


        <400> 232
agtaggtatt tcgtgagaag ttcaacacca aaactggaac atagttctcc ttcaagtgtt          60
ggcgacagcg gggcttcctg attctggaat ataactttgt gtaaattaac agccacctat          120
agaagagtcc atctgctgtg aaggagagac agagaactct gggttccgtc gtcctgtcca          180
cgtgctgtac caagtgctgg tgccagcctg ttacctgttc tcactgaaaa tctggctaat          240
gctcttgtgt atcacttctg attctgacaa tcaatcaatc aatggcctag agcactgact          300
g                                                                          301
```

```
        <210> 233
        <211> 301
        <212> DNA
        <213> Homo sapien


        <400> 233
atgactgact tcccagtaag gctctctaag gggtaagtag gaggatccac aggatttgag          60
atgctaaggc cccagagatc gtttgatcca accctcttat tttcagaggg gaaaatgggg          120
cctagaagtt acagagcatc tagctggtgc gctggcaccc ctggcctcac acagactccc          180
gagtagctgg gactacaggc acacagtcac tgaagcaggc cctgttagca attctatgcg          240
tacaaattaa catgagatga gtagagactt tattgagaaa gcaagagaaa atcctatcaa          300
c                                                                          301
```

```
        <210> 234
        <211> 301
        <212> DNA
        <213> Homo sapien


        <400> 234
aggtcctaca catcgagact catccatgat tgatatgaat ttaaaaatta caagcaaaga          60
cattttattc atcatgatgc tttcttttgt ttcttctttt cgttttcttc tttttctttt          120
tcaatttcag caacatactt ctcaatttct tcaggattta aaatcttgag ggattgatct          180
cgcctcatga cagcaagttc aatgtttttg ccacctgact gaaccacttc caggagtgcc          240
ttgatcacca gcttaatggt cagatcatct gcttcaatgg cttcgtcagt atagttcttc          300
t                                                                          301
```

81

```
        <210> 235
        <211> 283
        <212> DNA
        <213> Homo sapien

        <400> 235
tggggctgtg catcaggcgg gtttgagaaa tattcaattc tcagcagaag ccagaatttg      60
aattccctca tcttttaggg aatcatttac caggtttgga gaggattcag acagctcagg     120
tgctttcact aatgtctctg aacttctgtc cctctttgtt catggatagt ccaataaata     180
atgttatctt tgaactgatg ctcataggag agaatataag aactctgagt gatatcaaca     240
ttagggattc aaagaaatat tagatttaag ctcacactgg tca                       283

        <210> 236
        <211> 301
        <212> DNA
        <213> Homo sapien

        <400> 236
aggtcctcca ccaactgcct gaagcacggt taaaattggg aagaagtata gtgcagcata      60
aatactttta aatcgatcag atttccctaa cccacatgca atcttcttca ccagaagagg     120
tcggagcagc atcattaata ccaagcagaa tgcgtaatag ataaatacaa tggtatatag     180
tgggtagacg gcttcatgag tacagtgtac tgtggtatcg taatctggac ttgggttgta     240
aagcatcgtg taccagtcag aaagcatcaa tactcgacat gaacgaatat aaagaacacc     300
a                                                                      301

        <210> 237
        <211> 301
        <212> DNA
        <213> Homo sapien

        <400> 237
cagtggtagt ggtggtggac gtggcgttgg tcgtggtgcc ttttttggtg cccgtcacaa      60
actcaatttt tgttcgctcc ttttttggcct tttccaattt gtccatctca attttctggg     120
ccttggctaa tgcctcatag taggagtcct cagaccagcc atgggatca aacatatcct      180
ttgggtagtt ggtgccaagc tcgtcaatgg cacagaatgg atcagcttct cgtaaatcta     240
gggttccgaa attctttctt cctttggata atgtagttca tatccattcc ctcctttatc     300
t                                                                      301

        <210> 238
        <211> 301
        <212> DNA
        <213> Homo sapien

        <400> 238
gggcaggttt tttttttttt ttttttgatg gtgcagaccc ttgctttatt tgtctgactt      60
gttcacagtt cagccccctg ctcagaaaac caacgggcca gctaaggaga ggaggaggca     120
ccttgagact tccggagtcg aggctctcca gggttcccca gcccatcaat cattttctgc     180
accccctgcc tgggaagcag ctccctgggg ggtgggaatg ggtgactaga agggatttca     240
gtgtgggacc cagggtctgt tcttcacagt aggaggtgga agggatgact aatttctttta    300
t                                                                      301

        <210> 239
        <211> 239
        <212> DNA
        <213> Homo sapien

        <400> 239
ataagcagct agggaattct ttatttagta atgtcctaac ataaaagttc acataactgc      60
```

82

```
ttctgtcaaa ccatgatact gagctttgtg acaacccaga aataactaag agaaggcaaa       120
cataatacct tagagatcaa gaaacattta cacagttcaa ctgtttaaaa atagctcaac       180
attcagccag tgagtagagt gtgaatgcca gcatacacag tatacaggtc cttcaggga        239
```

        <210> 240
        <211> 300
        <212> DNA
        <213> Homo sapien

        <400> 240
```
ggtcctaatg aagcagcagc ttccacattt taacgcaggt ttacggtgat actgtccttt        60
gggatctgcc ctccagtgga accttttaag gaagaagtgg gcccaagcta agttccacat       120
gctgggtgag ccagatgact tctgttccct ggtcactttc ttcaatgggg cgaatggggg       180
ctgccaggtt tttaaaatca tgcttcatct tgaagcacac ggtcacttca ccctcctcac       240
gctgtgggtg tactttgatg aaaatacccca ctttgttggc ctttctgaag ctataatgtc      300
```

        <210> 241
        <211> 301
        <212> DNA
        <213> Homo sapien

        <400> 241
```
gaggtctggt gctgaggtct ctgggctagg aagaggagtt ctgtggagct ggaagccaga        60
cctctttgga ggaaactcca gcagctatgt tggtgtctct gagggaatgc aacaaggctg       120
ctcctccatg tattggaaaa ctgcaaactg gactcaactg gaaggaagtg ctgctgccag       180
tgtgaagaac cagcctgagg tgacagaaac ggaagcaaac aggaacagcc agtcttttct       240
tcctcctcct gtcatacggt ctctctcaag catcctttgt tgtcaggggc ctaaaaggga       300
g                                                                       301
```

        <210> 242
        <211> 301
        <212> DNA
        <213> Homo sapien

        <400> 242
```
ccgaggtcct gggatgcaac caatcactct gtttcacgtg acttttatca ccatacaatt        60
tgtggcattt cctcattttc tacattgtag aatcaagagt gtaaataaat gtatatcgat       120
gtcttcaaga atatatcatt ccttttttcac tagaacccat tcaaaatata agtcaagaat      180
cttaatatca acaaatatat caagcaaact ggaaggcaga ataactacca taatttagta       240
taagtaccca aagttttata aatcaaaagc cctaatgata accattttta gaattcaatc       300
a                                                                       301
```

        <210> 243
        <211> 301
        <212> DNA
        <213> Homo sapien

        <400> 243
```
aggtaagtcc cagtttgaag ctcaaaagat ctggtatgag cataggctca tcgacgacat        60
ggtggcccaa gctatgaaat cagagggagg cttcatctgg gcctgtaaaa actatgatgg       120
tgacgtgcag tcggactctg tggcccaagg gtatggctct ctcggcatga tgaccagcgt       180
gctggtttgt ccagatggca agacagtaga agcagaggct gcccacggga ctgtaacccg       240
tcactaccgc atgttccaga aaggacagga gacgtccacc aatcccattg cttccatttt       300
t                                                                       301
```

        <210> 244
        <211> 300
        <212> DNA

83

```
        <213> Homo sapien

        <400> 244
gctggtttgc aagaatgaaa tgaatgattc tacagctagg acttaacctt gaaatggaaa        60
gtcatgcaat cccatttgca ggatctgtct gtgcacatgc ctctgtagag agcagcattc       120
ccagggacct tggaaacagt tgacactgta aggtgcttgc tccccaagac acatcctaaa       180
aggtgttgta atggtgaaaa cgtcttcctt ctttattgcc ccttcttatt tatgtgaaca       240
actgtttgtc ttttgtgtat cttttttaaa ctgtaaagtt caattgtgaa aatgaatatc       300

        <210> 245
        <211> 301
        <212> DNA
        <213> Homo sapien

        <400> 245
gtctgagtat ttaaaatgtt attgaaatta tccccaacca atgttagaaa agaaagaggt        60
tatatactta gataaaaaat gaggtgaatt actatccatt gaaatcatgc tcttagaatt       120
aaggccagga gatattgtca ttaatgtara cttcaggaca ctagagtata gcagccctat       180
gttttcaaag agcagagatg caattaaaata ttgtttagca tcaaaaaggc cactcaatac       240
agctaataaa atgaaagacc taatttctaa agcaattctt tataatttac aaagtttttaa      300
g                                                                        301

        <210> 246
        <211> 301
        <212> DNA
        <213> Homo sapien

        <400> 246
ggtctgtcct acaatgcctg cttcttgaaa gaagtcggca ctttctagaa tagctaaata        60
acctgggctt attttaaaga actatttgta gctcagattg gttttcctat ggctaaaata       120
agtgcttctt gtgaaaatta aataaaacag ttaattcaaa gccttgatat atgttaccac       180
taacaatcat actaaatata ttttgaagta caaagtttga catgctctaa agtgacaacc       240
caaatgtgtc ttacaaaaca cgttcctaac aaggtatgct ttacactacc aatgcagaaa       300
c                                                                        301

        <210> 247
        <211> 301
        <212> DNA
        <213> Homo sapien

        <400> 247
aggtcctttg gcagggctca tggatcagag ctcaaactgg agggaaaggc atttcgggta        60
gcctaagagg gcgactggcg gcagcacaac caaggaaggc aaggttgttt cccccacgct       120
gtgtcctgtg ttcaggtgcg acacacaatc ctcatgggaa caggatcacc catgcgctgc       180
ccttgatgat caaggttggg gcttaagtgg attaagggag gcaagttctg ggttccttgc       240
cttttcaaac catgaagtca ggctctgtat ccctcctttt cctaactgat attctaacta       300
a                                                                        301

        <210> 248
        <211> 301
        <212> DNA
        <213> Homo sapien

        <400> 248
aggtccttgg agatgccatt tcagccgaag gactcttctw ttcggaagta caccctcact        60
attaggaaga ttcttagggg taatttttct gaggaaggag aactagccaa cttaagaatt       120
acaggaagaa agtggtttgg aagacagcca aagaaataaa agcagattaa attgtatcag       180
gtacattcca gcctgttggc aactccataa aaacatttca gattttaatc ccgaatttag       240
```

84

```
ctaatgagac tggattttttg ttttttatgt tgtgtgtcgc agagctaaaa actcagttcc      300
c                                                                       301
```

        <210> 249
        <211> 301
        <212> DNA
        <213> Homo sapien

        <400> 249
```
gtccagagga agcacctggt gctgaactag gcttgccctg ctgtgaactt gcacttggag      60
ccctgacgct gctgttctcc ccgaaaaacc cgaccgacct ccgcgatctc cgtcccgccc     120
ccagggagac acagcagtga ctcagagctg gtcgcacact gtgcctccct cctcaccgcc     180
catcgtaatg aattattttg aaaattaatt ccaccatcct·ttcagattct ggatggaaag     240
actgaatctt tgactcagaa ttgtttgctg aaaagaatga tgtgactttc ttagtcattt     300
a                                                                       301
```

        <210> 250
        <211> 301
        <212> DNA
        <213> Homo sapien

        <400> 250
```
ggtctgtgac aaggacttgc aggctgtggg aggcaagtga cccttaacac tacacttctc      60
cttatctttta ttggcttgat aaacataatt atttctaaca ctagcttatt tccagttgcc     120
cataagcaca tcagtacttt tctctggctg gaatagtaaa ctaaagtatg gtacatctac     180
ctaaaagact actatgtgga ataatacata ctaatgaagt attacatgat ttaaagacta     240
caataaaacc aaacatgctt ataacattaa gaaaaacaat aaagatacat gattgaaacc     300
a                                                                       301
```

        <210> 251
        <211> 301
        <212> DNA
        <213> Homo sapien

        <400> 251
```
gccgaggtcc tacatttggc ccagtttccc cctgcatcct ctccagggcc cctgcctcat      60
agacaacctc atagagcata ggagaactgg ttgccctggg ggcagggga ctgtctggat       120
ggcaggggtc ctcaaaaatg ccactgtcac tgccaggaaa tgcttctgag cagtacacct     180
cattgggatc aatgaaaagc ttcaagaaat cttcaggctc actctcttga aggcccggaa     240
cctctggagg ggggcagtgg aatcccagct ccaggacgga tcctgtcgaa aagatatcct     300
c                                                                       301
```

        <210> 252
        <211> 301
        <212> DNA
        <213> Homo sapien

        <400> 252
```
gcaaccaatc actctgtttc acgtgacttt tatcaccata caatttgtgg catttcctca      60
ttttctacat tgtagaatca agagtgtaaa taaatgtata tcgatgtctt caagaatata     120
tcattccttt ttcactagga acccattcaa aatataagtc aagaatctta atatcaacaa     180
atatatcaag caaactggaa ggcagaataa ctaccataat ttagtataag tacccaaagt     240
tttataaatc aaaagcccta atgataacca tttttagaat tcaatcatca ctgtagaatc     300
a                                                                       301
```

        <210> 253
        <211> 301
        <212> DNA

85

```
        <213> Homo sapien

        <400> 253
ttccctaaga agatgttatt ttgttgggtt ttgttccccc tccatctcga ttctcgtacc        60
caactaaaaa aaaaaaataa agaaaaaatg tgctgcgttc tgaaaaataa ctccttagct       120
tggtctgatt gttttcagac cttaaaatat aaacttgttt cacaagcttt aatccatgtg       180
gatttttttt cttagagaac cacaaaacat aaaaggagca agtcggactg aatacctgtt       240
tccatagtgc ccacagggta ttcctcacat tttctccata ggaaaatgct ttttcccaag       300
g                                                                       301

        <210> 254
        <211> 301
        <212> DNA
        <213> Homo sapien

        <400> 254
cgctgcgcct ttcccttggg ggaggggcaa ggccagaggg ggtccaagtg cagcacgagg        60
aacttgacca attcccttga agcgggtggg ttaaaccctg taaatgggaa caaaatcccc       120
ccaaatctct tcatcttacc ctggtggact cctgactgta gaatttttttg gttgaaacaa      180
gaaaaaaata aagctttgga cttttcaagg ttgcttaaca ggtactgaaa gactggcctc       240
acttaaactg agccaggaaa agctgcagat ttattaatgg gtgtgttagt gtgcagtgcc       300
t                                                                       301

        <210> 255
        <211> 302
        <212> DNA
        <213> Homo sapien

        <400> 255
agcttttttt ttttttttttt tttttttttt ttcattaaaa aatagtgctc tttattataa      60
attactgaaa tgtttctttt ctgaatataa atataaatat gtgcaaagtt tgacttggat       120
tgggattttg ttgagttctt caagcatctc ctaataccct caagggcctg agtaggggggg     180
aggaaaaagg actggaggtg gaatctttat aaaaaacaag agtgattgag gcagattgta       240
aacattatta aaaaacaaga aacaaacaaa aaaatagaga aaaaaaccac cccaacacac       300
aa                                                                      302

        <210> 256
        <211> 301
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(301)
        <223> n = A,T,C or G

        <400> 256
gttccagaaa acattgaagg tggcttccca aagtctaact agggataccc cctctagcct        60
aggaccctcc tccccacacc tcaatccacc aaaccatcca taatgcaccc agataggccc       120
acccccaaaa gcctggacac cttgagcaca cagttatgac caggacagac tcatctctat       180
aggcaaatag ctgctggcaa actggcatta cctggtttgt ggggatgggg gggcaagtgt       240
gtggcctctc ggcctggtta gcaagaacat tcagggtagg cctaagttan tcgtgttagt       300
t                                                                       301

        <210> 257
        <211> 301
        <212> DNA
        <213> Homo sapien
```

86

```
    <400> 257
gttgtggagg aactctggct tgctcattaa gtcctactga ttttcactat cccctgaatt        60
tccccactta ttttgtctt tcactatcgc aggccttaga agaggtctac ctgcctccag       120
tcttacctag tccagtctac ccctggagt tagaatggcc atcctgaagt gaaaagtaat       180
gtcacattac tcccttcagt gatttcttgt agaagtgcca atccctgaat gccaccaaga       240
tcttaatctt cacatcttta atcttatctc tttgactcct ctttacaccg gagaaggctc       300
c                                                                      301


    <210> 258
    <211> 301
    <212> DNA
    <213> Homo sapien

    <220>
    <221> misc_feature
    <222> (1)...(301)
    <223> n = A,T,C or G

    <400> 258
cagcagtagt agatgccgta tgccagcacg cccagcactc ccaggatcag caccagcacc        60
aggggcccag ccaccaggcg cagaagcaag ataaacagta ggctcaagac cagagccacc       120
cccagggcaa caagaatcca ataccaggac tgggcaaaat cttcaaagat cttaacactg       180
atgtctcggg cattgaggct gtcaataana cgctgatccc ctgctgtatg gtggtgtcat       240
tggtgatccc tgggagcgcc ggtggagtaa cgttggtcca tggaaagcag cgcccacaac       300
t                                                                      301


    <210> 259
    <211> 301
    <212> DNA
    <213> Homo sapien

    <220>
    <221> misc_feature
    <222> (1)...(301)
    <223> n = A,T,C or G

    <400> 259
tcatatatgc aaacaaatgc agactangcc tcaggcagag actaaaggac atctcttggg        60
gtgtcctgaa gtgatttgga cccctgaggg cagacaccta agtaggaatc ccagtgggaa       120
gcaaagccat aaggaagccc aggattcctt gtgatcagga agtgggccag gaaggtctgt       180
tccagctcac atctcatctg catgcagcac ggaccggatg cgcccactg gtcttggctt       240
ccctcccatc ttctcaagca gtgtccttgt tgagccattt gcatccttgg ctccaggtgg       300
c                                                                      301


    <210> 260
    <211> 301
    <212> DNA
    <213> Homo sapien

    <400> 260
tttttttct ccctaaggaa aaagaaggaa caagtctcat aaaaccaaat aagcaatggt        60
aaggtgtctt aacttgaaaa agattaggag tcactggttt acaagttata attgaatgaa       120
agaactgtaa cagccacagt tggccatttc atgccaatgg cagcaaacaa caggattaac       180
tagggcaaaa taaataagtg tgtggaagcc ctgataagtg cttaataaac agactgattc       240
actgagacat cagtacctgc ccgggcggcc gctcgagccg aattctgcag atatccatca       300
c                                                                      301
```

87

```
<210> 261
<211> 301
<212> DNA
<213> Homo sapien

<400> 261
aaatattcga gcaaatcctg taactaatgt gtctccataa aaggctttga actcagtgaa      60
tctgcttcca tccacgattc tagcaatgac ctctcggaca tcaaagctcc tcttaaggtt     120
agcaccaact attccataca attcatcagc aggaaataaa ggctcttcag aaggttcaat     180
ggtgacatcc aatttcttct gataatttag attcctcaca accttcctag ttaagtgaag     240
ggcatgatga tcatccaaag cccagtggtc acttactcca gactttctgc aatgaagatc     300
a                                                                      301

<210> 262
<211> 301
<212> DNA
<213> Homo sapien

<400> 262
gaggagagcc tgttacagca tttgtaagca cagaatactc caggagtatt tgtaattgtc      60
tgtgagcttc ttgccgcaag tctctcagaa atttaaaaag atgcaaatcc ctgagtcacc     120
cctagacttc ctaaaccaga tcctctgggg ctggaacctg gcactctgca tttgtaatga     180
gggctttctg gtgcacacct aattttgtgc atctttgccc taaatcctgg attagtgccc     240
catcattacc cccacattat aatgggatag attcagagca gatactctcc agcaaagaat     300
c                                                                      301

<210> 263
<211> 301
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(301)
<223> n = A,T,C or G

<400> 263
tttagcttgt ggtaaatgac tcacaaaact gattttaaaa tcaagttaat gtgaattttg      60
aaaattacta cttaatccta attcacaata acaatggcat taaggtttga cttgagttgg     120
ttcttagtat tatttatggt aaataggctc ttaccacttg caaataactg gccacatcat     180
taatgactga cttcccagta aggctctcta aggggtaagt angaggatcc acaggatttg     240
agatgctaag gccccagaga tcgtttgatc caaccctctt attttcagag gggaaaatgg     300
g                                                                      301

<210> 264
<211> 301
<212> DNA
<213> Homo sapien

<400> 264
aaagacgtta aaccactcta ctaccacttg tggaactctc aaagggtaaa tgacaaascc      60
aatgaatgac tctaaaaaca atatttacat ttaatggttt gtagacaata aaaaaacaag     120
gtggatagat ctagaattgt aacattttaa gaaaaccata scatttgaca gatgagaaag     180
ctcaattata gatgcaaagt tataactaaa ctactatagt agtaaagaaa tacatttcac     240
accctttcata taaattcact atcttggctt gaggcactcc ataaaatgta tcacgtgcat     300
a                                                                      301

<210> 265
```

88

```
        <211> 301
        <212> DNA
        <213> Homo sapien

        <400> 265
tgcccaagtt atgtgtaagt gtatccgcac ccagaggtaa aactacactg tcatctttgt          60
cttcttgtga cgcagtattt cttctctggg gagaagccgg gaagtcttct cctggctcta         120
catattcttg gaagtctcta atcaactttt gttccatttg tttcatttct tcaggaggga         180
ttttcagttt gtcaacatgt tctctaacaa cacttgccca tttctgtaaa gaatccaaag         240
cagtccaagg ctttgacatg tcaacaacca gcataactag agtatccttc agagatacgg         300
c                                                                        301


        <210> 266
        <211> 301
        <212> DNA
        <213> Homo sapien

        <400> 266
taccgtctgc ccttcctccc atccaggcca tctgcgaatc tacatgggtc ctcctattcg          60
acaccagatc actctttcct ctacccacag gcttgctatg agcaagagac acaacctcct         120
ctcttctgtg ttccagcttc tttttcctgtt cttcccaccc cttaagttct attcctgggg        180
atagagacac caatacccat aacctctctc ctaagcctcc ttataaccca gggtgcacag         240
cacagactcc tgacaactgg taaggccaat gaactgggag ctcacagctg gctgtgcctg         300
a                                                                        301


        <210> 267
        <211> 301
        <212> DNA
        <213> Homo sapien

        <400> 267
aaagagcaca ggccagctca gcctgccctg gccatctaga ctcagcctgg ctccatgggg          60
gttctcagtg ctgagtccat ccaggaaaag ctcacctaga ccttctgagg ctgaatcttc         120
atcctcacag gcagcttctg agagcctgat attcctagcc ttgatggtct ggagtaaagc         180
ctcattctga ttcctctcct tcttttcttt caagttggct ttcctcacat ccctctgttc         240
aattcgcttc agcttgtctg ctttagccct catttccaga agcttcttct ctttggcatc         300
t                                                                        301


        <210> 268
        <211> 301
        <212> DNA
        <213> Homo sapien

        <400> 268
aatgtctcac tcaactactt cccagcctac cgtggcctaa ttctgggagt tttcttctta          60
gatcttggga gagctggttc ttctaaggag aaggaggaag gacagatgta actttggatc         120
tcgaagagga agtctaatgg aagtaattag tcaacggtcc ttgtttagac tcttggaata         180
tgctgggtgg ctcagtgagc ccttttggag aaagcaagta ttattcttaa ggagtaacca         240
cttcccattg ttctactttc taccatcatc aattgtatat tatgtattct ttggagaact         300
a                                                                        301


        <210> 269
        <211> 301
        <212> DNA
        <213> Homo sapien

        <400> 269
taacaatata cactagctat cttttttaact gtccatcatt agcaccaatg aagattcaat          60
```

89

```
aaaattacct ttattcacac atctcaaaac aattctgcaa attcttagtg aagtttaact      120
atagtcacag accttaaata ttcacattgt tttctatgtc tactgaaaat aagttcacta      180
cttttctgga tattctttac aaaatcttat taaaattcct ggtattatca cccccaatta      240
tacagtagca caaccacctt atgtagtttt tacatgatag ctctgtagaa gtttcacatc      300
t                                                                      301
```

```
        <210> 270
        <211> 301
        <212> DNA
        <213> Homo sapien
```

```
        <400> 270
cattgaagag cttttgcgaa acatcagaac acaagtgctt ataaaattaa ttaagcctta       60
cacaagaata catattcctt ttatttctaa ggagttaaac atagatgtag ctgatgtgga      120
gagcttgctg gtgcagtgca tattggataa cactattcat ggccgaattg atcaagtcaa      180
ccaactcctt gaactggatc atcagaagaa gggtggtgca cgatatactg cactagataa      240
tggaccaacc aactaaattc tctcaccagg ctgtatcagt aaactggctt aacagaaaac      300
a                                                                      301
```

```
        <210> 271
        <211> 301
        <212> DNA
        <213> Homo sapien
```

```
        <220>
        <221> misc_feature
        <222> (1)...(301)
        <223> n = A,T,C or G
```

```
        <400> 271
aaaaggttct cataagatta acaatttaaa taaatatttg atagaacatt ctttctcatt       60
tttatagctc atctttaggg ttgatattca gttcatgctt cccttgctgt tcttgatcca      120
gaattgcaat cacttcatca gcctgtattc gctccaattc tctataaagt gggtccaagg      180
tgaaccacag agccacagca cacctctttc ccttggtgac tgccttcacc ccatganggt      240
tctctcctcc agatganaac tgatcatgcg cccacatttt gggtttttata gaagcagtca      300
c                                                                      301
```

```
        <210> 272
        <211> 301
        <212> DNA
        <213> Homo sapien
```

```
        <400> 272
taaattgcta agccacagat aacaccaatc aaatggaaca aatcactgtc ttcaaatgtc       60
ttatcagaaa accaaatgag cctggaatct tcataatacc taaacatgcc gtatttagga      120
tccaataatt ccctcatgat gagcaagaaa aattctttgc gcacccctcc tgcatccaca      180
gcatcttctc caacaaatat aaccttgagt ggcttcttgt aatctatgtt ctttgtttc      240
ctaaggactt ccattgcatc tcctacaata ttttctctac gcaccactag aattaagcag      300
g                                                                      301
```

```
        <210> 273
        <211> 301
        <212> DNA
        <213> Homo sapien
```

```
        <220>
        <221> misc_feature
        <222> (1)...(301)
```

90

```
        <223> n = A,T,C or G

        <400> 273
acatgtgtgt atgtgtatct ttgggaaaan aanaagacat cttgtttayt atttttttgg       60
agagangctg ggacatggat aatcacwtaa tttgctayta tyactttaat ctgactygaa      120
gaaccgtcta aaaataaaat ttaccatgtc dtatattcct tatagtatgc ttatttcacc      180
ttytttctgt ccagagagag tatcagtgac ananatttma gggtgaamac atgmattggt      240
gggacttnty tttacngagm accctgcccg sgcgccctcg makcngantt ccgcsananc      300
t                                                                      301


        <210> 274
        <211> 301
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(301)
        <223> n = A,T,C or G

        <400> 274
cttatatact ctttctcaga ggcaaaagag gagatgggta atgtagacaa ttctttgagg       60
aacagtaaat gattattaga gagaangaat ggaccaagga gacagaaatt aacttgtaaa      120
tgattctctt tggaatctga atgagatcaa gaggccagct ttagcttgtg gaaaagtcca      180
tctaggtatg gttgcattct cgtcttcttt tctgcagtag ataatgaggt aaccgaaggc      240
aattgtgctt cttttgataa gaagctttct tggtcatatc aggaaattcc aganaaagtc      300
c                                                                      301


        <210> 275
        <211> 301
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(301)
        <223> n = A,T,C or G

        <400> 275
tcggtgtcag cagcacgtgg cattgaacat tgcaatgtgg agcccaaacc acagaaaatg       60
gggtgaaatt ggccaacttt ctattaactt atgttggcaa ttttgccacc aacagtaagc      120
tggcccttct aataaaagaa aattgaaagg tttctcacta aacggaatta agtagtggag      180
tcaagagact cccaggcctc agcgtacctg cccgggcggc cgctcgaagc cgaattctgc      240
agatatccat cacactggcg gncgctcgan catgcatcta gaaggnccaa ttcgccctat      300
a                                                                      301


        <210> 276
        <211> 301
        <212> DNA
        <213> Homo sapien

        <400> 276
tgtacacata ctcaataaat aaatgactgc attgtggtat tattactata ctgattatat       60
ttatcatgtg acttctaatt agaaaatgta tccaaaagca aaacagcaga tatacaaaat      120
taaagagaca gaagatagac attaacagat aaggcaactt atacattgag aatccaaatc      180
caatacattt aaacatttgg gaaatgaggg ggacaaatgg aagccagatc aaatttgtgt      240
aaaactattc agtatgtttc ccttgcttca tgtctgagaa ggctctcctt caatggggat      300
g                                                                      301
```

91

```
<210> 277
<211> 301
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(301)
<223> n = A,T,C or G

<400> 277
tttgttgatg tcagtatttt attacttgcg ttatgagtgc tcacctggga aattctaaag      60
atacagagga cttggaggaa gcagagcaac tgaatttaat ttaaaagaag gaaaacattg     120
gaatcatggc actcctgata ctttcccaaa tcaacactct caatgcccca ccctcgtcct     180
caccatagtg gggagactaa agtggccacg gatttgcctt angtgtgcag tgcgttctga     240
gttcnctgtc gattacatct gaccagtctc cttttttccga agtccntccg ttcaatcttg     300
c                                                                     301

<210> 278
<211> 301
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(301)
<223> n = A,T,C or G

<400> 278
taccactaca ctccagcctg ggcaacagag caagacctgt ctcaaagcat aaaatggaat      60
aacatatcaa atgaaacagg gaaaatgaag ctgacaattt atggaagcca gggcttgtca     120
cagtctctac tgttattatg cattacctgg gaattatat aagcccttaa taataatgcc     180
aatgaacatc tcatgtgtgc tcacaatgtt ctggcactat tataagtgct tcacaggttt     240
tatgtgttct tcgtaacttt atggantagg tactcggccg cgaacacgct aagccgaatt     300
c                                                                     301

<210> 279
<211> 301
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(301)
<223> n = A,T,C or G

<400> 279
aaagcaggaa tgacaaagct tgctttttctg gtatgttcta ggtgtattgt gactttttact      60
gttatattaa ttgccaatat aagtaaatat agattatata tgtatagtgt ttcacaaagc     120
ttagaccttt accttccagc caccccacag tgcttgatat ttcagagtca gtcattggtt     180
atacatgtgt agttccaaag cacataagct agaanaanaa atatttctag ggagcactac     240
catctgtttt cacatgaaat gccacacaca tagaactcca acatcaattt cattgcacag     300
a                                                                     301

<210> 280
<211> 301
<212> DNA
```

92

```
        <213> Homo sapien

        <400> 280
ggtactggag ttttcctccc ctgtgaaaac gtaactactg ttgggagtga attgaggatg        60
tagaaaggtg gtggaaccaa attgtggtca atggaaatag gagaatatgg ttctcactct       120
tgagaaaaaa acctaagatt agcccaggta gttgcctgta acttcagttt ttctgcctgg       180
gtttgatata gtttagggtt ggggttagat taagatctaa attacatcag gacaaagaga       240
cagactatta actccacagt taattaagga ggtatgttcc atgtttattt gttaaagcag       300
t                                                                        301

        <210> 281
        <211> 301
        <212> DNA
        <213> Homo sapien

        <400> 281
aggtacaaga aggggaatgg gaaagagctg ctgctgtggc attgttcaac ttggatattc        60
gccgagcaat ccaaatcctg aatgaagggg catcttctga aaaaggagat ctgaatctca       120
atgtggtagc aatggctttta tcgggttata cggatgagaa gaactccctt tggagagaaa       180
tgtgtagcac actgcgatta cagctaaata acccgtattt gtgtgtcatg tttgcatttc       240
tgacaagtga aacaggatct tacgatggag ttttgtatga aaacaaagtt gcagtacctc       300
g                                                                        301

        <210> 282
        <211> 301
        <212> DNA
        <213> Homo sapien

        <400> 282
caggtactac agaattaaaa tactgacaag caagtagttt cttggcgtgc acgaattgca        60
tccagaaccc aaaaattaag aaattcaaaa agacattttg tgggcacctg ctagcacaga       120
agcgcagaag caaagcccag gcagaaccat gctaacctta cagctcagcc tgcacagaag       180
cgcagaagca aagcccaggc agaaccatgc taaccttaca gctcagcctg cacagaagcg       240
cagaagcaaa gcccaggcag aacatgctaa ccttacagct cagcctgcac agaagcacag       300
a                                                                        301

        <210> 283
        <211> 301
        <212> DNA
        <213> Homo sapien

        <400> 283
atctgtatac ggcagacaaa ctttatarag tgtagagagg tgagcgaaag gatgcaaaag        60
cactttgagg gctttataat aatatgctgc ttgaaaaaaa aaatgtgtag ttgatactca       120
gtgcatctcc agacatagta aggggttgct ctgaccaatc aggtgatcat ttttttctatc       180
acttcccagg ttttatgcaa aaattttgtt aaattctata atggtgatat gcatcttttta       240
ggaaacatat acatttttaa aaatctattt tatgtaagaa ctgacagacg aatttgcttt       300
g                                                                        301

        <210> 284
        <211> 301
        <212> DNA
        <213> Homo sapien

        <400> 284
caggtacaaa acgctattaa gtggcttaga atttgaacat ttgtggtctt tatttacttt        60
gcttcgtgtg tgggcaaagc aacatcttcc ctaaatatat attaccaaga aaagcaagaa       120
gcagattagg tttttgacaa aacaaacagg ccaaaagggg gctgacctgg agcagagcat       180
```

93

```
ggtgagaggc aaggcatgag agggcaagtt tgttgtggac agatctgtgc ctactttatt        240
actggagtaa aagaaaacaa agttcattga tgtcgaagga tatatacagt gttagaaatt        300
a                                                                        301
```

```
        <210> 285
        <211> 301
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(301)
        <223> n = A,T,C or G

        <400> 285
acatcaccat gatcggatcc cccacccatt atacgttgta tgtttacata aatactcttc        60
aatgatcatt agtgttttaa aaaaaatact gaaaactcct tctgcatccc aatctctaac        120
caggaaagca aatgctattt acagacctgc aagccctccc tcaaacnaaa ctatttctgg        180
attaaatatg tctgacttct tttgaggtca cacgactagg caaatgctat ttacgatctg        240
caaaagctgt ttgaagagtc aaagcccccca tgtgaacacg atttctggac cctgtaacag        300
t                                                                        301
```

```
        <210> 286
        <211> 301
        <212> DNA
        <213> Homo sapien

        <400> 286
taccactgca ttccagcctg ggtgacagag tgagactccg tctccaaaaa aaactttgct        60
tgtatattat tttttgcctta cagtggatca ttctagtagg aaaggacagt aagatttttt        120
atcaaaatgt gtcatgccag taagagatgt tatattcttt tctcatttct tccccaccca        180
aaaataagct accatatagc ttataagtct caaattttg ccttttacta aaatgtgatt        240
gtttctgttc attgtgtatg cttcatcacc tatattaggc aaattccatt ttttcccttg        300
t                                                                        301
```

```
        <210> 287
        <211> 301
        <212> DNA
        <213> Homo sapien

        <400> 287
tacagatctg ggaactaaat attaaaaatg agtgtggctg gatatatgga gaatgttggg        60
cccagaagga acgtagagat cagatattac aacagctttg ttttgagggt tagaaatatg        120
aaatgatttg gttatgaacg cacagtttag gcagcagggc cagaatcctg accctctgcc        180
ccgtggttat ctcctcccca gcttggctgc ctcatgttat cacagtattc cattttgttt        240
gttgcatgtc ttgtgaagcc atcaagattt tctcgtctgt tttcctctca ttggtaatgc        300
t                                                                        301
```

```
        <210> 288
        <211> 301
        <212> DNA
        <213> Homo sapien

        <400> 288
gtacacctaa ctgcaaggac agctgaggaa tgtaatgggc agccgctttt aaagaagtag        60
agtcaatagg aagacaaatt ccagttccag ctcagtctgg gtatctgcaa agctgcaaaa        120
gatctttaaa gacaatttca agagaatatt tccttaaagt tggcaatttg gagatcatac        180
aaaagcatct gcttttgtga tttaatttag ctcatctggc cactggaaga atccaaacag        240
```

```
tctgccttaa ttttggatga atgcatgatg gaaattcaat aatttagaaa gttaaaaaaa      300
a                                                                      301
```

            <210> 289
            <211> 301
            <212> DNA
            <213> Homo sapien

            <220>
            <221> misc_feature
            <222> (1)...(301)
            <223> n = A,T,C or G

            <400> 289
```
ggtacactgt ttccatgtta tgtttctaca cattgctacc tcagtgctcc tggaaactta      60
gcttttgatg tctccaagta gtccaccttc atttaactct ttgaaactgt atcatctttg     120
ccaagtaaga gtggtggcct atttcagctg ctttgacaaa atgactggct cctgacttaa     180
cgttctataa atgaatgtgc tgaagcaaag tgcccatggt ggcggcgaan aagagaaaga     240
tgtgttttgt tttggactct ctgtggtccc ttccaatgct gtgggtttcc aaccagngga     300
a                                                                      301
```

            <210> 290
            <211> 301
            <212> DNA
            <213> Homo sapien

            <220>
            <221> misc_feature
            <222> (1)...(301)
            <223> n = A,T,C or G

            <400> 290
```
acactgagct cttcttgata aatatacaga atgcttggca tatacaagat tctatactac      60
tgactgatct gttcatttct ctcacagctc ttacccccaa aagcttttcc accctaagtg     120
ttctgacctc cttttctaat cacagtaggg atagaggcag anccacctac aatgaacatg     180
gagttctatc aagaggcaga aacagcacag aatcccagtt ttaccattcg ctagcagtgc     240
tgccttgaac aaaaacattt ctccatgtct cattttcttc atgcctcaag taacagtgag     300
a                                                                      301
```

            <210> 291
            <211> 301
            <212> DNA
            <213> Homo sapien

            <400> 291
```
caggtaccaa tttcttctat cctagaaaca tttcatttta tgttgttgaa acataacaac      60
tatatcagct agattttttt tctatgcttt acctgctatg gaaaatttga cacattctgc     120
tttactcttt tgtttatagg tgaatcacaa aatgtatttt tatgtattct gtagttcaat     180
agccatggct gtttacttca tttaatttat ttagcataaa gacattatga aaaggcctaa     240
acatgagctt cacttcccca ctaactaatt agcatctgtt atttcttaac cgtaatgcct     300
a                                                                      301
```

            <210> 292
            <211> 301
            <212> DNA
            <213> Homo sapien

            <220>

95

```
      <221> misc_feature
      <222> (1)...(301)
      <223> n = A,T,C or G

      <400> 292
acctttttagt agtaatgtct aataataaat aagaaatcaa tttttataagg tccatatagc        60
tgtattaaat aattttttaag tttaaaagat aaaataccat cattttaaat gttggtattc       120
aaaaccaaag natataaccg aaaggaaaaa cagatgagac ataaaatgat ttgcnagatg       180
ggaaatatag tasttyatga atgttnatta aattccagtt ataatagtgg ctacacactc       240
tcactacaca cacagacccc acagtcctat atgccacaaa cacatttcca taacttgaaa       300
a                                                                         301

      <210> 293
      <211> 301
      <212> DNA
      <213> Homo sapien

      <400> 293
ggtaccaagt gctggtgcca gcctgttacc tgttctcact gaaaagtctg gctaatgctc        60
ttgtgtagtc acttctgatt ctgacaatca atcaatcaat ggcctagagc actgactgtt       120
aacacaaacg tcactagcaa agtagcaaca gctttaagtc taaatacaaa gctgttctgt       180
gtgagaattt tttaaaaggc tacttgtata ataaccttg tcatttttaa tgtacctcgg       240
ccgcgaccac gctaagccga attctgcaga tatccatcac actggcggcc gctcgagcat       300
g                                                                         301

      <210> 294
      <211> 301
      <212> DNA
      <213> Homo sapien

      <220>
      <221> misc_feature
      <222> (1)...(301)
      <223> n = A,T,C or G

      <400> 294
tgacccataa caatatacac tagctatctt tttaactgtc catcattagc accaatgaag        60
attcaataaa attacctta ttcacacatc tcaaaacaat tctgcaaatt cttagtgaag       120
tttaactata gtcacaganc ttaaatattc acattgtttt ctatgtctac tgaaaataag       180
ttcactactt ttctgggata ttctttacaa aatcttatta aaattcctgg tattatcacc       240
cccaattata cagtagcaca accaccttat gtagttttta catgatagct ctgtagaggt       300
t                                                                         301

      <210> 295
      <211> 305
      <212> DNA
      <213> Homo sapien

      <400> 295
gtactctttc tctcccctcc tctgaattta attctttcaa cttgcaattt gcaaggatta        60
cacatttcac tgtgatgtat attgtgttgc aaaaaaaaaa gtgtctttgt ttaaaattac       120
ttggtttgtg aatccatctt gcttttccc cattggaact agtcattaac ccatctctga       180
actggtagaa aaacrtctga agagctagtc tatcagcatc tgacaggtga attggatggt       240
tctcagaacc atttcaccca gacagcctgt ttctatcctg tttaataaat tagtttgggt       300
tctct                                                                     305

      <210> 296
      <211> 301
```

96

```
        <212> DNA
        <213> Homo sapien

        <400> 296
aggtactatg ggaagctgct aaaataatat ttgatagtaa aagtatgtaa tgtgctatct        60
cacctagtag taaactaaaa ataaactgaa actttatgga atctgaagtt attttccttg       120
attaaataga attaataaac caatatgagg aaacatgaaa ccatgcaatc tactatcaac       180
tttgaaaaag tgattgaacg aaccacttag ctttcagatg atgaacactg ataagtcatt       240
tgtcattact ataaatttta aaatctgtta ataagatggc ctataggggag gaaaaagggg       300
c                                                                        301

        <210> 297
        <211> 300
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(300)
        <223> n = A,T,C or G

        <400> 297
actgagtttt aactggacgc caagcaggca aggctggaag gttttgctct ctttgtgcta        60
aaggttttga aaaccttgaa ggagaatcat tttgacaaga agtacttaag agtctagaga       120
acaaagangt gaaccagctg aaagctctcg ggggaanctt acatgtgttg ttaggcctgt       180
tccatcattg ggagtgcact ggccatccct caaaatttgt ctgggctggc ctgagtggtc       240
accgcacctc ggccgcgacc acgctaagcc gaattctgca gatatccatc acactggcgg       300

        <210> 298
        <211> 301
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(301)
        <223> n = A,T,C or G

        <400> 298
tatggggttt gtcacccaaa agctgatgct gagaaaggcc tccctggggc ccctcccgcg        60
ggcatctgag agacctggtg ttccagtgtt tctggaaatg ggtcccagtg ccgccggctg       120
tgaagctctc agatcaatca cgggaagggc ctggcggtgg tggccacctg gaaccaccct       180
gtcctgtctg tttacatttc actaycaggt tttctctggg cattacnatt tgttcccta        240
caacagtgac ctgtgcattc tgctgtggcc tgctgtgtct gcaggtggct ctcagcgagg       300
t                                                                        301

        <210> 299
        <211> 301
        <212> DNA
        <213> Homo sapien

        <400> 299
gttttgagac ggagtttcac tcttgttgcc cagactggac tgcaatggca gggtctctgc        60
tcactgcacc ctctgcctcc caggttcgag caattctcct gcctcagcct cccaggtagc       120
tgggattgca ggctcacgcc accataccca gctaattttt ttgtattttt agtagagacg       180
gagtttcgcc atgttggcca gctggtctca aactcctgac ctcaagcgac ctgcctgcct       240
cggcctccca aagtgctgga attataggca tgagtcaaca cgcccagcct aaagatattt       300
t                                                                        301
```

```
        <210> 300
        <211> 301
        <212> DNA
        <213> Homo sapien

        <400> 300
attcagtttt atttgctgcc ccagtatctg taaccaggag tgccacaaaa tcttgccaga      60
tatgtcccac acccactggg aaaggctccc acctggctac ttcctctatc agctgggtca     120
gctgcattcc acaaggttct cagcctaatg agtttcacta cctgccagtc tcaaaactta     180
gtaaagcaag accatgacat tcccccacgg aaatcagagt ttgccccacc gtcttgttac     240
tataaagcct gcctctaaca gtccttgctt cttcacacca atcccgagcg catcccccat     300
g                                                                     301

        <210> 301
        <211> 301
        <212> DNA
        <213> Homo sapien

        <400> 301
ttaaattttt gagaggataa aaaggacaaa taatctagaa atgtgtcttc ttcagtctgc      60
agaggacccc aggtctccaa gcaaccacat ggtcaagggc atgaataatt aaaagttggt     120
gggaactcac aaagaccctc agagctgaga cacccacaac agtgggagct cacaaagacc     180
ctcagagctg agacacccac aacagtggga gctcacaaag accctcagag ctgagacacc     240
cacaacagca cctcgttcag ctgccacatg tgtgaataag gatgcaatgt ccagaagtgt     300
t                                                                     301

        <210> 302
        <211> 301
        <212> DNA
        <213> Homo sapien

        <400> 302
aggtacacat ttagcttgtg gtaaatgact cacaaaactg attttaaaat caagttaatg      60
tgaattttga aaattactac ttaatcctaa ttcacaataa caatggcatt aaggtttgac     120
ttgagttggt tcttagtatt atttatggta aataggctct taccacttgc aaataactgg     180
ccacatcatt aatgactgac ttcccagtaa ggctctctaa ggggtaagta ggaggatcca     240
caggatttga gatgctaagg ccccagagat cgtttgatcc aaccctctta ttttcagagg     300
g                                                                     301

        <210> 303
        <211> 301
        <212> DNA
        <213> Homo sapien

        <400> 303
aggtaccaac tgtggaaata ggtagaggat catttttttct ttccatatca actaagttgt      60
atattgtttt ttgacagttt aacacatctt cttctgtcag agattctttc acaatagcac     120
tggctaatgg aactaccgct tgcatgttaa aaatggtggt ttgtgaaatg atcataggcc     180
agtaacgggt atgtttttct aactgatctt ttgctcgttc caaagggacc tcaagacttc     240
catcgatttt atatctgggg tctagaaaag gagttaatct gttttcccatc ataaattcac     300
c                                                                     301

        <210> 304
        <211> 301
        <212> DNA
        <213> Homo sapien
```

98

```
        <400> 304
acatggatgt tattttgcag actgtcaacc tgaatttgta tttgcttgac attgcctaat          60
tattagtttc agtttcagct tacccacttt ttgtctgcaa catgcaraas agacagtgcc         120
cttttagtg tatcatatca ggaatcatct cacattggtt tgtgccatta ctggtgcagt          180
gactttcagc cacttgggta aggtggagtt ggccatatgt ctccactgca aaattactga         240
ttttccttt gtaattaata agtgtgtgtg tgaagattct ttgagatgag gtatatatct          300
c                                                                         301
```

        <210> 305
        <211> 301
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(301)
        <223> n = A,T,C or G

```
        <400> 305
gangtacagc gtggtcaagg taacaagaag aaaaaaatgt gagtggcatc ctgggatgag          60
caggggaca gacctggaca gacacgttgt catttgctgc tgtgggtagg aaaatgggcg         120
taaaggagga gaaacagata caaaatctcc aactcagtat taaggtattc tcatgcctag          180
aatattggta gaaacaagaa tacattcata tggcaaataa ctaaccatgg tggaacaaaa         240
ttctgggatt taagttggat accaangaaa ttgtattaaa agagctgttc atggaataag         300
a                                                                         301
```

        <210> 306
        <211> 8
        <212> PRT
        <213> Homo sapien

        <400> 306
Val Leu Gly Trp Val Ala Glu Leu
 1   5

        <210> 307
        <211> 637
        <212> DNA
        <213> Homo sapien

```
        <400> 307
acagggratg aaggaaagg gagaggatga ggaagccccc ctggggattt ggtttggtcc          60
ttgtgatcag gtggtctatg gggcttatcc ctacaaagaa gaatccagaa ataggggcac         120
attgaggaat gatacttgag cccaaagagc attcaatcat tgttttatt gccttmtttt          180
cacaccattg gtgaggagg gattaccacc ctggggttat gaagatggtt gaacacccca         240
cacatagcac cggagatatg agatcaacag tttcttagcc atagagattc acagcccaga         300
gcaggaggac gcttgcacac catgcaggat gacatggggg atgcgctcgg gattggtgtg         360
aagaagcaag gactgttaga ggcaggcttt atagtaacaa gacggtgggg caaactctga         420
tttccgtggg ggaatgtcat ggtcttgctt tactaagttt tgagactggc aggtagtgaa         480
actcattagg ctgagaacct tgtggaatgc acttgaccca sctgatagag gaagtagcca         540
ggtgggagcc tttcccagtg ggtgtgggac atatctggca agattttgtg gcactcctgg         600
ttacagatac tggggcagca aataaaactg aatcttg                                  637
```

        <210> 308
        <211> 647
        <212> DNA
        <213> Homo sapien

99

```
<220>
<221> misc_feature
<222> (1)...(647)
<223> n = A,T,C or G

<400> 308
acgattttca ttatcatgta aatcgggtca ctcaaggggc caaccacagc tgggagccac     60
tgctcagggg aaggttcata tgggactttc tactgcccaa ggttctatac aggatataaa    120
ggngcctcac agtatagatc tggtagcaaa gaagaagaaa caaacactga tctctttctg    180
ccacccctct gaccctttgg aactcctctg accctttaga acaagcctac ctaatatctg    240
ctagagaaaa gaccaacaac ggcctcaaag gatctcttac catgaaggtc tcagctaatt    300
cttggctaag atgtgggttc cacattaggt tctgaatatg gggggaaggg tcaatttgct    360
cattttgtgt gtggataaag tcaggatgcc caggggccag agcaggggc tgcttgcttt      420
gggaacaatg gctgagcata taaccatagg ttatggggaa caaaacaaca tcaaagtcac    480
tgtatcaatt gccatgaaga cttgagggac ctgaatctac cgattcatct taaggcagca    540
ggaccagttt gagtggcaac aatgcagcag cagaatcaat ggaaacaaca gaatgattgc    600
aatgtccttt tttttctcct gcttctgact tgataaaagg ggaccgt                  647

<210> 309
<211> 460
<212> DNA
<213> Homo sapien

<400> 309
actttatagt ttaggctgga cattggaaaa aaaaaaaagc cagaacaaca tgtgatagat     60
aatatgattg gctgcacact tccagactga tgaatgatga acgtgatgga ctattgtatg    120
gagcacatct tcagcaagag ggggaaatac tcatcatttt tggccagcag ttgtttgatc    180
accaaacatc atgccagaat actcagcaaa ccttcttagc tcttgagaag tcaaagtccg    240
ggggaattta ttcctggcaa ttttaattgg actccttatg tgagagcagc ggctacccag    300
ctggggtggt ggagcgaacc cgtcactagt ggacatgcag tggcagagct cctggtaacc    360
acctagagga atacacaggc acatgtgtga tgccaagcgt gacacctgta gcactcaaat    420
ttgtcttgtt tttgtctttc ggtgtgtaag attcttaagt                         460

<210> 310
<211> 539
<212> DNA
<213> Homo sapien

<400> 310
acgggactta tcaaataaag ataggaaaag aagaaaactc aaatattata ggcagaaatg     60
ctaaaggttt taaaatatgt caggattgga agaaggcatg gataaagaac aaagttcagt    120
taggaaagag aaacacagaa ggaagagaca caataaaagt cattatgtat tctgtgagaa    180
gtcagacagt aagatttgtg ggaaatgggt tggtttgttg tatggtatgt attttagcaa    240
taatctttat ggcagagaaa gctaaaatcc tttagcttgc gtgaatgatc acttgctgaa    300
ttcctcaagg taggcatgat gaaggagggt ttagaggaga cacagacaca atgaactgac    360
ctagatagaa agccttagta tactcagcta ggaatagtga ttctgagggc acactgtgac    420
atgattatgt cattacatgt atggtagtga tggggatgat aggaaggaag aacttatggc    480
atattttcac ccccacaaaa gtcagttaaa tattgggaca ctaaccatcc aggtcaaga    539

<210> 311
<211> 526
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(526)
<223> n = A,T,C or G
```

100

```
    <400> 311
caaatttgag ccaatgacat agaattttac aaatcaagaa gcttattctg gggccatttc      60
ttttgacgtt ttctctaaac tactaaagag gcattaatga tccataaatt atattatcta     120
catttacagc atttaaaatg tgttcagcat gaaatattag ctacagggga agctaaataa     180
attaaacatg gaataaagat ttgtccttaa atataatcta caagaagact ttgatatttg     240
tttttcacaa gtgaagcatt cttataaagt gtcataacct ttttgggaa  actatgggaa     300
aaaatgggga aactctgaag ggttttaagt atcttacctg aagctacaga ctccataacc     360
·tctctttaca gggagctcct gcagccccta cagaaatgag tggctgagat tcttgattgc     420
acagcaagag cttctcatct aaaccctttc cctttttagt atctgtgtat caagtataaa     480
agttctataa actgtagtnt acttatttta atccccaaag cacagt                    526
```

```
    <210> 312
    <211> 500
    <212> DNA
    <213> Homo sapien

    <220>
    <221> misc_feature
    <222> (1)...(500)
    <223> n = A,T,C or G
```

```
    <400> 312
cctctctctc cccacccct  gactctagag aactgggttt tctcccagta ctccagcaat      60
tcatttctga aagcagttga gccactttat tccaaagtac actgcagatg ttcaaactct     120
ccatttctct ttcccttcca cctgccagtt ttgctgactc tcaacttgtc atgagtgtaa     180
gcattaagga cattatgctt cttcgattct gaagacaggc cctgctcatg gatgactctg     240
gcttcttagg aaaaatattt tcttccaaaa tcagtaggaa atctaaactt atcccctctt     300
tgcagatgtc tagcagcttc agacatttgg ttaagaaccc atgggaaaaa aaaaaatcct     360
tgctaatgtg gtttcctttg taaaccanga ttcttatttg nctggtatag aàtatcagct     420
ctgaacgtgt ggtaaagatt tttgtgtttg aatataggag aaatcagttt gctgaaaagt     480
tagtcttaat tatctctattgg                                               500
```

```
    <210> 313
    <211> 718
    <212> DNA
    <213> Homo sapien

    <220>
    <221> misc_feature
    <222> (1)...(718)
    <223> n = A,T,C or G
```

```
    <400> 313
ggagatttgt gtggtttgca gccgagggag accaggaaga tctgcatggt gggaaggacc      60
tgatgataca gaggtgagaa ataagaaagg ctgctgactt taccatctga ggccacacat     120
ctgctgaaat ggagataatt aacatcacta gaaacagcaa gatgacaata taatgtctaa     180
gtagtgacat gttttttgcac atttccagcc ctttttaaata tccacacaca caggaagcac     240
aaaaggaagc acagagatcc ctgggagaaa tgcccggccg ccatcttggg tcatcgatga     300
gcctcgccct gtgcctgntc ccgcttgtga gggaaggaca ttagaaaatg aattgatgtg     360
ttccttaaag gatggcagga aaacagatcc tgttgtggat atttatttga acgggattac     420
agatttgaaa tgaagtcaca aagtgaagcat taccaatgag aggaaaacag acgagaaat     480
cttgatggtt cacaagacat gcaacaaaca aaatggaata ctgtgatgac acgagcagcc     540
aactggggag gagataccac ggggcagagg tcaggattct ggccctgctg cctaactgtg  .  600
cgttatacca atcatttcta tttctaccct caaacaagct gtngaatatc tgacttacgg     660
ttcttntggc ccacattttc atnatccacc ccntcntttt aannttantc caaantgt       718
```

```
    <210> 314
```

101

```
        <211> 358
        <212> DNA
        <213> Homo sapien

        <400> 314
gtttatttac attacagaaa aaacatcaag acaatgtata ctatttcaaa tatatccata          60
cataatcaaa tatagctgta gtacatgttt tcattggtgt agattaccac aaatgcaagg         120
caacatgtgt agatctcttg tcttattctt ttgtctataa tactgtattg tgtagtccaa         180
gctctcggta gtccagccac tgtgaaacat gctcccttta gattaacctc gtggacgctc         240
ttgttgtatt gctgaactgt agtgccctgt attttgcttg tgtctgtgaa ttctgttgct         300
tctggggcat ttccttgtga tgcagaggac caccacacag atgacagcaa tctgaatt          358

        <210> 315
        <211> 341
        <212> DNA
        <213> Homo sapien

        <400> 315
taccacctcc ccgctggcac tgatgagccg catcaccatg gtcaccagca ccatgaaggc          60
ataggtgatg atgaggacat ggaatgggcc cccaaggatg gtctgtccaa agaagcgagt         120
gacccccatt ctgaagatgt ctggaacctc taccagcagg atgatgatag ccccaatgac         180
agtcaccagc tccccgacca gccggatatc gtccttaggg gtcatgtagg cttcctgaag         240
tagcttctgc tgtaagaggg tgttgtcccg ggggctcgtg cggttattgg tcctgggctt         300
gagggggcgg tagatgcagc acatggtgaa gcagatgatg t                            341

        <210> 316
        <211> 151
        <212> DNA
        <213> Homo sapien

        <400> 316
agactgggca agactcttac gccccacact gcaatttggt cttgttgccg tatccatta           60
tgtgggcctt tctcgagttt ctgattataa acaccactgg agcgatgtgt tgactggact         120
cattcaggga gctctggttg caatattagt t                                       151

        <210> 317
        <211> 151
        <212> DNA
        <213> Homo sapien

        <400> 317
agaactagtg gatcctaatg aaatacctga aacatatatt ggcatttatc aatggctcaa          60
atcttcattt atctctggcc ttaaccctgg ctcctgaggc tgcggccagc agatcccagg         120
ccagggctct gttcttgcca cacctgcttg a                                       151

        <210> 318
        <211> 151
        <212> DNA
        <213> Homo sapien

        <400> 318
actggtggga ggcgctgttt agttggctgt tttcagaggg gtctttcgga gggacctcct          60
gctgcaggct ggagtgtctt tattcctggc gggagaccgc acattccact gctgaggctg         120
tggggcggt ttatcaggca gtgataaaca t                                        151

        <210> 319
        <211> 151
        <212> DNA
```

102

```
        <213> Homo sapien

        <400> 319
aactagtgga tccagagcta taggtacagt gtgatctcag ctttgcaaac acattttcta        60
catagatagt actaggtatt aatagatatg taaagaaaga aatcacacca ttaataatgg       120
taagattggg tttatgtgat tttagtgggt a                                       151

        <210> 320
        <211> 150
        <212> DNA
        <213> Homo sapien

        <400> 320
aactagtgga tccactagtc cagtgtggtg gaattccatt gtgttggggt tctagatcgc        60
gagcggctgc cctttttttt ttttttttg ggggggaatt tttttttttt aatagttatt       120
gagtgttcta cagcttacag taaataccat                                         150

        <210> 321
        <211> 151
        <212> DNA
        <213> Homo sapien

        <400> 321
agcaactttg tttttcatcc aggttatttt aggcttagga tttcctctca cactgcagtt        60
tagggtggca ttgtaaccag ctatggcata ggtgttaacc aaaggctgag taaacatggg       120
tgcctctgag aaatcaaagt cttcatacac t                                       151

        <210> 322
        <211> 151
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(151)
        <223> n = A,T,C or G

        <400> 322
atccagcatc ttctcctgtt tcttgccttc cttttcttc ttcttasatt ctgcttgagg         60
tttgggcttg gtcagtttgc cacagggctt ggagatggtg acagtcttct ggcattcggc       120
attgtgcagg gctcgcttca nacttccagt t                                       151

        <210> 323
        <211> 151
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(151)
        <223> n = A,T,C or G

        <400> 323
tgaggacttg tkttcttttt ctttattttt aatcctctta ckttgtaaat atattgccta        60
nagactcant tactacccag tttgtggttt twtgggagaa atgtaactgg acagttagct       120
gttcaatyaa aaagacactt ancccatgtg g                                       151

        <210> 324
```

103

```
<211> 461
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(461)
<223> n = A,T,C or G

<400> 324
acctgtgtgg aatttcagct ttcctcatgc aaaaggattt tgtatccccg gcctacttga        60
agaagtggtc agctaaagga atccaggttg ttggttggac tgttaatacc tttgatgaaa       120
agagttacta cgaatcccat cttggttcca gctatatcac tgacagcatg gtagaagact       180
gcgaacctca cttctagact ttcacggtgg dacgaaacgg gttcagaaac tgccagggggc       240
ctcatacagg gatatcaaaa tacccttgt gctacccagg ccctgggaa tcaggtgact       300
cacacaaatg caatagttgg tcactgcatt tttacctgaa ccaaagctaa acccggtgtt       360
gccaccatgc accatgccat gccagagttc aacactgttg ctcttgaaaa ttgggtctga       420
aaaaacgcac aagagccccc tgccctgccct agctgangca c                         461

<210> 325
<211> 400
<212> DNA
<213> Homo sapien

<400> 325
acactgtttc catgttatgt ttctacacat tgctacctca gtgctcctgg aaacttagct        60
tttgatgtct ccaagtagtc caccttcatt taactctttg aaactgtatc atctttgcca       120
agtaagagtg gtggcctatt tcagctgctt tgacaaaatg actggctcct gacttaacgt       180
tctataaatg aatgtgctga agcaaagtgc ccatggtggc ggcgaagaag agaaagatgt       240
gtttttgtttt ggactctctg tggtcccttc caatgctgtg ggtttccaac caggggaagg       300
gtccctttttg cattgccaag tgccataacc atgagcacta cgctaccatg gttctgcctc       360
ctggccaagc aggctggttt gcaagaatga aatgaatgat                            400

<210> 326
<211> 1215
<212> DNA
<213> Homo sapien

<400> 326
ggaggactgc agcccgcact cgcagccctg gcaggcggca ctggtcatgg aaaacgaatt        60
gttctgctcg ggcgtcctgg tgcatccgca gtgggtgctg tcagccgcac actgtttcca       120
gaactcctac accatcgggc tgggcctgca cagtcttgag gccgaccaag agccagggag       180
ccagatggtg gaggccagcc tctccgtacg gcacccagag tacaacagac ccttgctcgc       240
taacgacctc atgctcatca agttggacga atccgtgtcc gagtctgaca ccatccggag       300
catcagcatt gcttcgcagt gccctaccgc ggggaactct tgcctcgttt ctggctgggg       360
tctgctggcg aacggcagaa tgcctaccgt gctgcagtgc gtgaacgtgt cggtggtgtc       420
tgaggaggtc tgcagtaagc tctatgaccc gctgtaccac cccagcatgt tctgcgccgg       480
cggaggcaa gaccagaagg actcctgcaa cggtgactct gggggggccc tgatctgcaa       540
cgggtacttg cagggccttg tgtctttcgg aaaagccccg tgtggccaag ttggcgtgcc       600
aggtgtctac accaacctct gcaaattcac tgagtggata gagaaaaccg tccaggccag       660
ttaactctgg ggactgggaa cccatgaaat tgaccccaa atacatcctg cggaaggaat       720
tcaggaatat ctgttcccag cccctcctcc ctcaggccca ggagtccagg cccccagccc       780
ctcctccctc aaaccaaggg tacagatccc cagcccctcc tccctcagac ccaggagtcc       840
agaccccca gccctcctc cctcagaccc aggagtccag cccctcctcc ctcagaccca       900
ggagtccaga ccccccagcc cctcctccct cagacccagg gtccaggcc cccaacccct       960
cctccctcag actcagaggt ccaagccccc aaccctcct tccccagacc cagaggtcca      1020
ggtccagcc cctcctccct cagacccagc ggtccaatgc cacctagact ctccctgtac      1080
acagtgcccc cttgtggcac gttgacccaa ccttaccagt tggttttca ttttttgtcc      1140
```

104

```
ctttccccta gatccagaaa taaagtctaa gagaagcgca aaaaaaaaaa aaaaaaaaaa      1200
aaaaaaaaaa aaaaa                                                       1215
```

```
        <210> 327
        <211> 220
        <212> PRT
        <213> Homo sapien

        <400> 327
Glu Asp Cys Ser Pro His Ser Gln Pro Trp Gln Ala Ala Leu Val Met
 1               5                  10                  15
Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln Trp Val
            20                  25                  30
Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu Gly
   .35           .        40                  45
Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val Glu
    50                  55                  60
Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro Leu Leu Ala
65                  70              .       75                  80
Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser Asp
                85                  ·90                  95
Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly Asn
            100                 105                 110
Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly Arg Met Pro
            115                 120                 125
Thr Val Leu Gln Cys Val Asn Val Ser Val Val Ser Glu Glu Val Cys
    130                 135                 140
Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe Cys Ala Gly
145                 150                 155  --               160
Gly Gly Gln Asp Gln Lys Asp Ser Cys Asn Gly Asp Ser Gly Gly Pro
                165                 170                 175
Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe Gly Lys Ala
                180                 185                 190
Pro Cys Gly Gln Val Gly Val Pro Gly Val Tyr Thr Asn Leu Cys Lys
            195                 200                 205
Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser
 .210                 215                 220

        <210> .328
        <211> 234
        <212> DNA
        <213> Homo sapien

        <400> 328
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agccctggca ggcggcactg gtcatggaaa acgaattgtt ctgctcgggc gtcctggtgc      120
atccgcagtg ggtgctgtca gccacacact gtttccagaa ctcctacacc atcgggctgg      180
gcctgcacag tcttgaggcc gaccaagagc cagggagcca gatggtggag gcca            234

        <210> 329
        <211> 77
        <212> PRT
        <213> Homo sapien

        <400> 329
Leu Val Ser Gly Ser Cys Ser Gln Ile Ile Asn Gly Glu Asp Cys Ser
 1               5                  10                  15
Pro His Ser Gln Pro Trp Gln Ala Ala Leu Val Met Glu Asn Glu Leu
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105

```
                    20              25              30
Phe Cys Ser Gly Val Leu Val His Pro Gln Trp Val Leu Ser Ala Thr
        35              40              45
His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu Gly Leu His Ser Leu
    50              55              60
Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val Glu Ala
65              70              75
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        <210> 330
        <211> 70
        <212> DNA
        <213> Homo sapien

        <400> 330
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gctgcagcca                                                               70

        <210> 331
        <211> 22
        <212> PRT
        <213> Homo sapien

        <400> 331
Gln His Asn Gly Pro Ile Pro Ser Leu Thr Pro Pro Ser Gly Ser Leu
 1               5              10              15
Val Ser Gly Ser Cys Ser
                20

        <210> 332
        <211> 2507
        <212> DNA
        <213> Homo sapien

        <400> 332
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tgcccttcct tctgtatatg gctgcgcccc aaatcaggaa aatgctgtcc agtggggtgt      120
gtacatcaac tgttcagctt cctgggaaag tagttgtggt cacaggagct aatacaggta      180
tcgggaagga gacagccaaa gagctggctc agagaggagc tcgagtatat ttagcttgcc      240
gggatgtgga aaagggggaa ttggtggcca aagagatcca gaccacgaca gggaaccagc      300
aggtgttggt gcggaaactg gacctgtctg atactaagtc tattcgagct tttgctaagg      360
gcttcttagc tgaggaaaag cacctccacg ttttgatcaa caatgcagga gtgatgatgt      420
gtccgtactc gaagacagca gatggctttg agatgcacat aggagtcaac cacttgggtc      480
acttcctcct aacccatctg ctgctagaga aactaaagga atcagcccca tcaaggatag      540
taaatgtgtc ttccctcgca catcacctgg gaaggatcca cttccataac ctgcagggcg      600
agaaattcta caatgcaggc ctggcctact gtcacagcaa gctagccaac atcctcttca      660
cccaggaact ggcccggaga ctaaaaggct ctggcgttac gacgtattct gtacaccctg      720
gcacagtcca atctgaactg gttcggcact catctttcat gagatggatg tggtggcttt      780
tctcctttttt catcaagact cctcagcagg gagcccagac cagcctgcac tgtgccttaa      840
cagaaggtct tgagattcta agtgggaatc atttcagtga ctgtcatgtg gcatgggtct      900
ctgcccaagc tcgtaatgag actatagcaa ggcggctgtg ggacgtcagt tgtgacctgc      960
tgggcctccc aatagactaa caggcagtgc cagttggacc caagagaaga ctgcagcaga     1020
ctacacagta cttcttgtca aatgattct ccttcaaggt tttcaaaacc tttagcacaa     1080
agagagcaaa accttccagc cttgcctgct tggtgtccag ttaaaactca gtgtactgcc     1140
agattcgtct aaatgtctgt catgtccaga tttactttgc ttctgttact gccagagtta     1200
ctagagatat cataatagga taagaagacc ctcatatgac ctgcacagct cattttcctt     1260
ctgaaagaaa ctactaccta ggagaatcta agctatagca gggatgattt atgcaaattt     1320
gaactagctt ctttgttcac aattcagttc ctcccaacca accagtcttc acttcaagag     1380
ggccacactg caacctcagc ttaacatgaa taacaaagac tggctcagga gcagggcttg     1440
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106

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cccaggcatg gtggatcacc ggaggtcagt agttcaagac cagcctggcc aacatggtga    1500
aaccccacct ctactaaaaa ttgtgtatat ctttgtgtgt cttcctgttt atgtgtgcca    1560
agggagtatt ttcacaaagt tcaaaacagc cacaataatc agagatggag caaaccagtg    1620
ccatccagtc tttatgcaaa tgaaatgctg caaagggaag cagattctgt atatgttggt    1680
aactacccac caagagcaca tgggtagcag ggaagaagta aaaaaagaga aggagaatac    1740
tggaagataa tgcacaaaat gaagggacta gttaaggatt aactagccct ttaaggatta    1800
actagttaag gattaatagc aaaagayatt aaatatgcta acatagctat ggaggaattg    1860
agggcaagca cccaggactg atgaggtctt aacaaaaacc agtgtggcaa aaaaaaaaa    1920
aaaaaaaaaa aaaaatccta aaaacaaaca aacaaaaaaa acaattcttc attcagaaaa    1980
attatcttag ggactgatat tggtaattat ggtcaattta ataatatttt ggggcatttc    2040
cttacattgt cttgacaaga ttaaaatgtc tgtgccaaaa ttttgtattt tatttggaga    2100
cttcttatca aaagtaatgc tgccaaagga agtctaagga attagtagtg ttcccatcac    2160
ttgtttggag tgtgctattc taaaagattt tgatttcctg gaatgacaat tatattttaa    2220
ctttggtggg ggaaagagtt ataggaccac agtcttcact tctgatactt gtaaattaat    2280
cttttattgc acttgttttg accattaagc tatatgttta gaaatggtca ttttacggaa    2340
aaattagaaa aattctgata atagtgcaga ataaatgaat taatgtttta cttaatttat    2400
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aataaaaacg taagaattaa aagtttgatt acaaaaaaaa aaaaaa                    2507
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    <210> 333
    <211> 3030
    <212> DNA
    <213> Homo sapien

    <400> 333
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gctccatgga gcccggcaat tatgccacct tggatggagc caaggatatc gaaggcttgc     180
tgggagcggg aggggggcgg aatctggtcg cccactcccc tctgaccagc cacccagcgg     240
cgcctacgct gatgcctgct gtcaactatg cccccttgga tctgccaggc tcggcggagc     300
cgccaaagca atgccaccca tgccctgggg tgccccaggg gacgtccccca gctcccgtgc     360
cttatggtta ctttggaggc gggtactact cctgccgagt gtcccggagc tcgctgaaac     420
cctgtgccca ggcagccacc ctggccgcgt accccgcgga gactcccacg gccggggaag     480
agtaccccag ycgccccact gagtttgcct tctatccggg atatccggga acctaccagc     540
ctatggccag ttacctggac gtgtctgtgg tgcagactct gggtgctcct ggagaaccgc     600
gacatgactc cctgttgcct gtggacagtt accagtcttg ggctcctcgc ggtggctgga     660
acagccagat gtgttgccag ggagaacaga acccaccagg tcccttttgg aaggcagcat     720
ttgcagactc cagcgggcag caccctcctg acgcctgcgc ctttcgtcgc ggccgcaaga     780
aacgcattcc gtacagcaag gggcagttgc gggagctgga gcgggagtat gcggctaaca     840
agttcatcac caaggacaag aggcgcaaga tctcggcagc caccagcctc tcggagcgcc     900
agattaccat ctggtttcag aaccgccggg tcaaagagaa gaaggttctc gccaaggtga     960
agaacagcgc tacccccttaa gagatctcct tgcctgggtg ggaggagcga aagtgggggt    1020
gtcctgggga gaccaggaac ctgccaagcc caggctgggg ccaaggactc tgctgagagg    1080
cccctagaga caacacccctt cccaggccac tggctgctgg actgttcctc aggagcggcc    1140
tgggtaccca gtatgtgcag ggagacggaa ccccatgtga cagcccactc caccagggtt    1200
cccaaagaac ctggcccagt cataatcatt catcctgaca gtggcaataa tcacgataac    1260
cagtactagc tgccatgatc gttagcctca tattttctat ctagagctct gtagagcact    1320
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cagggaagct ttctctcaga ccccccttcca ttacacctct caccctggta acagcaggaa    1440
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tctcagctga cagctgggta ggtggacaat tgtagaggct gtctcttcct ccctccttgt    1560
ccacccccata gggtgtaccc actggtcttg gaagcaccca tccttaatac gatgattttt    1620
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tcttcccttá atatttctgg tggttctgac caaagcaggt catggtttgt tgagcatttg    1800
ggatcccagt gaagtagatg tttgtagcct tgcatactta gcccttccca ggcacaaacg    1860
gagtggcaga gtggtgccaa ccctgttttc ccagtccacg tagacagatt cacagtgcgg    1920
aattctggaa gctggagaca gacgggctct ttgcagagcc gggactctga gagggacatg    1980
```

```
agggcctctg cctctgtgtt cattctctga tgtcctgtac ctgggctcag tgcccggtgg    2040
gactcatctc ctggccgcgc agcaaagcca gcgggttcgt gctggtcctt cctgcacctt    2100
aggctggggg tggggggcct gccggcgcat tctccacgat tgagcgcaca ggcctgaagt    2160
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tggcgagcag ttggtggtgg gccgcgccg ccactacctc gaggacattt ccctcccgga     2280
gccagctctc ctagaaaccc cgcggcggcc gccgcagcca agtgtttatg gcccgcggtc     2340
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gatcgggcaa gtaaacccc tccctcgccg acttcggaac tggcgagagt tcagcgcaga      2760
tgggcctgtg gggaggggc aagatagatg aggggagcg gcatggtgcg gggtgacccc .    2820
ttggagagag gaaaaaggcc acaagagggg ctgccaccgc cactaacgga gatggccctg     2880
gtagagacct ttggggggtct ggaacctctg gactccccat gctctaactc ccacactctg    2940
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aacaaaaaaa aaaaaaaaaa aaaactcgag                                      3030
```

    <210> 334
    <211> 2417
    <212> DNA
    <213> Homo sapien

    <400> 334

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agtttacaaa tgaggaaaca ggtgcaaaaa ggttgttacc tgtcaaaggt cgtatgtggc    180
agagccaaga tttgagccca gttatgtctg atgaacttag cctatgctct ttaaacttct    240
gaatgctgac cattgaggat atctaaactt agatcaattg cattttccct ccaagactat    300
ttacttatca atacaataat accacctta ccaatctatt gtttttgatac gagactcaaa     360
tatgccagat atatgtaaaa gcaacctaca agctctctaa tcatgctcac ctaaaagatt     420
cccgggatct aataggctca aagaaacttc ttctagaaat ataaaagaga aaattggatt     480
atgcaaaaat tcattattaa ttttttttcat ccatcctta attcagcaaa catttatctg     540
ttgttgactt tatgcagtat ggccttttaa ggattggggg acaggtgaag aacgggtgc      600
cagaatgcat cctcctacta atgaggtcag tacacatttg cattttaaaa tgccctgtcc     660
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gcttcagccc aggagttcaa gaccagcctg ggcaacatag aaagacccca tctctcaatc     780
aatcaatcaa tgccctgtct ttgaaaataa aactctttaa gaaaggttta atgggcaggg     840
tgtggtagct catgcctata atacagcact ttgggaggct gaggcaggag gatcacttta .   900
gcccagaagt tcaagaccag cctgggcaac aagtgacacc tcatctcaat tttttaataa     960
aatgaataca tacataagga aagataaaaa gaaaagttta atgaaagaat acagtataaa    1020
acaaatctct tggacctaaa agtatttttg ttcaagccaa atattgtgaa tcacctatct    1080
gtgttgagga tacagaatat ctaagcccag gaaactgagc agaaagttca tgtactaact    1140
aatcaacccg aggcaaggca aaaatgagac taactaatca atccgaggca aggggcaaat    1200
tagacggaac ctgactctgg tctattaagc gacaactttc cctctgttgt attttttcttt   1260
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cacagactgg gaggcttaag taacagaaat tcatttctca cagttctggg ggctggaagt    1560
ccacgatcaa ggtgcaggaa aggcaggctt cattctgagg cccctctctt ggctcacatg    1620
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tggccaagat aaagcaacag aaaaatgtcc aaagctgtgc agcaaagaca agccaccgaa    1860
cagggatctg ctcatcagtg tggggacctc caagtcggcc accctggagg caagcccca     1920
cagagcccat gcaaggtggc agcagcagaa gaagggaatt gtccctgtcc ttggcacatt    1980
```

108

```
cctcaccgac ctggtgatgc tggacactgc gatgaatggt aatgtggatg agaatatgat   2040
ggactcccag aaaaggagac ccagctgctc aggtggctgc aaatcattac agccttcatc   2100
ctggggagga actggggggcc tggttctggg tcagagagca gcccagtgag ggtgagagct   2160
acagcctgtc ctgccagctg gatccccagt cccggtcaac cagtaatcaa ggctgagcag   2220
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ggtactgaga caatattgtc ataaattcaa tgcgcccttg tatccctttt tctttttttat  2340
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```

        <210> 335
        <211> 2984
        <212> DNA
        <213> Homo sapien

        <400> 335
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cccgagctgc cttctcccac actcaggtga tcgagttgga gaggaagttc agccatcaga   180
agtacctgtc ggccctgaa cgggcccacc tggccaagaa cctcaagctc acggagaccc   240
aagtgaagat atggttccag aacagacgct ataagactaa gcgaaagcag ctctcctcgg   300
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aatgaaacaa cagagacagt gaaagttta atacctaagt cattcccca gtgcatactg   660
taggtcattt tttttgcttc tggctacctg tttgaagggg agagagggaa aatcaagtgg   720
tattttccag cactttgtat gattttggat gagctgtaca cccaaggatt ctgttctgca   780
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gccttggaat atggccaagg ctctctctgt ccctgtaaaa gagaggggca aatagagagt   960
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cagtccactg agcaagcaag ggactgagtg agccttttgc aggaaaaggc taagaaaaag   1980
gaaaaccatt ctaaaacaca acaagaaact gtccaaatgc tttgggaact gtgtttattg   2040
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```

109

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tgatgtatat tgtgttgcaa aaaaaaaaaa aagtgtcttt gtttaaaatt acttggtttg   2640
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ccatttcacc cagacagcct gtttctatcc tgtttaataa attagtttgg gttctctaca   2820
tgcataacaa accctgctcc aatctgtcac ataaaagtct gtgacttgaa gtttagtcag   2880
cacccccacc aaactttatt tttctatgtg ttttttgcaa catatgagtg ttttgaaaat   2940
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```

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        <210> 336
        <211> 147
        <212> PRT
        <213> Homo sapien


        <400> 336
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            20                  25                  30
Pro Lys Gln Pro Gln Lys Arg Ser Arg Ala Ala Phe Ser His Thr Gln
        35                  40                  45
Val Ile Glu Leu Glu Arg Lys Phe Ser His Gln Lys Tyr Leu Ser Ala
    50                  55                  60
Pro Glu Arg Ala His Leu Ala Lys Asn Leu Lys Leu Thr Glu Thr Gln
65                  70                  75                  80
Val Lys Ile Trp Phe Gln Asn Arg Arg Tyr Lys Thr Lys Arg Lys Gln
                85                  90                  95
Leu Ser Ser Glu Leu Gly Asp Leu Glu Lys His Ser Ser Leu Pro Ala
            100                 105                 110
Leu Lys Glu Glu Ala Phe Ser Arg Ala Ser Leu Val Ser Val Tyr Asn
        115                 120                 125
Ser Tyr Pro Tyr Tyr Pro Tyr Leu Tyr Cys Val Gly Ser Trp Ser Pro
    130                 135                 140
Ala Phe Trp
145


        <210> 337
        <211> 9
        <212> PRT
        <213> Homo sapien


        <400> 337
Ala Leu Thr Gly Phe Thr Phe Ser Ala
 1               5


        <210> 338
        <211> 9
        <212> PRT
        <213> Homo sapien


        <400> 338
Leu Leu Ala Asn Asp Leu Met Leu Ile
 1               5


        <210> 339
        <211> 318
        <212> PRT
        <213> Homo sapien
```

```
        <400> 339
Met Val Glu Leu Met Phe Pro Leu Leu Leu Leu Leu Leu Pro Phe Leu
1               5                   10                  15
Leu Tyr Met Ala Ala Pro Gln Ile Arg Lys Met Leu Ser Ser Gly Val
            20                  25                  30
Cys Thr Ser Thr Val Gln Leu Pro Gly Lys Val Val Val Thr Gly
            35                  40                  45
Ala Asn Thr Gly Ile Gly Lys Glu Thr Ala Lys Glu Leu Ala Gln Arg
    50                  55                  60
Gly Ala Arg Val Tyr Leu Ala Cys Arg Asp Val Glu Lys Gly Glu Leu
65                  70                  75                  80
Val Ala Lys Glu Ile Gln Thr Thr Thr Gly Asn Gln Gln Val Leu Val
                85                  90                  95
Arg Lys Leu Asp Leu Ser Asp Thr Lys Ser Ile Arg Ala Phe Ala Lys
            100                 105                 110
Gly Phe Leu Ala Glu Glu Lys His Leu His Val Leu Ile Asn Asn Ala
            115                 120                 125
Gly Val Met Met Cys Pro Tyr Ser Lys Thr Ala Asp Gly Phe Glu Met
    130                 135                 140
His Ile Gly Val Asn His Leu Gly His Phe Leu Leu Thr His Leu Leu
145                 150                 155                 160
Leu Glu Lys Leu Lys Glu Ser Ala Pro Ser Arg Ile Val Asn Val Ser
            165                 170                 175
Ser Leu Ala His His Leu Gly Arg Ile His Phe His Asn Leu Gln Gly
        180                 185                 190
Glu Lys Phe Tyr Asn Ala Gly Leu Ala Tyr Cys His Ser Lys Leu Ala
        195                 200                 205
Asn Ile Leu Phe Thr Gln Glu Leu Ala Arg Arg Leu Lys Gly Ser Gly
    210                 215                 220
Val Thr Thr Tyr Ser Val His Pro Gly Thr Val Gln Ser Glu Leu Val
225                 230                 235                 240
Arg His Ser Ser Phe Met Arg Trp Met Trp Trp Leu Phe Ser Phe Phe
                245                 250                 255
Ile Lys Thr Pro Gln Gln Gly Ala Gln Thr Ser Leu His Cys Ala Leu
            260                 265                 270
Thr Glu Gly Leu Glu Ile Leu Ser Gly Asn His Phe Ser Asp Cys His
        275                 280                 285
Val Ala Trp Val Ser Ala Gln Ala Arg Asn Glu Thr Ile Ala Arg Arg
    290                 295                 300
Leu Trp Asp Val Ser Cys Asp Leu Leu Gly Leu Pro Ile Asp
305                 310                 315

        <210> 340
        <211> 483
        <212> DNA
        <213> Homo sapien

        <400> 340
gccgaggtct gccttcacac ggaggacacg agactgcttc ctcaagggct cctgcctgcc     60
tggacactgg tgggaggcgc tgtttagttg gctgttttca gaggggtctt tcggagggac    120
ctcctgctgc aggctggagt gtctttattc ctggcgggag accgcacatt ccactgctga    180
ggttgtgggg gcggtttatc aggcagtgat aaacataaga tgtcatttcc ttgactccgg    240
ccttcaattt tctctttggc tgacgacgga gtccgtggtg tcccgatgta actgacccct    300
gctccaaacg tgacatcact gatgctcttc tcggggggtgc tgatggcccg cttggtcacg    360
tgctcaatct cgccattcga ctcttgctcc aaactgtatg aagacacctg actgcacgtt    420
ttttctgggc ttccagaatt taaagtgaaa ggcagcactc ctaagctccg actccgatgc    480
ctg                                                                   483
```

```
<210> 341
<211> 344
<212> DNA
<213> Homo sapien

<400> 341
ctgctgctga gtcacagatt tcattataaa tagcctccct aaggaaaata cactgaatgc      60
tattttttact aaccattcta tttttataga aatagctgag agtttctaaa ccaactctct    120
gctgccttac aagtattaaa tattttactt ctttccataa agagtagctc aaaatatgca     180
attaatttaa taatttctga tgatggtttt atctgcagta atatgtatat catctattag     240
aatttactta atgaaaaact gaagagaaca aaatttgtaa ccactagcac ttaagtactc     300
ctgattctta acattgtctt taatgaccac aagacaacca acag                      344


<210> 342
<211> 592
<212> DNA
<213> Homo sapien

<400> 342
acagcaaaaa agaaactgag aagcccaaty tgctttcttg ttaacatcca cttatccaac      60
caatgtggaa acttcttata cttggttcca ttatgaagtt ggacaattgc tgctatcaca     120
cctggcaggt aaaccaatgc caagagagtg atggaaacca ttggcaagac tttgttgatg     180
accaggattg gaattttata aaaatattgt tgatgggaag ttgctaaagg gtgaattact     240
tccctcagaa gagtgtaaag aaaagtcaga gatgctataa tagcagctat tttaattggc     300
aagtgccact gtggaaagag ttcctgtgtg tgctgaagtt ctgaagggca gtcaaattca     360
tcagcatggg ctgtttggtg caaatgcaaa agcacaggtc tttttagcat gctggtctct     420
cccgtgtcct tatgcaaata atcgtcttct tctaaatttc tcctaggctt cattttccaa     480
agttcttctt ggtttgtgat gtctttttctg ctttccatta attctataaa atagtatggc    540
ttcagccacc cactcttcgc cttagcttga ccgtgagtct cggctgccgc tg             592


<210> 343
<211> 382
<212> DNA
<213> Homo sapien

<400> 343
ttcttgacct cctcctcctt caagctcaaa caccacctcc cttattcagg accggcactt      60
cttaatgttt gtggctttct ctccagcctc tcttaggagg ggtaatggtg gagttggcat     120
cttgtaactc tcctttctcc tttcttcccc tttctctgcc cgcctttccc atcctgctgt     180
agacttcttg attgtcagtc tgtgtcacat ccagtgattg ttttggtttc tgttcccttt     240
ctgactgccc aaggggctca gaaccccagc aatcccttcc tttcactacc ttcttttttg     300
ggggtagttg gaagggactg aaattgtggg gggaaggtag gaggcacatc aataaagagg     360
aaaccaccaa gctgaaaaaa aa                                              382


<210> 344
<211> 536
<212> DNA
<213> Homo sapien

<400> 344
ctgggcctga agctgtaggg taaatcagag gcaggcttct gagtgatgag agtcctgaga      60
caataggcca cataaacttg gctggatgga acctcacaat aaggtggtca cctcttgttt     120
gtttaggggg atgccaagga taaggccagc tcagttatat gaagagaagc agaacaaaca     180
agtctttcag agaaatggat gcaatcagag tgggatcccg gtcacatcaa ggtcacactc     240
caccttcatg tgcctgaatg gttgccaggt cagaaaaatc caccccttac gagtgcggct     300
tcgaccctat atcccccgcc cgcgtccctt tctccataaa attcttctta gtagctatta     360
ccttcttatt atttgatcta gaaattgccc tccttttacc cctaccatga gccctacaaa     420
```

112

```
caactaacct gccactaata gttatgtcat ccctcttatt aatcatcatc ctagccctaa     480
gtctggccta tgagtgacta caaaaaggat tagactgagc cgaataacaa aaaaaa         536


        <210> 345
        <211> 251
        <212> DNA
        <213> Homo sapien


        <400> 345
accttttgag gtctctctca ccacctccac agccaccgtc accgtgggat gtgctggatg      60
tgaatgaagc ccccatcttt gtgcctcctg aaaagagagt ggaagtgtcc gaggactttg     120
gcgtgggcca ggaaatcaca tcctacactg cccaggagcc agacacattt atggaacaga     180
aaataacata tcggatttgg agagacactg ccaactggct ggagattaat ccggacactg     240
gtgccatttc c                                                         251


        <210> 346
        <211> 282
        <212> DNA
        <213> Homo sapien


        <220>
        <221> misc_feature
        <222> (1)...(282)
        <223> n = A,T,C or G


<400> 346
cgcgtctctg acactgtgat catgacaggg gttcaaacag aaagtgcctg ggccctcctt      60
ctaagtcttg ttaccaaaaa aaggaaaaag aaaagatctt ctcagttaca aattctggga     120
agggagacta tacctggctc ttgccctaag tgagaggtct tccctcccgc accaaaaaat     180
agaaaggctt tctatttcac tggcccaggt aggggaagg agagtaactt tgagtctgtg      240
ggtctcattt cccaaggtgc cttcaatgct catnaaaacc aa                       282


        <210> 347
        <211> 201
        <212> DNA
        <213> Homo sapien


        <220>
        <221> misc_feature
        <222> (1)...(201)
        <223> n = A,T,C or G


        <400> 347
acacacataa tattataaaa tgccatctaa ttggaaggag ctttctatca ttgcaagtca      60
taaatataac ttttaaaana ntactancag cttttaccta ngctcctaaa tgcttgtaaa     120
tctgagactg actggaccca cccagaccca gggcaaagat acatgttacc atatcatctt     180
tataaagaat ttttttttgt c                                               201


        <210> 348
        <211> 251
        <212> DNA
        <213> Homo sapien


        <400> 348
ctgttaatca caacatttgt gcatcacttg tgccaagtga gaaaatgttc taaaatcaca      60
agagagaaca gtgccagaat gaaactgacc ctaagtccca ggtgcccctg ggcaggcaga     120
aggagacact cccagcatgg aggagggttt atcttttcat cctaggtcag gtctacaatg     180
ggggaaggtt ttattataga actcccaaca gcccacctca ctcctgccac ccacccgatg     240
```

113

```
gccctgcctc c                                                            251

        <210> 349
        <211> 251
        <212> DNA
        <213> Homo sapien

        <400> 349
taaaaatcaa gccatttaat tgtatctttg aaggtaaaca atatatggga gctggatcac        60
aacccctgag gatgccagag ctatgggtcc agaacatggt gtggtattat caacagagtt       120
cagaagggtc tgaactctac gtgttaccag agaacataat gcaattcatg cattccactt       180
agcaattttg taaaatacca gaaacagacc ccaagagtct ttcaagatga ggaaaattca       240
actcctggtt t                                                            251

        <210> 350
        <211> 908
        <212> DNA
        <213> Homo sapien

        <400> 350
ctggacactt tgcgagggct tttgctggct gctgctgctg cccgtcatgc tactcatcgt        60
agcccgcccg gtgaagctcg ctgctttccc tacctcctta agtgactgcc aaacgcccac       120
cggctggaat tgctctggtt atgatgacag agaaaatgat ctcttcctct gtgacaccaa       180
cacctgtaaa tttgatgggg aatgtttaag aattggagac actgtgactt gcgtctgtca       240
gttcaagtgc aacaatgact atgtgcctgt gtgtggctcc aatggggaga gctaccagaa       300
tgagtgttac ctgcgacagg ctgcatgcaa acagcagagt gagatacttg tggtgtcaga       360
aggatcatgt gccacagtcc atgaaggctc tggagaaact agtcaaaagg agacatccac       420
ctgtgatatt tgccagtttg gtgcagaatg tgacgaagat gccgaggatg tctggtgtgt       480
gtgtaatatt gactgttctc aaaccaactt caatcccctc tgcgcttctg atgggaaatc       540
ttatgataat gcatgccaaa tcaaagaagc atcgtgtcag aaacaggaga aaattgaagt       600
catgtctttg ggtcgatgtc aagataacac aactacaact actaagtctg aagatgggca       660
ttatgcaaga acagattatg cagagaatgc taacaaatta gaagaaagtg ccagagaaca       720
ccacatacct tgtccggaac attacaatgg cttctgcatg catgggaagt gtgagcattc       780
tatcaatatg caggagccat cttgcaggtg tgatgctggt tatactggac aacactgtga       840
aaaaaaggac tacagtgttc tatacgttgt tcccggtcct gtacgatttc agtatgtctt       900
aatcgcag                                                                908

        <210> 351
        <211> 472
        <212> DNA
        <213> Homo sapien

        <400> 351
ccagttattt gcaagtggta agagcctatt taccataaat aatactaaga accaactcaa        60
gtcaaacctt aatgccattg ttattgtgaa ttaggattaa gtagtaattt tcaaaattca       120
cattaacttg attttaaaat cagwtttgyg agtcatttac cacaagctaa atgtgtacac       180
tatgataaaa acaaccattg tattcctgtt tttctaaaca gtcctaattt ctaacactgt       240
atatatcctt cgacatcaat gaactttgtt ttcttttact ccagtaataa agtaggcaca       300
gatctgtcca caacaaactt gccctctcat gccttgcctc tcaccatgct ctgctccagg       360
tcagcccct tttggcctgt ttgttttgtc aaaaacctaa tctgcttctt gctttttcttg      420
gtaatatata tttaggaag atgttgcttt gcccacacac gaagcaaagt aa                472

        <210> 352
        <211> 251
        <212> DNA
        <213> Homo sapien

        <400> 352
```

114

```
ctcaaagcta atctctcggg aatcaaacca gaaaagggca aggatcttag gcatggtgga      60
tgtggataag gccaggtcaa tggctgcaag catgcagaga aagaggtaca tcggagcgtg     120
caggctgcgt tccgtcctta cgatgaagac cacgatgcag tttccaaaca ttgccactac     180
atacatggaa aggaggggga agccaaccca gaaatgggct ttctctaatc ctgggatacc     240
aataagcaca a                                                          251
```

```
        <210> 353
        <211> 436
        <212> DNA
        <213> Homo sapien


        <400> 353
tttttttttt tttttttttt tttttacaa caatgcagtc atttatttat tgagtatgtg      60
cacattatgg tattattact atactgatta tatttatcat gtgacttcta attaraaaat     120
gtatccaaaa gcaaaacagc agatatacaa aattaaagag acagaagata gacattaaca     180
gataaggcaa cttatacatt gacaatccaa atccaataca tttaaacatt tgggaaatga     240
gggggacaaa tggaagccar atcaaatttg tgtaaaacta ttcagtatgt ttcccttgct     300
tcatgtctga raaggctctc ccttcaatgg ggatgacaaa ctccaaatgc cacacaaatg     360
ttaacagaat actagattca cactggaacg ggggtaaaga agaaattatt ttctataaaa     420
gggctcctaa tgtagt                                                     436
```

```
        <210> 354
        <211> 854
        <212> DNA
        <213> Homo sapien


        <400> 354
cctttctag ttcaccagtt ttctgcaagg atgctggtta gggagtgtct gcaggaggag       60
caagtctgaa accaaatcta ggaaacatag gaaacgagcc aggcacaggg ctggtgggcc     120
atcagggacc acccttgggg ttgatatttt gcttaatctg catcttttga gtaagatcat     180
ctggcagtag aagctgttct ccaggtacat ttctctagct catgtacaaa aacatcctga     240
aggactttgt caggtgcctt gctaaaagcc agatgcgttc ggcacttcct tggtctgagg     300
ttaattgcac acctacaggc actgggctca tgctttcaag tattttgtcc tcactttagg     360
gtgagtgaaa gatccccatt ataggagcac ttgggagaga tcatataaaa gctgactctt     420
gagtacatgc agtaatgggg tagatgtgtg tggtgtgtct tcattcctgc aagggtgctt     480
gttagggagt gtttccagga ggaacaagtc tgaaaccaat catgaaataa atggtaggtg     540
tgaactggaa aactaattca aaagagagat cgtgatatca gtgtggttga tacaccttgg     600
caatatggaa ggctctaatt tgcccatatt tgaaataata attcagcttt ttgtaataca     660
aaataacaaa ggattgagaa tcatggtgtc taatgtataa aagacccagg aaacataaat     720
atatcaactg cataaatgta aaatgcatgt gacccaagaa ggccccaaag tggcagacaa     780
cattgtaccc attttccctt ccaaaatgtg agcggcgggc ctgctgcttt caaggctgtc     840
acacgggatg tcag                                                       854
```

```
        <210> 355
        <211> 676
        <212> DNA
        <213> Homo sapien


        <400> 355
gaaattaagt atgagctaaa ttccctgtta aaacctctag gggtgacaga tctcttcaac      60
caggtcaaag ctgatctttc tggaatgtca ccaaccaagg gcctatattt atcaaaagcc     120
atccacaagt catacctgga tgtcagcgaa gagggcacgg aggcagcagc agccactggg     180
gacagcatcg ctgtaaaaag cctaccaatg agagctcagt tcaaggcgaa ccaccccttc     240
ctgttcttta taaggcacac tcataccaac acgatcctat tctgtggcaa gcttgcctct     300
ccctaatcag atggggttga gtaaggctca gagttgcaga tgaggtgcag agacaatcct     360
gtgactttcc cacggccaaa aagctgttca cacctcacgc acctctgtgc ctcagtttgc     420
tcatctgcaa aataggtcta ggatttcttc caaccatttc atgagttgtg aagctaaggc     480
tttgttaatc atggaaaaag gtagacttat gcagaaagcc tttctggctt tcttatctgt     540
```

```
ggtgtctcat ttgagtgctg tccagtgaca tgatcaagtc aatgagtaaa attttaaggg      600
attagatttt cttgacttgt atgtatctgt gagatcttga ataagtgacc tgacatctct      660
gcttaaagaa aaccag                                                       676
```

        <210> 356
        <211> 574
        <212> DNA
        <213> Homo sapien

        <400> 356
```
ttttttttt tttttcagga aaacattctc ttactttatt tgcatctcag caaaggttct       60
catgtggcac ctgactggca tcaaaccaaa gttcgtaggc caacaaagat gggccactca      120
caagcttccc atttgtagat ctcagtgcct atgagtatct gacacctgtt cctctcttca      180
gtctcttagg gaggcttaaa tctgtctcag gtgtgctaag agtgccagcc caaggkggtc      240
aaaagtccac aaaactgcag tctttgctgg gatagtaagc caagcagtgc ctggacagca      300
gagttctttt cttgggcaac agataaccag acaggactct aatcgtgctc ttattcaaca      360
ttcttctgtc tctgcctaga ctggaataaa aagccaatct ctctcgtggc acagggaagg      420
agatacaagc tcgtttacat gtgatagatc taacaaaggc atctaccgaa gtctggtctg      480
gatagacggc acagggagct cttaggtcag cgctgctggt tggaggacat tcctgagtcc      540
agctttgcag cctttgtgca acagtacttt ccca                                  574
```

        <210> 357
        <211> 393
        <212> DNA
        <213> Homo sapien

        <400> 357
```
ttttttttt tttttttttt tttttttttt tacagaatat aratgcttta tcactgkact       60
taatatggkg kcttgttcac tatacttaaa aatgcaccac tcataaatat ttaattcagc      120
aagccacaac caaracttga ttttatcaac aaaaacccct aaatataaac ggsaaaaaag      180
atagatataa ttattccagt tttttaaaa cttaaaarat attccattgc cgaattaara      240
araarataag tgttatatgg aaagaagggc attcaagcac actaaaraaa cctgaggkaa      300
gcataatctg tacaaaatta aactgtcctt tttggcattt taacaaattt gcaacgktct      360
ttttttctt tttctgtttt tttttttttt tac                                    393
```

        <210> 358
        <211> 630
        <212> DNA
        <213> Homo sapien

        <400> 358
```
acagggtaaa caggaggatc cttgctctca cggagcttac attctagcag gaggacaata       60
ttaatgttta taggaaaatg atgagtttat gacaaaggaa gtagatagtg ttttacaaga      120
gcatagagta gggaagctaa tccagcacag ggaggtcaca gagacatccc taaggaagtg      180
gagtttaaac tgagagaagc aagtgcttaa actgaaggat gtgttgaaga agaagggaga      240
gtagaacaat ttgggcagag ggaaccttat agaccctaag gtgggaaggt tcaaagaact      300
gaaagagagc tagaacagct ggagccgttc tccggtgtaa agaggagtca aagagataag      360
attaaagatg tgaagattaa gatcttggtg gcattcaggg attggcactt ctacaagaaa      420
tcactgaagg gagtaatgtg acattacttt tcacttcagg atggccattc taactccagg      480
gggtagactg gactaggtaa gactggaggc aggtagacct cttctaaggc ctgcgatagt      540
gaaagacaaa aataagtggg gaaattcagg ggatagtgaa aatcagtagg acttaatgag      600
caagccagag gttcctccac aacaaccagt                                       630
```

        <210> 359
        <211> 620
        <212> DNA
        <213> Homo sapien

116

```
<400> 359
acagcattcc aaaatataca tctagagact aarrgtaaat gctctatagt gaagaagtaa        60
taattaaaaa atgctactaa tatagaaaat ttataatcag aaaaataaat attcagggag       120
ctcaccagaa gaataaagtg ctctgccagt tattaaagga ttactgctgg tgaattaaat       180
atggcattcc ccaagggaaa tagagagatt cttctggatt atgttcaata tttatttcac       240
aggattaact gttttaggaa cagatataaa gcttcgccac ggaagagatg gacaaagcac       300
aaagacaaca tgatacctta ggaagcaaca ctacccttc aggcataaaa tttggagaaa        360
tgcaacatta tgcttcatga ataatatgta gaaagaaggt ctgatgaaaa tgacatcctt       420
aatgtaagat aactttataa gaattctggg tcaaataaaa ttctttgaag aaaacatcca       480
aatgtcattg acttatcaaa tactatcttg gcatataacc tatgaaggca aaactaaaca       540
aacaaaaagc tcacaccaaa caaaaccatc aacttatttt gtattctata acatacgaga       600
ctgtaaagat gtgacagtgt                                                    620
```

```
<210> 360
<211> 431
<212> DNA
<213> Homo sapien
```

```
<400> 360
aaaaaaaaaa agccagaaca acatgtgata gataatatga ttggctgcac acttccagac        60
tgatgaatga tgaacgtgat ggactattgt atggagcaca tcttcagcaa gaggggggaaa      120
tactcatcat ttttggccag cagttgtttg atcaccaaac atcatgccag aatactcagc       180
aaaccttctt agctcttgag aagtcaaagt ccggggggaat ttattcctgg caattttaat      240
tggactcctt atgtgagagc agcggctacc cagctggggt ggtggagcga acccgtcact       300
agtggacatg cagtggcaga gctcctggta accacctaga ggaatacaca ggcacatgtg       360
tgatgccaag cgtgacacct gtagcactca aatttgtctt gtttttgtct ttcggtgtgt       420
agattcttag t                                                            431
```

```
<210> 361
<211> 351
<212> DNA
<213> Homo sapien
```

```
<400> 361
acactgattt ccgatcaaaa gaatcatcat ctttaccttg acttttcagg gaattactga        60
actttcttct cagaagatag ggcacagcca ttgccttggc ctcacttgaa gggtctgcat       120
ttgggtcctc tggtctcttg ccaagtttcc cagccactcg agggagaaat atcgggaggt       180
ttgacttcct ccggggcttt cccgagggct tcaccgtcga ccctgcggcc ctcagggctg       240
caatcctgga ttcaatgtct gaaacctcgc tctctgcctg ctggacttct gaggccgtca       300
ctgccactct gtcctccagc tctgacagct cctcatctgt ggtcctgttg t               351
```

```
<210> 362
<211> 463
<212> DNA
<213> Homo sapien
```

```
<400> 362
acttcatcag gccataatgg gtgcctcccg tgagaatcca agcacctttg gactgcgcga        60
tgtagatgag ccggctgaag atcttgcgca tgcgcggctt cagggcgaag ttcttggcgc       120
ccccggtcac agaaatgacc aggttgggtg ttttcaggtg ccagtgctgg gtcagcagct       180
cgtaaaggat ttccgcgtcc gtgtcgcagg acagacgtat atacttccct ttcttcccca       240
gtgtctcaaa ctgaatatcc ccaaaggcgt cggtaggaaa ttccttggtg tgtttcttgt       300
agttccattt ctcactttgg ttgatctggg tgccttccat gtgctggctc tgggcatagc       360
cacacttgca cacattctcc ctgataagca cgatggtgtg gacaggaagg aaggatttca       420
ttgagcctgc ttatggaaac tggtattgtt agcttaaata gac                        463
```

```
<210> 363
<211> 653
```

117

```
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(653)
<223> n = A,T,C or G

<400> 363
accccccgagt ncctgnctgg catactgnga acgaccaacg acacacccaa gctcggcctc      60
ctcttggnga ttctgggtga catcttcatg aatggcaacc gtgccagwga ggctgtcctc     120
tgggaggcac tacgcaagat gggactgcgt cctggggtga gacatcctct ccttggagat     180
ctaacgaaac ttctcaccta tgagttgtaa agcagaaata cctgnactac agacgagtgc     240
ccaacagcaa ccccccggaa gtatgagttc ctctrgggcc tccgttccta ccatgagasc     300
tagcaagatg naagtgttga gantcattgc agaggttcag aaaagagacc cntcgtgact     360
ggtctgcaca gttcatggag gctgcagatg aggccttgga tgctctggat gctgctgcag     420
ctgaggccga agcccgggct gaagcaagaa cccgcatggg aattggagat gaggctgtgt     480
ntgggccctg gagctgggat gacattgagt ttgagctgct gacctgggat gaggaaggag     540
attttggaga tccntggtcc agaattccat ttaccttctg ggccagatac caccagaatg     600
cccgctccag attccctcag acctttgccg gtcccattat tggtcstggt ggt            653

       <210> 364
       <211> 401
       <212> DNA
       <213> Homo sapien

<400> 364
actagaggaa agacgttaaa ccactctact accacttgtg gaactctcaa agggtaaatg      60
acaaagccaa tgaatgactc taaaaacaat atttacattt aatggtttgt agacaataaa     120
aaaacaaggt ggatagatct agaattgtaa cattttaaga aaaccatagc atttgacaga     180
tgagaaagct caattataga tgcaaagtta taactaaact actatagtag taaagaaata     240
catttcacac ccttcatata aattcactat cttggcttga ggcactccat aaaatgtatc     300
acgtgcatag taaatcttta tatttgctat ggcgttgcac tagaggactt ggactgcaac     360
aagtggatgc gcggaaaatg aaatcttctt caatagccca g                        401

       <210> 365
       <211> 356
       <212> DNA
       <213> Homo sapien

<400> 365
ccagtgtcat atttgggctt aaaatttcaa gaagggcact tcaaatggct ttgcatttgc      60
atgtttcagt gctagagcgt aggaatagac cctggcgtcc actgtgagat gttcttcagc     120
taccagagca tcaagtctct gcagcaggtc attcttgggt aaagaaatga cttccacaaa     180
ctctccatcc cctggctttg gcttcggcct tgcgttttcg gcatcatctc cgttaatggt     240
gactgtcacg atgtgtatag tacagtttga caagcctggg tccatacaga ccgctggaga     300
acattcggca atgtcccctt tgtagccagt ttcttcttcg agctcccgga gagcag        356

       <210> 366
       <211> 1851
       <212> DNA
       <213> Homo sapien

<400> 366
tcatcaccat tgccagcagc ggcaccgtta gtcaggtttt ctgggaatcc cacatgagta      60
cttccgtgtt cttcattctt cttcaatagc cataaatctt ctagctctgg ctggctgttt     120
tcacttcctt taagcctttg tgactcttcc tctgatgtca gctttaagtc ttgttctgga     180
ttgctgtttt cagaagagat ttttaacatc tgttttctt tgtagtcaga aagtaactgg     240
```

118

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caaattacat gatgatgact agaaacagca tactctctgg ccgtctttcc agatcttgag        300
aagatacatc aacattttgc tcaagtagag ggctgactat acttgctgat ccacaacata        360
cagcaagtat gagagcagtt cttccatatc tatccagcgc atttaaattc gctttttct         420
tgattaaaaa tttcaccact tgctgttttt gctcatgtat accaagtagc agtggtgtga        480
ggccatgctt gtttttgat tcgatatcag caccgtataa gagcagtgct ttggccatta         540
atttatcttc attgtagaca gcatagtgta gagtggtatt tccatactca tctggaatat        600
ttggatcagt gccatgttcc agcaacatta acgcacattc atcttcctgg cattgtacgg        660
cctttgtcag agctgtcctc ttttttgttgt caaggacatt aagttgacat cgtctgtcca        720
gcacgagttt tactacttct gaattcccat tggcagaggc cagatgtaga gcagtcctct        780
tttgcttgtc cctcttgttc acatccgtgt ccctgagcat gacgatgaga tcctttctgg        840
ggactttacc ccaccaggca gctctgtgga gcttgtccag atcttctcca tggacgtggt        900
acctgggatc catgaaggcg ctgtcatcgt agtctcccca agcgaccacg ttgctcttgc        960
cgctcccctg cagcaggga agcagtggca gcaccacttg cacctcttgc tcccaagcgt         1020
cttcacagag gagtcgttgt ggtctccaga agtgcccacg ttgctcttgc cgctccccct        1080
gtccatccag ggaggaagaa atgcaggaaa tgaaagatgc atgcacgatg gtatactcct         1140
cagccatcaa acttctggac agcaggtcac ttccagcaag gtggagaaag ctgtccaccc        1200
acagaggatg agatccagaa accacaatat ccattcacaa acaaacactt ttcagccaga        1260
cacaggtact gaaatcatgt catctgcggc aacatggtgg aacctaccca atcacacatc        1320
aagagatgaa gacactgcag tatatctgca caacgtaata ctcttcatcc ataacaaaat        1380
aatataattt tcctctggag ccatatggat gaactatgaa ggaagaactc cccgaagaag        1440
ccagtcgcag agaagccaca ctgaagctct gtcctcagcc atcagcgcca cggacaggar        1500
tgtgtttctt ccccagtgat gcagcctcaa gttatcccga agctgccgca gcacacggtg        1560
gctcctgaga aacaccccag ctcttccggt ctaacacagg caagtcaata aatgtgataa        1620
tcacataaac agaattaaaa gcaaagtcac ataagcatct caacagacac agaaaaggca        1680
tttgacaaaa tccagcatcc ttgtatttat tgttgcagtt ctcagaggaa atgcttctaa        1740
cttttcccca tttagtatta tgttggctgt gggcttgtca taggtggttt ttattacttt        1800
aaggtatgtc ccttctatgc ctgttttgct gagggtttta attctcgtgc c                1851
```

        <210> 367
        <211> 668
        <212> DNA
        <213> Homo sapien

        <400> 367

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cttgagcttc caaataygga agactggccc ttacacasgt caatgttaaa atgaatgcat        60
ttcagtattt tgaagataaa attrgtagat ctataccttg ttttttgatt cgatatcagc        120
accrtataag agcagtgctt tggccattaa tttatctttc attrtagaca gcrtagtgya        180
gagtggtatt tccatactca tctggaatat ttggatcagt gccatgttcc agcaacatta        240
acgcacattc atcttcctgg cattgtacgg cctgtcagta ttagacccaa aaacaaatta        300
catatcttag gaattcaaaa taacattcca cagctttcac caactagtta tatttaaagg        360
agaaactca ttttatgcc atgtattgaa atcaaaccca cctcatgctg atatagttgg         420
ctactgcata cctttatcag agctgtcctc ttttttgttgt caaggacatt aagttgacat        480
cgtctgtcca gcaggagttt tactacttct gaattcccat tggcagaggc cagatgtaga        540
gcagtcctat gagagtgaga agactttta ggaaattgta gtgcactagc tacagccata         600
gcaatgattc atgtaactgc aaacactgaa tagcctgcta ttactctgcc ttcaaaaaaa        660
aaaaaaaa                                                                 668
```

        <210> 368
        <211> 1512
        <212> DNA
        <213> Homo sapien

        <400> 368

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gggtcgccca gggggsgcgt gggctttcct cgggtgggtg tgggtttttcc ctgggtgggg       60
tgggctgggc trgaatcccc tgctggggtt ggcaggtttt ggctgggatt gactttttytc       120
ttcaaacaga ttggaaaccc ggagttacct gctagttggt gaaactggtt ggtagacgcg        180
atctgttggc tactactggc ttctcctggc tgttaaaagc agatggtggt tgaggttgat        240
tccatgccgg ctgcttcttc tgtgaagaag ccatttggtc tcaggagcaa gatgggcaag        300
```

119

```
tggtgctgcc gttgcttccc ctgctgcagg gagagcggca agagcaacgt gggcacttct    360
ggagaccacg acgactctgc tatgaagaca ctcaggagca agatgggcaa gtggtgccgc    420
cactgcttcc cctgctgcag gggggagtggc aagagcaacg tgggcgcttc tggagaccac    480
gacgaytctg ctatgaagac actcaggaac aagatgggca agtggtgctg ccactgcttc    540
ccctgctgca ggggggagcrg caagagcaag gtgggcgctt ggggagacta cgatgacagt    600
gccttcatgg agcccaggta ccacgtccgt ggagaagatc tggacaagct ccacagagct    660
gcctggtggg gtaaagtccc cagaaaggat ctcatcgtca tgctcaggga cactgacgtg    720
aacaagaagg acaagcaaaa gaggactgct ctacatctgg cctctgccaa tgggaattca    780
gaagtagtaa aactcstgct ggacagacga tgtcaactta atgtccttga caacaaaaag    840
aggacagctc tgayaaaggc cgtacaatgc caggaagatg aatgtgcgtt aatgttgctg    900
gaacatggca ctgatccaaa tattccagat gagtatggaa ataccactct rcactaygct    960
rtctayaatg aagataaatt aatggccaaa gcactgctct tatayggtgc tgatatcgaa   1020
tcaaaaaaca aggtatagat ctactaattt tatcttcaaa atactgaaat gcattcattt    1080
taacattgac gtgtgtaagg gccagtcttc cgtatttgga agctcaagca taacttgaat   1140
gaaaatattt tgaaatgacc taattatctm agactttatt ttaaatattg ttattttcaa   1200
agaagcatta gagggtacag ttttttttttt ttaaatgcac ttctggtaaa tacttttgtt   1260
gaaaacactg aatttgtaaa aggtaatact tactatttt caattttttcc ctcctaggat   1320
ttttttcccc taatgaatgt aagatggcaa aatttgccct gaaataggtt ttacatgaaa   1380
actccaagaa aagttaaaca tgtttcagtg aatagagatc ctgctccttt ggcaagttcc   1440
taaaaaacag taatagatac gaggtgatgc gcctgtcagt ggcaaggttt aagatatttc   1500
tgatctcgtg cc                                                       1512
```

        <210> 369
        <211> 1853
        <212> DNA
        <213> Homo sapien

        <400> 369

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gggtcgccca gggggsgcgt gggctttcct cgggtgggtg tgggtttttcc ctgggtgggg     60
tgggctgggc trgaatcccc tgctgggggtt ggcaggtttt ggctgggatt gacttttytc    120
ttcaaacaga ttggaaaccc ggagttacct gctagttggt gaaactggtt ggtagacgcg    180
atctgttggc tactactggc ttctcctggc tgttaaaagc agatggtggt tgaggttgat    240
tccatgccgg ctgcttcttc tgtgaagaag ccatttggtc tcaggagcaa gatgggacagt    300
tggtgctgcc gttgcttccc ctgctgcagg gagagcggca agagcaacgt gggcacttct    360
ggagaccacg acgactctgc tatgaagaca ctcaggagca agatgggcaa gtggtgccgc    420
cactgcttcc cctgctgcag gggggagtggc aagagcaacg tgggcgcttc tggagaccac    480
gacgaytctg ctatgaagac actcaggaac aagatgggca agtggtgctg ccactgcttc    540
ccctgctgca ggggggagcrg caagagcaag gtgggcgctt ggggagacta cgatgacagy    600
gccttcatgg akcccaggta ccacgtccrt ggagaagatc tggacaagct ccacagagct    660
gcctggtggg gtaaagtccc cagaaaggat ctcatcgtca tgctcaggga cackgaygtg    720
aacaagargg acaagcaaaa gaggactgct ctacatctgg cctctgccaa tgggaattca    780
gaagtagtaa aactcstgct ggacagacga tgtcaactta atgtccttga caacaaaaag    840
aggacagctc tgayaaaggc cgtacaatgc caggaagatg aatgtgcgtt aatgttgctg    900
gaacatggca ctgatccaaa tattccagat gagtatggaa ataccactct rcactaygct    960
rtctayaatg aagataaatt aatggccaaa gcactgctct tatayggtgc tgatatcgaa   1020
tcaaaaaaca agcatggcct cacaccactg ytacttggtr tacatgagca aaaacagcaa   1080
gtsgtgaaat ttttaatyaa gaaaaaagcg aatttaaaat gcrctggata gatatggaag   1140
ractgctctc atacttgctg tatgttgtgg atcagcaagt atagtcagcc ytctacttga   1200
gcaaaatrtt gatgtatctt ctcaagatct ggaaagacgg ccagagagta tgctgtttct   1260
agtcatcatc atgtaatttg ccagttactt tctgactaca aagaaaaaca gatgttaaaa   1320
atctcttctg aaaacagcaa tccagaacaa gacttaaagc tgacatcaga ggaagagtca   1380
caaaggctta aaggaagtga aaacagccag ccagaggcat ggaaactttt aaatttaaac   1440
ttttggttta atgttttttt ttttttgcctt aataatatta gatagtccca aatgaaatwa   1500
cctatgagac taggctttga gaatcaatag attcttttttt taagaatctt ttggctagga   1560
gcggtgtctc acgcctgtaa ttccagcacc ttgagaggct gaggtgggca gatcacgaga   1620
tcaggagatc gagaccatcc tggctaacac ggtgaaaccc catctctact aaaaatacaa   1680
aaacttagct gggtgtggtg gcgggtgcct gtagtcccag ctactcagga rgctgaggca   1740
ggagaatggc atgaacccgg gaggtggagg ttgcagtgag ccgagatccg ccactacact   1800
```

120

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ccagcctggg tgacagagca agactctgtc tcaaaaaaaa aaaaaaaaaa aaa                  1853

        <210> 370
        <211> 2184
        <212> DNA
        <213> Homo sapien

        <400> 370
ggcacgagaa ttaaaaccct cagcaaaaca ggcatagaag ggacatacct taaagtaata         60
aaaaccacct atgacaagcc cacagccaac ataatactaa atggggaaaa gttagaagca        120
tttcctctga gaactgcaac aataaataca aggatgctgg attttgtcaa atgccttttc        180
tgtgtctgtt gagatgctta tgtgactttg cttttaattc tgtttatgtg attatcacat        240
ttattgactt gcctgtgtta gaccggaaga gctggggtgt ttctcaggag ccaccgtgtg        300
ctgcggcagc ttcgggataa cttgaggctg catcactggg gaagaaacac aytcctgtcc        360
gtggcgctga tggctgagga cagagcttca gtgtggcttc tctgcgactg gcttcttcgg        420
ggagttcttc cttcatagtt catccatatg gctccagagg aaaattatat tattttgtta        480
tggatgaaga gtattacgtt gtgcagatat actgcagtgt cttcatctct tgatgtgtga        540
ttgggtaggt tccaccatgt tgccgcagat gacatgattt cagtacctgt gtctggctga        600
aaagtgtttg tttgtgaatg gatattgtgg tttctggatc tcatcctctg tgggtggaca        660
gctttctcca ccttgctgga agtgacctgc tgtccagaag tttgatggct gaggagtata        720
ccatcgtgca tgcatctttc atttcctgca tttcttcctc cctggatgga cagggggagc        780
ggcaagagca acgtgggcac ttctggagac cacaacgact cctctgtgaa gacgcttggg        840
agcaagaggt gcaagtggtg ctgccactgc ttcccctgct gcaggggagc ggcaagagca        900
acgtggtcgc ttggggagac tacgatgaca gcgccttcat ggatcccagg taccacgtcc        960
atggagaaga tctggacaag ctcccacagag ctgcctggtg gggtaaagtc cccagaaagg       1020
atctcatcgt catgctcagg gacacggatg tgaacaagag ggacaagcaa aagaggactg       1080
ctctacatct ggcctctgcc aatgggaatt cagaagtagt aaaactcgtg ctggacagac       1140
gatgtcaact taatgtcctt gacaacaaaa agaggacagc tctgacaaag gccgtacaat       1200
gccaggaaga tgaatgtgcg ttaatgttgc tggaacatgg cactgatcca aatattccag       1260
atgagtatgg aaataccact ctacactatg ctgtctacaa tgaagataaa ttaatggcca       1320
aagcactgct cttatacggt gctgatatcg aatcaaaaaa caagcatggc ctcacaccac       1380
tgctacttgg tatacatgag caaaaacagc aagtggtgaa attttttaatc aagaaaaaag       1440
cgaatttaaa tgcgctggat agatatggaa gaactgctct catacttgct gtatgttgtg       1500
gatcagcaag tatagtcagc cctctacttg agcaaaatgt tgatgtatct tctcaagatc       1560
tggaaagacg gccagagagt atgctgtttc tagtcatcat catgtaattt gccagttact       1620
ttctgactac aaagaaaaac agatgttaaa aatctcttct gaaaacagca atccagaaca       1680
agacttaaag ctgacatcag aggaagagtc acaaaggctt aaaggaagtg aaaacagcca       1740
gccagaggca tggaaacttt taaatttaaa cttttggttt aatgtttttt tttttttgcct       1800
taataatatt agatagtccc aaatgaaatw acctatgaga ctaggctttg agaatcaata       1860
gattctttt ttaagaatct tttggctagg agcggtgtct cacgcctgta attccagcac       1920
cttgagaggc tgaggtgggc agatcacgag atcaggagat cgagaccatc ctggctaaca       1980
cggtgaaacc ccatctctac taaaaataca aaaacttagc tgggtgtggt ggcgggtgcc       2040
tgtagtccca gctactcagg argctgaggc aggagaatgg catgaacccg ggaggtggag       2100
gttgcagtga gccgagatcc gccactacac tccagcctgg tgacagagc aagactctgt       2160
ctcaaaaaaa aaaaaaaaaa aaaa                                             2184

        <210> 371
        <211> 1855
        <212> DNA
        <213> Homo sapien

        <220>
        <221> misc_feature
        <222> (1)...(1855)
        <223> n = A,T,C or G

        <400> 371
tgcacgcatc ggccagtgtc tgtgccacgt acactgacgc cccctgagat gtgcacgccg        60
```

121

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cacgcgcacg ttgcacgcgc ggcagcggct tggctggctt gtaacggctt gcacgcgcac      120
gccgccccg cataaccgtc agactggcct gtaacggctt gcaggcgcac gccgcacgcg      180
cgtaacggct tggctgccct gtaacggctt gcacgtgcat gctgcacgcg cgttaacggc      240
ttggctggca tgtagccgct tggcttggct ttgcattytt tgctkggctk ggcgttgkty     300
tcttggattg acgcttcctc cttggatkga cgtttcctcc ttggatkgac gtttcytyty     360
tcgcgttcct ttgctggact tgacctttty tctgctgggt ttggcattcc tttggggtgg     420
gctgggtgtt ttctccgggg gggktkgccc ttcctggggt gggcgtgggk cgccccagg     480
gggcgtgggc tttccccggg tgggtgtggg ttttcctggg gtggggtggg ctgtgctggg     540
atccccctgc tggggttggc agggattgac ttttttcttc aaacagattg gaaacccgga     600
gtaacntgct agttggtgaa actggttggt agacgcgatc tgctggtact actgtttctc      660
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agaagccatt tggtctcagg agcaagatgg gcaagtggtg cgccactgct tcccctgctg      780
caggggagc ggcaagagca acgtgggcac ttctggagac cacaacgact cctctgtgaa     840
gacgcttggg agcaagaggt gcaagtggtg ctgcccactg cttcccctgc tgcaggggag      900
cggcaagagc aacgtggkcg cttggggaga ctacgatgac agcgccttca tggakcccag      960
gtaccacgtc crtggagaag atctggacaa gctccacaga gctgcctggt ggggtaaagt     1020
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aaagaggact gctctacatc tggcctctgc caatgggaat tcagaagtag taaaactcgt     1140
gctggacaga cgatgtcaac ttaatgtcct tgacaacaaa aagaggacag ctctgacaaa     1200
ggccgtacaa tgccaggaag atgaatgtgc gttaatgttg ctggaacatg gcactgatcc     1260
aaatattcca gatgagtatg gaaataccac tctacactat gctgtctaca atgaagataa     1320
attaatggcc aaagcactgc tcttatacgg tgctgatatc gaatcaaaaa acaaggtata     1380
gatctactaa ttttatcttc aaaatactga aatgcattca ttttaacatt gacgtgtgta     1440
agggccagtc ttccgtattt ggaagctcaa gcataacttg aatgaaaata ttttgaaatg     1500
acctaattat ctaagacttt attttaaata ttgttatttt caaagaagca ttagagggta     1560
cagtttttt tttttaaatg cacttctggt aaatacttt gttgaaaaca ctgaatttgt      1620
aaaaggtaat acttactatt tttcaatttt tccctcctag gatttttttc ccctaatgaa     1680
tgtaagatgg caaaatttgc cctgaaatag gttttacatg aaaactccaa gaaaagttaa      1740
acatgtttca gtgaatagag atcctgctcc tttggcaagt tcctaaaaaa cagtaataga      1800
tacgaggtga tgcgcctgtc agtggcaagg tttaagatat ttctgatctc gtgcc          1855
```

        <210> 372
        <211> 1059
        <212> DNA
        <213> Homo sapien

        <400> 372
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gcaacgtggg cacttctgga gaccacaacg actcctctgt gaagacgctt gggagcaaga      60
ggtgcaagtg gtgctgccca ctgcttcccc tgctgcaggg gagcggcaag agcaacgtgg      120
gcgcttgrgg agactmcgat gacagygcct tcatggagcc caggtaccac gtccgtggag      180
aagatctgga caagctccac agagctgccc tggtggggta aagtccccag aaaggatctc      240
atcgtcatgc tcagggacac tgaygtgaac aagarggaac agcaaaagag gactgctcta      300
catctggcct ctgccaatgg gaattcagaa gtagtaaaac tcstgctgga cagacgatgt      360
caacttaatg tccttgacaa caaaaagagg acagctctga yaaaggccgt acaatgccag      420
gaagatgaat gtgcgttaat gttgctggaa catggcactg atccaaatat tccagatgag      480
tatgaaaata ccactctrca ctaygctrtc tayaatgaag ataaattaat ggccaaagca      540
ctgctcttat ayggtgctga tatcgaatca aaaacaagg tatagatcta ctaattttat      600
cttcaaaata ctgaaatgca ttcattttaa cattgacgtg tgtaagggcc agtcttccgt      660
atttggaagc tcaagcataa cttgaatgaa aatattttga aatgacctaa ttatctaaga      720
cttttatttta aatattgtta ttttcaaaga agcattagag ggtacagttt ttttttttta      780
aatgcacttc tggtaaatac ttttgttgaa aacactgaat ttgtaaaagg taatacttac      840
tattttccctc ctaggatttt tttccccctaa tgaatgtaag atggcaaaat      900
ttgccctgaa ataggtttta catgaaaact ccaagaaaag ttaaacatgt ttcagtgaat      960
agagatcctg ctcctttggc aagttcctaa aaaacagtaa tagatacgag gtgatgcgcc     1020
tgtcagtggc aaggtttaag atatttctga tctcgtgcc                          1059
```

        <210> 373
        <211> 1155

122

<210> 374

```
    <212> DNA
    <213> Homo sapien

    <400> 373
atggtggttg aggttgattc catgccggct gcctcttctg tgaagaagcc atttggtctc         60
aggagcaaga tgggcaagtg gtgctgccgt tgcttcccct gctgcaggga gagcggcaag        120
agcaacgtgg gcacttctgg agaccacgac gactctgcta tgaagacact caggagcaag        180
atgggcaagt ggtgccgcca ctgcttcccc tgctgcaggg ggagtggcaa gagcaacgtg        240
ggcgcttctg gagaccacga cgactctgct atgaagacac tcaggaacaa gatgggcaag        300
tggtgctgcc actgcttccc ctgctgcagg gggagcggca gagcaaggt gggcgcttgg        360
ggagactacg atgacagtgc cttcatggag cccaggtacc acgtccgtgg agaagatctg        420
gacaagctcc acagagctgc ctggtggggt aaagtcccca gaaaggatct catcgtcatg        480
ctcagggaca ctgacgtgaa caagaaggac aagcaaaaga ggactgctct acatctggcc        540
tctgccaatg ggaattcaga agtagtaaaa ctcctgctgg acagacgatg tcaacttaat        600
gtccttgaca acaaaaagag gacagctctg ataaaggccg tacaatgcca ggaagatgaa        660
tgtgcgttaa tgttgctgga acatggcact gatccaaata ttccagatga gtatggaaat        720
accactctgc actacgctat ctataatgaa gataaattaa tggccaaagc actgctctta        780
tatggtgctg atatcgaatc aaaaaacaag catggcctca caccactgtt acttggtgta        840
catgagcaaa aacagcaagt cgtgaaattt ttaatcaaga aaaaagcgaa tttaaatgca        900
ctggatagat atggaaggac tgctctcata cttgctgtat gttgtggatc agcaagtata        960
gtcagccttc tacttgagca aaatattgat gtatcttctc aagatctatc tggacagacg       1020
gccagagagt atgctgtttc tagtcatcat catgtaattt gccagttact ttctgactac       1080
aaagaaaaac agatgctaaa aatctcttct gaaacagca atccagaaaa tgtctcaaga       1140
accagaaata aataa                                                        1155
```

```
        <210> 374
        <211> 2000
        <212> DNA
        <213> Homo sapien

        <400> 374
atggtggttg aggttgattc catgccggct gcctcttctg tgaagaagcc atttggtctc         60
aggagcaaga tgggcaagtg gtgctgccgt tgcttcccct gctgcaggga gagcggcaag        120
agcaacgtgg gcacttctgg agaccacgac gactctgcta tgaagacact caggagcaag        180
atgggcaagt ggtgccgcca ctgcttcccc tgctgcaggg ggagtggcaa gagcaacgtg        240
ggcgcttctg gagaccacga cgactctgct atgaagacac tcaggaacaa gatgggcaag        300
tggtgctgcc actgcttccc ctgctgcagg gggagcggca gagcaaggt gggcgcttgg        360
ggagactacg atgacagtgc cttcatggag cccaggtacc acgtccgtgg agaagatctg        420
gacaagctcc acagagctgc ctggtggggt aaagtcccca gaaaggatct catcgtcatg        480
ctcagggaca ctgacgtgaa caagaaggac aagcaaaaga ggactgctct acatctggcc        540
tctgccaatg ggaattcaga agtagtaaaa ctcctgctgg acagacgatg tcaacttaat        600
gtccttgaca acaaaaagag gacagctctg ataaaggccg tacaatgcca ggaagatgaa        660
tgtgcgttaa tgttgctgga acatggcact gatccaaata ttccagatga gtatggaaat        720
accactctgc actacgctat ctataatgaa gataaattaa tggccaaagc actgctctta        780
tatggtgctg atatcgaatc aaaaaacaag catggcctca caccactgtt acttggtgta        840
catgagcaaa aacagcaagt cgtgaaattt ttaatcaaga aaaaagcgaa tttaaatgca        900
ctggatagat atggaaggac tgctctcata cttgctgtat gttgtggatc agcaagtata        960
gtcagccttc tacttgagca aaatattgat gtatcttctc aagatctatc tggacagacg       1020
gccagagagt atgctgtttc tagtcatcat catgtaattt gccagttact ttctgactac       1080
aaagaaaaac agatgctaaa aatctcttct gaaacagca atccagaaca agacttaaag       1140
ctgacatcag aggaagagtc acaaaggttc aaaggcagtg aaaatagcca gccagagaaa       1200
atgtctcaag aaccagaaat aaataaggat ggtgatagag aggttgaaga agaaatgaag       1260
aagcatgaaa gtaataatgt gggattacta gaaaacctga ctaatggtgt cactgctggc       1320
aatggtgata atggattaat tcctcaaagg aagagcagaa cacctgaaaa tcagcaattt       1380
cctgacaacg aaagtgaaga gtatcacaga atttgcgaat tagtttctga ctacaaagaa       1440
aaacagatgc caaaatactc ttctgaaaac agcaacccag aacaagactt aaagctgaca       1500
tcagaggaag agtcacaaag gcttgagggc agtgaaaatg ccagccaga gctagaaaat       1560
tttatggcta tcgaagaaat gaagaagcac ggaagtactc atgtcggatt cccagaaaac       1620
```

123

```
ctgactaatg gtgccactgc tggcaatggt gatgatggat taattcctcc aaggaagagc    1680
agaacacctg aaagccagca atttcctgac actgagaatg aagagtatca cagtgacgaa    1740
caaaatgata ctcagaagca attttgtgaa gaacagaaca ctggaatatt acacgatgag    1800
attctgattc atgaagaaaa gcagatagaa gtggttgaaa aaatgaattc tgagctttct    1860
cttagttgta agaaagaaaa agacatcttg catgaaaata gtacgttgcg ggaagaaatt    1920
gccatgctaa gactggagct agacacaatg aaacatcaga gccagctaaa aaaaaaaaaa    1980
aaaaaaaaaa aaaaaaaaaa                                                2000
```

        <210> 375
        <211> 2040
        <212> DNA
        <213> Homo sapien

        <400> 375
```
atggtggttg aggttgattc catgccggct gcctcttctg tgaagaagcc atttggtctc     60
aggagcaaga tgggcaagtg gtgctgccgt tgcttcccct gctgcaggga gagcggcaag    120
agcaacgtgg gcacttctgg agaccacgac gactctgcta tgaagacact caggagcaag    180
atgggcaagt ggtgccgcca ctgcttcccc tgctgcaggg ggagtggcaa gagcaacgtg    240
ggcgcttctg agaccacga cgactctgct atgaagacac tcaggaacaa gatgggcaag    300
tggtgctgcc actgcttccc ctgctgcagg gggagcggca gagcaaggt gggcgcttgg    360
ggagactacg atgacagtgc cttcatggag cccaggtacc acgtccgtgg agaagatctg    420
gacaagctcc acagagctgc ctggtggggt aaagtcccca gaaaggatct catcgtcatg    480
ctcagggaca ctgacgtgaa caagaaggac aagcaaaaga ggactgctct acatctggcc    540
tctgccaatg ggaattcaga agtagtaaaa ctcctgctgg acagacgatg tcaacttaat    600
gtccttgaca acaaaaagag gacagctctg ataaaggccg tacaatgcca ggaagatgaa    660
tgtgcgttaa tgttgctgga acatggcact gatccaaata ttccagatga gtatggaaat    720
accactctgc actacgctat ctataatgaa gataaattaa tggccaaagc actgctctta    780
tatggtgctg atatcgaatc aaaaaacaag catggcctca caccactgtt acttggtgta    840
catgagcaaa aacagcaagt cgtgaaattt ttaatcaaga aaaaagcgaa tttaaatgca    900
ctggatagat atggaaggac tgctctcata cttgctgtat gttgtggatc agcaagtata    960
gtcagccttc tacttgagca aaatattgat gtatcttctc aagatctatc tggacagacg   1020
gccagagagt atgctgtttc tagtcatcat catgtaattt gccagttact ttctgactac   1080
aaagaaaaac agatgctaaa aatctcttct gaaaacagca atccagaaca agacttaaag   1140
ctgacatcag aggaagagtc acaaaggttc aaaggcagtg aaaatagcca gccagagaaa   1200
atgtctcaag aaccagaaat aaataaggat ggtgatagag aggttgaaga agaaatgaag   1260
aagcatgaaa gtaataatgt gggattacta gaaaacctga ctaatggtgt cactgctggc   1320
aatggtgata atggattaat tcctcaaagg aagagcagaa cacctgaaaa tcagcaattt   1380
cctgacaacg aaagtgaaga gtatcacaga atttgcgaat tagtttctga ctacaaagaa   1440
aaacagatgc caaaatactc ttctgaaaac agcaacccag aacaagactt aaagctgaca   1500
tcagaggaag agtcacaaag gcttgagggc agtgaaaatg gccagccaga gaaaagatct   1560
caagaaccag aaataaataa ggatggtgat agagagctag aaaattttat ggctatcgaa   1620
gaaatgaaga agcacggaag tactcatgtc ggattcccag aaaacctgac taatggtgcc   1680
actgctggca atggtgatga tggattaatt cctccaagga gagcagaac acctgaaagc   1740
cagcaatttc ctgacactga gaatgaagag tatcacagtg acgaacaaaa tgatactcag   1800
aagcaatttt gtgaagaaca gaacactgga atattacacg atgagattct gattcatgaa   1860
gaaaagcaga tagaagtggt tgaaaaaatg aattctgagc tttctcttag ttgtaagaaa   1920
gaaaaagaca tcttgcatga aaatagtacg ttgcgggaag aaattgccat gctaagactg   1980
gagctagaca caatgaaaca tcagagccag ctaaaaaaaa aaaaaaaaaa aaaaaaaaaa   2040
```

        <210> 376
        <211> 329
        <212> PRT
        <213> Homo sapien

        <400> 376
```
Met Asp Ile Val Val Ser Gly Ser His Pro Leu Trp Val Asp Ser Phe
1               5                   10                  15
Leu His Leu Ala Gly Ser Asp Leu Leu Ser Arg Ser Leu Met Ala Glu
```

```
            20                    25                    30
Glu Tyr Thr Ile Val His Ala Ser Phe Ile Ser Cys Ile Ser Ser Ser
        35                    40                    45
Leu Asp Gly Gln Gly Glu Arg Gln Glu Gln Arg Gly His Phe Trp Arg
    50                    55                    60
Pro Gln Arg Leu Leu Cys Glu Asp Ala Trp Glu Gln Glu Val Gln Val
65                    70                    75                    80
Val Leu Pro Leu Leu Pro Leu Leu Gln Gly Ser Gly Lys Ser Asn Val
                85                    90                    95
Val Ala Trp Gly Asp Tyr Asp Asp Ser Ala Phe Met Asp Pro Arg Tyr
            100                   105                   110
His Val His Gly Glu Asp Leu Asp Lys Leu His Arg Ala Ala Trp Trp
        115                   120                   125
Gly Lys Val Pro Arg Lys Asp Leu Ile Val Met Leu Arg Asp Thr Asp
    130                   135                   140
Val Asn Lys Arg Asp Lys Gln Lys Arg Thr Ala Leu His Leu Ala Ser
145                  ·150                   155                   160
Ala Asn Gly Asn Ser Glu Val Val Lys Leu Val Leu Asp Arg Arg Cys
                165                   170                   175
Gln Leu Asn Val Leu Asp Asn Lys Lys Arg Thr Ala Leu Thr Lys Ala
            180                   185                   190
Val Gln Cys Gln Glu Asp Glu Cys Ala Leu Met Leu Leu Glu His Gly
        195                   200                   205
Thr Asp Pro Asn Ile Pro Asp Glu Tyr Gly Asn Thr Thr Leu His Tyr
    210                   215                   220
Ala Val Tyr Asn Glu Asp Lys Leu Met Ala Lys Ala Leu Leu Leu Tyr
225                   230                   235                   240
Gly Ala Asp Ile Glu Ser Lys Asn Lys His Gly Leu Thr Pro Leu Leu
                245                   250                   255
Leu Gly Ile His Glu Gln Lys Gln Gln Val Val Lys Phe Leu Ile Lys
            260                   265                   270
Lys Lys Ala Asn Leu Asn Ala Leu Asp Arg Tyr Gly Arg Thr Ala Leu
        275                   280                   285
Ile Leu Ala Val Cys Cys Gly Ser Ala Ser Ile Val Ser Pro Leu Leu
    290                   295                   300
Glu Gln Asn Val Asp Val Ser Ser Gln Asp Leu Glu Arg Arg Pro Glu
305                   310                   315                   320
Ser Met Leu Phe Leu Val Ile Ile Met
                325
```

```
        <210> 377
        <211> 148
        <212> PRT
        <213> Homo sapien

        <220>
        <221> VARIANT
        <222> (1)...(148)
        <223> Xaa = Any Amino Acid

        <400> 377
Met Thr Xaa Pro Ser Trp Ser Pro Gly Thr Thr Ser Val Glu Lys Ile
1                5                    10                   15
Trp Thr Ser Ser Thr Glu Leu Pro Trp Trp Gly Lys Val Pro Arg Lys
            20                    25                    30
Asp Leu Ile Val Met Leu Arg Asp Thr Asp Val Asn Lys Xaa Asp Lys
        35                    40                    45
Gln Lys Arg Thr Ala Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu
```

125

```
       50                    55                    60
Val Val Lys Leu Xaa Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp
65                    70                    75                    80
Asn Lys Lys Arg Thr Ala Leu Xaa Lys Ala Val Gln Cys Gln Glu Asp
              85                    90                    95
Glu Cys Ala Leu Met Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro
              100                   105                   110
Asp Glu Tyr Gly Asn Thr Thr Leu His Tyr Ala Xaa Tyr Asn Glu Asp
          115                   120                   125
Lys Leu Met Ala Lys Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu Ser
    130                   135                   140
Lys Asn Lys Val
145


        <210> 378
        <211> 1719
        <212> PRT
        <213> Homo sapien


        <400> 378
Met Val Val Glu Val Asp Ser Met Pro Ala Ala Ser Ser Val Lys Lys
1                 5                    10                   15
Pro Phe Gly Leu Arg Ser Lys Met Gly Lys Trp Cys Cys Arg Cys Phe
              20                    25                   30
Pro Cys Cys Arg Glu Ser Gly Lys Ser Asn Val Gly Thr Ser Gly Asp
          35                    40                    45
His Asp Asp Ser Ala Met Lys Thr Leu Arg Ser Lys Met Gly Lys Trp
    50                    55                    60
Cys Arg His Cys Phe Pro Cys Cys Arg Gly Ser Gly Lys Ser Asn Val
65                    70                    75                    80
Gly Ala Ser Gly Asp His Asp Asp Ser Ala Met Lys Thr Leu Arg Asn
              85                    90                    95
Lys Met Gly Lys Trp Cys Cys His Cys Phe Pro Cys Cys Arg Gly Ser
              100                   105                   110
Gly Lys Ser Lys Val Gly Ala Trp Gly Asp Tyr Asp Asp Ser Ala Phe
          115                   120                   125
Met Glu Pro Arg Tyr His Val Arg Gly Glu Asp Leu Asp Lys Leu His
    130                   135                   140
Arg Ala Ala Trp Trp Gly Lys Val Pro Arg Lys Asp Leu Ile Val Met
145                   150                   155                   160
Leu Arg Asp Thr Asp Val Asn Lys Lys Asp Lys Gln Lys Arg Thr Ala
              165                   170                   175
Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu Val Val Lys Leu Leu
          180                   185                   190
Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp Asn Lys Lys Arg Thr
          195                   200                   205
Ala Leu Ile Lys Ala Val Gln Cys Gln Glu Asp Glu Cys Ala Leu Met
    210                   215                   220
Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro Asp Glu Tyr Gly Asn
225                   230                   235                   240
Thr Thr Leu His Tyr Ala Ile Tyr Asn Glu Asp Lys Leu Met Ala Lys
              245                   250                   255
Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu Ser Lys Asn Lys His Gly
          260                   265                   270
Leu Thr Pro Leu Leu Leu Gly Val His Glu Gln Lys Gln Gln Val Val
          275                   280                   285
Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu Asn Ala Leu Asp Arg Tyr
    290                   295                   300
```

126

```
Gly Arg Thr Ala Leu Ile Leu Ala Val Cys Cys Gly Ser Ala Ser Ile
305                 310                 315                 320
Val Ser Leu Leu Leu Glu Gln Asn Ile Asp Val Ser Ser Gln Asp Leu
                325                 330                 335
Ser Gly Gln Thr Ala Arg Glu Tyr Ala Val Ser Ser His His His Val
            340                 345                 350
Ile Cys Gln Leu Leu Ser Asp Tyr Lys Glu Lys Gln Met Leu Lys Ile
        355                 360                 365
Ser Ser Glu Asn Ser Asn Pro Glu Asn Val Ser Arg Thr Arg Asn Lys
    370                 375                 380
Pro Arg Thr His Met Val Val Glu Val Asp Ser Met Pro Ala Ala Ser
385                 390                 395                 400
Ser Val Lys Lys Pro Phe Gly Leu Arg Ser Lys Met Gly Lys Trp Cys
                405                 410                 415
Cys Arg Cys Phe Pro Cys Cys Arg Glu Ser Gly Lys Ser Asn Val Gly
            420                 425                 430
Thr Ser Gly Asp His Asp Asp Ser Ala Met Lys Thr Leu Arg Ser Lys
            435                 440                 445
Met Gly Lys Trp Cys Arg His Cys Phe Pro Cys Cys Arg Gly Ser Gly
    450                 455                 460
Lys Ser Asn Val Gly Ala Ser Gly Asp His Asp Asp Ser Ala Met Lys
465                 470                 475                 480
Thr Leu Arg Asn Lys Met Gly Lys Trp Cys Cys His Cys Phe Pro Cys
            485                 490                 495
Cys Arg Gly Ser Gly Lys Ser Lys Val Gly Ala Trp Gly Asp Tyr Asp
            500                 505                 510
Asp Ser Ala Phe Met Glu Pro Arg Tyr His Val Arg Gly Glu Asp Leu
        515                 520                 525
Asp Lys Leu His Arg Ala Ala Trp Trp Gly Lys Val Pro Arg Lys Asp
    530                 535                 540
Leu Ile Val Met Leu Arg Asp Thr Asp Val Asn Lys Lys Asp Lys Gln
545                 550                 555                 560
Lys Arg Thr Ala Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu Val
            565                 570                 575
Val Lys Leu Leu Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp Asn
            580                 585                 590
Lys Lys Arg Thr Ala Leu Ile Lys Ala Val Gln Cys Gln Glu Asp Glu
    595                 600                 605
Cys Ala Leu Met Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro Asp
610                 615                 620
Glu Tyr Gly Asn Thr Thr Leu His Tyr Ala Ile Tyr Asn Glu Asp Lys
625                 630                 635                 640
Leu Met Ala Lys Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu Ser Lys
                645                 650                 655
Asn Lys His Gly Leu Thr Pro Leu Leu Leu Gly Val His Glu Gln Lys
            660                 665                 670
Gln Gln Val Val Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu Asn Ala
        675                 680                 685
Leu Asp Arg Tyr Gly Arg Thr Ala Leu Ile Leu Ala Val Cys Cys Gly
    690                 695                 700
Ser Ala Ser Ile Val Ser Leu Leu Leu Glu Gln Asn Ile Asp Val Ser
705                 710                 715                 720
Ser Gln Asp Leu Ser Gly Gln Thr Ala Arg Glu Tyr Ala Val Ser Ser
            725                 730                 735
His His His Val Ile Cys Gln Leu Leu Ser Asp Tyr Lys Glu Lys Gln
            740                 745                 750
Met Leu Lys Ile Ser Ser Glu Asn Ser Asn Pro Glu Gln Asp Leu Lys
        755                 760                 765
```

127

```
Leu Thr Ser Glu Glu Glu Ser Gln Arg Phe Lys Gly Ser Glu Asn Ser
    770             775             780
Gln Pro Glu Lys Met Ser Gln Glu Pro Glu Ile Asn Lys Asp Gly Asp
785             790             795             800
Arg Glu Val Glu Glu Glu Met Lys Lys His Glu Ser Asn Asn Val Gly
            805             810             815
Leu Leu Glu Asn Leu Thr Asn Gly Val Thr Ala Gly Asn Gly Asp Asn
        .820             825             830
Gly Leu Ile Pro Gln Arg Lys Ser Arg Thr Pro Glu Asn Gln Gln Phe
        835             840             845
Pro Asp Asn Glu Ser Glu Glu Tyr His Arg Ile Cys Glu Leu Val Ser
    850             855             860
Asp Tyr Lys Glu Lys Gln Met Pro Lys Tyr Ser Ser Glu Asn Ser Asn
865             870             875             880
Pro Glu Gln Asp Leu Lys Leu Thr Ser Glu Glu Glu Ser Gln Arg Leu
            885             890             895
Glu Gly Ser Glu Asn Gly Gln Pro Glu Leu Glu Asn Phe Met Ala Ile
            900             905             910
Glu Glu Met Lys Lys His Gly Ser Thr His Val Gly Phe Pro Glu Asn
    915             920             925
Leu Thr Asn Gly Ala Thr Ala Gly Asn Gly Asp Asp Gly Leu Ile Pro
    930             935             940
Pro Arg Lys Ser Arg Thr Pro Glu Ser Gln Gln Phe Pro Asp Thr Glu
945             950             955             960
Asn Glu Glu Tyr His Ser Asp Glu Gln Asn Asp Thr Gln Lys Gln Phe
            965             970             975
Cys Glu Glu Gln Asn Thr Gly Ile Leu His Asp Glu Ile Leu Ile His
            980             985             990
Glu Glu Lys Gln⁺ Ile Glu Val Val Glu Lys Met Asn Ser Glu Leu Ser
            995             1000            1005
Leu Ser Cys Lys Lys Glu Lys Asp Ile Leu His Glu Asn Ser Thr Leu
    1010            1015            1020
Arg Glu Glu Ile Ala Met Leu Arg Leu Glu Leu Asp Thr Met Lys His
1025            1030            1035            1040
Gln Ser Gln Leu Pro Arg Thr His Met Val Val Glu Val Asp Ser Met
            1045            1050            1055
Pro Ala Ala Ser Ser Val Lys Lys Pro Phe Gly Leu Arg Ser Lys Met
            1060            1065            1070
Gly Lys Trp Cys Cys Arg Cys Phe Pro Cys Cys Arg Glu Ser Gly Lys
            1075            1080            1085
Ser Asn Val Gly Thr Ser Gly Asp His Asp Asp Ser Ala Met Lys Thr
    1090            1095            1100
Leu Arg Ser Lys Met Gly Lys Trp Cys Arg His Cys Phe Pro Cys Cys
1105            1110            1115            1120
Arg Gly Ser Gly Lys Ser Asn Val Gly Ala Ser Gly Asp His Asp Asp
            1125            1130            1135
Ser Ala Met Lys Thr Leu Arg Asn Lys Met Gly Lys Trp Cys Cys His
            1140.           1145            1150
Cys Phe Pro Cys Cys Arg Gly Ser Gly Lys Ser Lys Val Gly Ala Trp
    1155            1160            1165
Gly Asp Tyr Asp Asp Ser Ala Phe Met Glu Pro Arg Tyr His Val Arg
    1170            1175            1180
Gly Glu Asp Leu Asp Lys Leu His Arg Ala Ala Trp Trp Gly Lys Val
1185            1190            1195            1200
Pro Arg Lys Asp Leu Ile Val Met Leu Arg Asp Thr Asp Val Asn Lys
            1205            1210            1215
Lys Asp Lys Gln Lys Arg Thr Ala Leu His Leu Ala Ser Ala Asn Gly
            1220            1225            1230
```

```
Asn Ser Glu Val Val Lys Leu Leu Leu Asp Arg Arg Cys Gln Leu Asn
        1235                1240                1245
Val Leu Asp Asn Lys Lys Arg Thr Ala Leu Ile Lys Ala Val Gln Cys
    1250                1255                1260
Gln Glu Asp Glu Cys Ala Leu Met Leu Leu Glu His Gly Thr Asp Pro
1265                1270                1275                1280
Asn Ile Pro Asp Glu Tyr Gly Asn Thr Thr Leu His Tyr Ala Ile Tyr
            1285                1290                1295
Asn Glu Asp Lys Leu Met Ala Lys Ala Leu Leu Leu Tyr Gly Ala Asp
        1300                1305                1310
Ile Glu Ser Lys Asn Lys His Gly Leu Thr Pro Leu Leu Leu Gly Val
        1315                1320                1325
His Glu Gln Lys Gln Gln Val Lys Phe Leu Ile Lys Lys Lys Ala
    1330                1335                1340
Asn Leu Asn Ala Leu Asp Arg Tyr Gly Arg Thr Ala Leu Ile Leu Ala
1345                1350                1355                1360
Val Cys Cys Gly Ser Ala Ser Ile Val Ser Leu Leu Leu Glu Gln Asn
            1365                1370                1375
Ile Asp Val Ser Ser Gln Asp Leu Ser Gly Gln Thr Ala Arg Glu Tyr
        1380                1385                1390
Ala Val Ser Ser His His His Val Ile Cys Gln Leu Leu Ser Asp Tyr
    1395                1400                1405
Lys Glu Lys Gln Met Leu Lys Ile Ser Ser Glu Asn Ser Asn Pro Glu
    1410                1415                1420
Gln Asp Leu Lys Leu Thr Ser Glu Glu Glu Ser Gln Arg Phe Lys Gly
1425                1430                1435                1440
Ser Glu Asn Ser Gln Pro Glu Lys Met Ser Gln Glu Pro Glu Ile Asn
            1445                1450                1455
Lys Asp Gly Asp Arg Glu Val Glu Glu Glu Met Lys Lys His Glu Ser
        1460                1465                1470
Asn Asn Val Gly Leu Leu Glu Asn Leu Thr Asn Gly Val Thr Ala Gly
        1475                1480                1485
Asn Gly Asp Asn Gly Leu Ile Pro Gln Arg Lys Ser Arg Thr Pro Glu
    1490                1495                1500
Asn Gln Gln Phe Pro Asp Asn Glu Ser Glu Glu Tyr His Arg Ile Cys
1505                1510                1515                1520
Glu Leu Val Ser Asp Tyr Lys Glu Lys Gln Met Pro Lys Tyr Ser Ser
            1525                1530                1535
Glu Asn Ser Asn Pro Glu Gln Asp Leu Lys Leu Thr Ser Glu Glu Glu
        1540                1545                1550
Ser Gln Arg Leu Glu Gly Ser Glu Asn Gly Gln Pro Glu Lys Arg Ser
    1555                1560                1565
Gln Glu Pro Glu Ile Asn Lys Asp Gly Asp Arg Glu Leu Glu Asn Phe
    1570                1575                1580
Met Ala Ile Glu Glu Met Lys Lys His Gly Ser Thr His Val Gly Phe
1585                1590                1595                1600
Pro Glu Asn Leu Thr Asn Gly Ala Thr Ala Gly Asn Gly Asp Asp Gly
            1605                1610                1615
Leu Ile Pro Pro Arg Lys Ser Arg Thr Pro Glu Ser Gln Gln Phe Pro
        1620                1625                1630
Asp Thr Glu Asn Glu Glu Tyr His Ser Asp Glu Gln Asn Asp Thr Gln
        1635                1640                1645
Lys Gln Phe Cys Glu Glu Gln Asn Thr Gly Ile Leu His Asp Glu Ile
    1650                1655                1660
Leu Ile His Glu Glu Lys Gln Ile Glu Val Val Glu Lys Met Asn Ser
1665                1670                1675                1680
Glu Leu Ser Leu Ser Cys Lys Lys Glu Lys Asp Ile Leu His Glu Asn
            1685                1690                1695
```

Ser Thr Leu Arg Glu Glu Ile Ala Met Leu Arg Leu Glu Leu Asp Thr
        1700   1705   1710
Met Lys His Gln Ser Gln Leu
    1715

        <210> 379
        <211> 656
        <212> PRT
    .   <213> Homo sapien

        <400> 379
Met Val Val Glu Val Asp Ser Met Pro Ala Ala Ser Ser Val Lys Lys
1 ·   5   10   15
Pro Phe Gly Leu Arg Ser Lys Met Gly Lys Trp Cys Cys Arg Cys Phe
        20   25   30
Pro Cys Cys Arg Glu Ser Gly Lys Ser Asn Val Gly Thr Ser Gly Asp
        35   40   45
His Asp Asp Ser Ala Met Lys Thr Leu Arg Ser Lys Met Gly Lys Trp
    50   55   60
Cys Arg His Cys Phe Pro Cys Cys Arg Gly Ser Gly Lys Ser Asn Val
65   70   75   80
Gly Ala Ser Gly Asp His Asp Asp Ser Ala Met Lys Thr Leu Arg Asn
            85   90   95
Lys Met Gly Lys Trp Cys Cys His Cys Phe Pro Cys Cys Arg Gly Ser
        100   105   110
Gly Lys Ser Lys Val Gly Ala Trp Gly Asp Tyr Asp Asp Ser Ala Phe
        115   120   125
Met Glu Pro Arg Tyr His Val Arg Gly Glu Asp Leu Asp Lys Leu His
    130   135   140
Arg Ala Ala Trp Trp Gly Lys Val Pro Arg Lys Asp Leu Ile Val Met
145   150   155   160
Leu Arg Asp Thr Asp Val Asn Lys Lys Asp Lys Gln Lys Arg Thr Ala
            165   170   175
Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu Val Val Lys Leu Leu
        180   185   190
Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp Asn Lys Lys Arg Thr
        195   200   205
Ala Leu Ile Lys Ala Val Gln Cys Gln Glu Asp Glu Cys Ala Leu Met
    210   215   220
Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro Asp Glu Tyr Gly Asn
225   230   235   240
Thr Thr Leu His Tyr Ala Ile Tyr Asn Glu Asp Lys Leu Met Ala Lys
            245   250   255
Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu Ser Lys Asn Lys His Gly
        260   265   270
Leu Thr Pro Leu Leu Leu Gly Val His Glu Gln Lys Gln Gln Val Val
        275   280   285
· Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu Asn Ala Leu Asp Arg Tyr
    290   295   300
Gly Arg Thr Ala Leu Ile Leu Ala Val Cys Cys Gly Ser Ala Ser Ile
305   310   315   320
Val Ser Leu Leu Leu Glu Gln Asn Ile Asp Val Ser Ser Gln Asp Leu
            325   330   335
Ser Gly Gln Thr Ala Arg Glu Tyr Ala Val Ser Ser His His His Val
            340   345   350
Ile Cys Gln Leu Leu Ser Asp Tyr Lys Glu Lys Gln Met Leu Lys Ile
        355   360   365
Ser Ser Glu Asn Ser Asn Pro Glu Gln Asp Leu Lys Leu Thr Ser Glu

130

```
        370                    375                    380
Glu Glu Ser Gln Arg Phe Lys Gly Ser Glu Asn Ser Gln Pro Glu Lys
385                    390                    395                    400
Met Ser Gln Glu Pro Glu Ile Asn Lys Asp Gly Asp Arg Glu Val Glu
                405                    410                    415
Glu Glu Met Lys Lys His Glu Ser Asn Asn Val Gly Leu Leu Glu Asn
            420                    425                    430
Leu Thr Asn Gly Val Thr Ala Gly Asn Gly Asp Asn Gly Leu Ile Pro
            435                    440                    445
Gln Arg Lys Ser Arg Thr Pro Glu Asn Gln Gln Phe Pro Asp Asn Glu
        450                    455                    460
Ser Glu Glu Tyr His Arg Ile Cys Glu Leu Val Ser Asp Tyr Lys Glu
465                    470                    475                    480
Lys Gln Met Pro Lys Tyr Ser Ser Glu Asn Ser Asn Pro Glu Gln Asp
                485                    490                    495 .
Leu Lys Leu Thr Ser Glu Glu Glu Ser Gln Arg Leu Glu Gly Ser Glu
            500                    505                    510
Asn Gly Gln Pro Glu Leu Glu Asn Phe Met Ala Ile Glu Glu Met Lys
            515                    520                    525
Lys His Gly Ser Thr His Val Gly Phe Pro Glu Asn Leu Thr Asn Gly
    530                    535                    540
Ala Thr Ala Gly Asn Gly Asp Asp Gly Leu Ile Pro Pro Arg Lys Ser
545                    550                    555                    560
Arg Thr Pro Glu Ser Gln Gln Phe Pro Asp Thr Glu Asn Glu Glu Tyr
                565                    570                    575
His Ser Asp Glu Gln Asn Asp Thr Gln Lys Gln Phe Cys Glu Glu Gln
            580                    585                    590
Asn Thr Gly Ile Leu His Asp Glu Ile Leu Ile His Glu Glu Lys Gln
        595                    600                    605
Ile Glu Val Val Glu Lys Met Asn Ser Glu Leu Ser Leu Ser Cys Lys
    610                    615                    620
Lys Glu Lys Asp Ile Leu His Glu Asn Ser Thr Leu Arg Glu Glu Ile
625                    630                    635                    640
Ala Met Leu Arg Leu Glu Leu Asp Thr Met Lys His Gln Ser Gln Leu
            645                    650                    655
```

```
        <210> 380
        <211> 671
        <212> PRT
        <213> Homo sapien
```

```
        <400> 380
Met Val Val Glu Val Asp Ser Met Pro Ala Ala Ser Ser Val Lys Lys
1                   5                   10                  15
Pro Phe Gly Leu Arg Ser Lys Met Gly Lys Trp Cys Cys Arg Cys Phe
                20                  25                  30
Pro Cys Cys Arg Glu Ser Gly Lys Ser Asn Val Gly Thr Ser Gly Asp
        35                  40                  45
His Asp Asp Ser Ala Met Lys Thr Leu Arg Ser Lys Met Gly Lys Trp
    50                  55                  60
Cys Arg His Cys Phe Pro Cys Cys Arg Gly Ser Gly Lys Ser Asn Val
65                  70                  75                  80
Gly Ala Ser Gly Asp His Asp Asp Ser Ala Met Lys Thr Leu Arg Asn
                85                  90                  95
Lys Met Gly Lys Trp Cys Cys His Cys Phe Pro Cys Cys Arg Gly Ser
            100                 105                 110
Gly Lys Ser Lys Val Gly Ala Trp Gly Asp Tyr Asp Asp Ser Ala Phe
        115                 120                 125
```

Met Glu Pro Arg Tyr His Val Arg Gly Glu Asp Leu Asp Lys Leu His
    130   135   140
Arg Ala Ala Trp Trp Gly Lys Val Pro Arg Lys Asp Leu Ile Val Met
145   150   155   160
Leu Arg Asp Thr Asp Val Asn Lys Lys Asp Lys Gln Lys Arg Thr Ala
                165   170   175
Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu Val Val Lys Leu Leu
            180   185   190
Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp Asn Lys Lys Arg Thr
        195   200   205
Ala Leu Ile Lys Ala Val Gln Cys Gln Glu Asp Glu Cys Ala Leu Met
    210   215   220
Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro Asp Glu Tyr Gly Asn
225   230   235   240
Thr Thr Leu His Tyr Ala Ile Tyr Asn Glu Asp Lys Leu Met Ala Lys
                245   250   255
Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu Ser Lys Asn Lys His Gly
            260   265   270
Leu Thr Pro Leu Leu Leu Gly Val His Glu Gln Lys Gln Gln Val Val
        275   280   285
Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu Asn Ala Leu Asp Arg Tyr
    290   295   300
Gly Arg Thr Ala Leu Ile Leu Ala Val Cys Cys Gly Ser Ala Ser Ile
305   310   315   320
Val Ser Leu Leu Leu Glu Gln Asn Ile Asp Val Ser Ser Gln Asp Leu
                325   330   335
Ser Gly Gln Thr Ala Arg Glu Tyr Ala Val Ser Ser His His His Val
            340   345   350
Ile Cys Gln Leu Leu Ser Asp Tyr Lys Glu Lys Gln Met Leu Lys Ile
        355   360   365
Ser Ser Glu Asn Ser Asn Pro Glu Gln Asp Leu Lys Leu Thr Ser Glu
370   375   380
Glu Glu Ser Gln Arg Phe Lys Gly Ser Glu Asn Ser Gln Pro Glu Lys
385   390   395   400
Met Ser Gln Glu Pro Glu Ile Asn Lys Asp Gly Asp Arg Glu Val Glu
                405   410   415
Glu Glu Met Lys Lys His Glu Ser Asn Asn Val Gly Leu Leu Glu Asn
            420   425   430
Leu Thr Asn Gly Val Thr Ala Gly Asn Gly Asp Asn Gly Leu Ile Pro
        435   440   445
Gln Arg Lys Ser Arg Thr Pro Glu Asn Gln Gln Phe Pro Asp Asn Glu
    450   455   460
Ser Glu Glu Tyr His Arg Ile Cys Glu Leu Val Ser Asp Tyr Lys Glu
465   470   475   480
Lys Gln Met Pro Lys Tyr Ser Ser Glu Asn Ser Asn Pro Glu Gln Asp
                485   490   495
Leu Lys Leu Thr Ser Glu Glu Glu Ser Gln Arg Leu Glu Gly Ser Glu
            500   505   510
Asn Gly Gln Pro Glu Lys Arg Ser Gln Glu Pro Glu Ile Asn Lys Asp
        515   520   525
Gly Asp Arg Glu Leu Glu Asn Phe Met Ala Ile Glu Glu Met Lys Lys
    530   535   540
His Gly Ser Thr His Val Gly Phe Pro Glu Asn Leu Thr Asn Gly Ala
545   550   555   560
Thr Ala Gly Asn Gly Asp Asp Gly Leu Ile Pro Pro Arg Lys Ser Arg
                565   570   575
Thr Pro Glu Ser Gln Gln Phe Pro Asp Thr Glu Asn Glu Glu Tyr His
            580   585   590

132

```
Ser Asp Glu Gln Asn Asp Thr Gln Lys Gln Phe Cys Glu Glu Gln Asn
        595             600             605
Thr Gly Ile Leu His Asp Glu Ile Leu Ile His Glu Glu Lys Gln Ile
    610             615             620
Glu Val Val Glu Lys Met Asn Ser Glu Leu Ser Leu Ser Cys Lys Lys
625             630             635             640
Glu Lys Asp Ile Leu His Glu Asn Ser Thr Leu Arg Glu Glu Ile Ala
            645             650             655
Met Leu Arg Leu Glu Leu Asp Thr Met Lys His Gln Ser Gln Leu
        660             665             670
```

```
        <210> 381
        <211> 251
        <212> DNA
        <213> Homo sapien

        <400> 381
ggagaagcgt ctgctggggc aggaaggggt ttccctgccc tctcacctgt ccctcaccaa        60
ggtaacatgc ttcccctaag ggtatcccaa cccaggggcc tcaccatgac ctctgagggg       120
ccaatatccc aggagaagca ttggggagtt gggggcaggt gaaggaccca ggactcacac       180
atcctgggcc tccaaggcag aggagagggt cctcaagaag gtcaggagga aaatccgtaa       240
caagcagtca g                                                            251
```

```
<210> 382
<211> 3279
<212> DNA
<213> Homo sapiens

<400> 382
cttcctgcag cccccatgct ggtgaggggc acgggcagga acagtggacc caacatggaa 60
atgctggagg gtgtcaggaa gtgatcgggc tctgggcag ggaggagggg tggggagtgt 120
cactgggagg ggacatcctg cagaaggtag gagtgagcaa acacccgctg caggggaggg 180
gagagccctg cggcacctgg gggagcagag ggagcagcac ctgcccaggc ctgggaggag 240
gggcctggag ggcgtgagga ggagcgaggg ggctgcatgg ctggagtgag ggatcagggg 300
cagggcgcga gatggcctca cacagggaag agagggcccc tcctgcaggg cctcacctgg 360
gccacaggag gacactgctt ttcctctgag gagtcaggag ctgtggatgg tgctggacag 420
aagaaggaca gggcctggct caggtgtcca gaggctgtcg ctggcttccc tttgggatca 480
gactgcaggg agggaggcg gcaggggttgt ggggggagtg acgatgagga tgacctgggg 540
gtggctccag gccttgcccc tgcctgggcc ctcacccagc ctccctcaca gtctcctggc 600
cctcagtctc tcccctccac tccatcctcc atctggcctc agtgggtcat tctgatcact 660
gaactgacca tacccagccc tgcccacggc cctccatggc tccccaatgc cctggagagg 720
ggacatctag tcagagagta gtcctgaaga ggtggcctct gcgatgtgcc tgtgggggca 780
gcatcctgca gatgctcccg gccctcatcc tgctgacctg tctgcaggga ctgtcctcct 840
ggaccttgcc ccttgtgcag gagctggacc ctgaagtccc ctccccatag gccaagactg 900
gagccttgtt ccctctgttg gactccctgc ccatattctt gtgggagtgg gttctggaga 960
catttctgtc tgttcctgag agctgggaat tgctctcagt catctgcctg cgcggttctg 1020
agagatggag ttgcctaggc agttattggg gccaatcttt ctcactgtgt ctctcctcct 1080
ttacccttag ggtgattctg ggggtccact tgtctgtaat ggtgtgcttc aaggtatcac 1140
atcatggggc cctgagccat gtgccctgcc tgaaaagcct gctgtgtaca ccaaggtggt 1200
gcattaccgg aagtggatca aggacaccat cgcagccaac ccctgagtgc ccctgtccca 1260
cccctacctc tagtaaattt aagtccacct cacgttctgg catcacttgg cctttctgga 1320
tgctggacac ctgaagcttg gaactcacct ggccgaagct cgagcctcct gagtcctact 1380
gacctgtgct ttctggtgtg gagtccaggg ctgctaggaa aaggaatggg cagacacagg 1440
tgtatgccaa tgtttctgaa atgggtataa tttcgtcctc tccttcggaa cactggctgt 1500
ctctgaagac ttctcgctca gtttcagtga ggacacacac aaagacgtgg gtgaccatgt 1560
tgtttgtggg gtgcagagat gggaggggtg gggcccaccc tggaagagtg gacagtgaca 1620
caaggtggac actctctaca gatcactgag gataagctgg agccacaatg catgaggcac 1680
acacacagca aggttgacgc tgtaaacata gcccacgctg tcctggggggc actgggaagc 1740
```

```
ctagataagg ccgtgagcag aaagaagggg aggatcctcc tatgttgttg aaggagggac 1800
tagggggaga aactgaaagc tgattaatta caggaggttt gttcaggtcc cccaaaccac 1860
cgtcagattt gatgatttcc tagcaggact tacagaaata aagagctatc atgctgtggt 1920
ttattatggt ttgttacatt gataggatac atactgaaat cagcaaacaa aacagatgta 1980
tagattagag tgtggagaaa acagaggaaa acttgcagtt acgaagactg gcaacttggc 2040
tttactaagt tttcagactg gcaggaagtc aaacctatta ggctgaggac cttgtggagt 2100
gtagctgatc cagctgatag aggaactagc caggtggggg cctttccctt tggatggggg 2160
gcatatccga cagttattct ctccaagtgg agacttacgg acagcatata attctccctg 2220
caaggatgta tgataatatg tacaaagtaa ttccaactga ggaagctcac ctgatcctta 2280
gtgtccaggg tttttactgg gggtctgtag gacgagtatg gagtacttga ataattgacc 2340
tgaagtcctc agacctgagg ttccctagag ttcaaacaga tacagcatgg tccagagtcc 2400
cagatgtaca aaaacaggga ttcatcacaa atcccatctt tagcatgaag ggtctggcat 2460
ggcccaaggc cccaagtata tcaaggcact tgggcagaac atgccaagga atcaaatgtc 2520
atctcccagg agttattcaa gggtgagccc tttacttggg atgtacaggc tttgagcagt 2580
gcagggctgc tgagtcaacc tttattgta cagggatga gggaaaggga gaggatgagg 2640
aagcccccct ggggatttgg tttggtcttg tgatcaggtg gtctatgggg ctatccctac 2700
aaagaagaat ccagaaatag gggcacattg aggaatgata ctgagcccaa agagcattca 2760
atcattgttt tatttgcctt cttttcacac cattggtgag ggagggatta ccaccctggg 2820
gttatgaaga tggttgaaca ccccacacat agcaccggag atatgagatc aacagtttct 2880
tagccataga gattcacagc ccagagcagg aggacgctgc acaccatgca ggatgacatg 2940
ggggatgcgc tcgggattgg tgtgaagaag caaggactgt tagaggcagg ctttatagta 3000
acaagacggt ggggcaaact ctgatttccg tgggggaatg tcatggtctt gctttactaa 3060
gttttgagac tggcaggtag tgaaactcat taggctgaga accttgtgga atgcagctga 3120
cccagctgat agaggaagta gccaggtggg agcctttccc agtgggtgtg ggacatatct 3180
ggcaagattt tgtggcactc ctggttacag atactggggc agcaaataaa actgaatctt 3240
gttttcagac cttaaaaaaa aaaaaaaaa aaaagtttt                            3279
```

<210> 383
<211> 154
<212> PRT
<213> Homo sapiens

<400> 383

```
Met Ala Gly Val Arg Asp Gln Gly Gln Gly Ala Arg Trp Pro His Thr
                  5                  10                  15
Gly Lys Arg Gly Pro Leu Leu Gln Gly Leu Thr Trp Ala Thr Gly Gly
                 20                  25                  30
His Cys Phe Ser Ser Glu Glu Ser Gly Ala Val Asp Gly Ala Gly Gln
             35                  40                  45
Lys Lys Asp Arg Ala Trp Leu Arg Cys Pro Glu Ala Val Ala Gly Phe
         50                  55                  60
Pro Leu Gly Ser Asp Cys Arg Glu Gly Gly Arg Gln Gly Cys Gly Gly
65                  70                  75                  80
Ser Asp Asp Glu Asp Asp Leu Gly Val Ala Pro Gly Leu Ala Pro Ala
                     85                  90                  95
Trp Ala Leu Thr Gln Pro Pro Ser Gln Ser Pro Gly Pro Gln Ser Leu
                100                 105                 110
Pro Ser Thr Pro Ser Ser Ile Trp Pro Gln Trp Val Ile Leu Ile Thr
            115                 120                 125
Glu Leu Thr Ile Pro Ser Pro Ala His Gly Pro Pro Trp Leu Pro Asn
        130                 135                 140
Ala Leu Glu Arg Gly His Leu Val Arg Glu
145                 150
```

<210> 384
<211> 557
<212> DNA
<213> Homo sapiens

```
<400> 384
ggatcctcta gagcggccgc ctactactac taaattcgcg gccgcgtcga cgaagaagag 60
aaagatgtgt tttgtttttgg actctctgtg gtcccttcca atgctgtggg tttccaacca 120
ggggaagggt cccttttgca ttgccaagtg ccataaccat gagcactact ctaccatggt 180
tctgcctcct ggccaagcag gctggtttgc aagaatgaaa tgaatgattc tacagctagg 240
acttaacctt gaaatggaaa gtcttgcaat cccatttgca ggatccgtct gtgcacatgc 300
ctctgtagag agcagcattc ccagggacct tggaaacagt tggcactgta aggtgcttgc 360
tccccaagac acatcctaaa aggtgttgta atggtgaaaa cgtcttcctt ctttattgcc 420
ccttcttatt tatgtgaaca actgtttgtc ttttttttgta tcttttttaa actgtaaagt 480
tcaattgtga aaatgaatat catgcaaata aattatgcga ttttttttttc aaagtaaaaa 540
aaaaaaaaaa aaaaaaa                                                557
```

```
<210> 385
<211> 337
<212> DNA
<213> Homo sapiens
```

```
<400> 385
ttcccaggtg atgtgcgagg gaagacacat ttactatcct tgatggggct gattccttta 60
gtttctctag cagcagatgg gttaggagga agtgacccaa gtggttgact cctatgtgca 120
tctcaaagcc atctgctgtc ttcgagtacg gacacatcat cactcctgca ttgttgatca 180
aaacgtggag gtgcttttcc tcagctaaga agcccttagc aaaagctcga atagacttag 240
tatcagacag gtccagtttc cgcaccaaca cctgctggtt ccctgtcgtg gtctggatct 300
ctttggccac caattccccc ttttccacat cccggca                          337
```

```
<210> 386
<211> 300
<212> DNA
<213> Homo sapiens
```

```
<400> 386
gggcccgcta ccggcccagg ccccgcctcg cgagtcctcc tccccgggtg cctgcccgca 60
gcccgctcgg cccagagggt gggcgcgggg ctgcctctac cggctggcgg ctgtgccgca 120
gcgaccttgg cccgaaggct ctagcaagga cccaccgacc ccagccgcgg cggcggcggc 180
gcggactttg cccggtgtgt ggggcggagc ggactgcgtg tccgcggacg ggcagcgaag 240
atgttagcct tcgctgccag gaccgtggac cgatcccagg gctgtggtgt aacctcagcc 300
```

```
<210> 387
<211> 537
<212> DNA
<213> Homo sapiens
```

```
<400> 387
gggccgagtc gggcaccaag ggactctttg caggcttcct tcctcggatc atcaaggctg 60
cccctcctg tgccatcatg atcagcacct atgagttcgg caaaagcttc ttccagaggc 120
tgaaccagga ccggcttctg gcggctgaa aggggcaagg aggcaaggac ccgtctctc 180
ccacggatgg ggagaggca ggaggagacc cagccaagtg ccttttcctc agcactgagg 240
gagggggctt gtttcccttc cctccggcg acaagctcca gggcagggct gtccctctgg 300
gcggcccagc acttcctcag acacaacttc ttcctgctgc tccagtcgtg gggatcatca 360
cttacccacc ccccaagttc aagaccaaat cttccagctg ccccccttcgt gtttccctgt 420
gtttgctgta gctgggcatg tctccaggaa ccaagaagcc ctcagcctgg tgtagtctcc 480
ctgacccttg ttaattcctt aagtctaaag atgatgaact tcaaaaaaaa aaaaaaa  537
```

```
<210> 388
<211> 520
<212> DNA
<213> Homo sapiens
```

135

```
<400> 388
aggataattt ttaaaccaat caaatgaaaa aaacaaacaa acaaaaaagg aaatgtcatg 60
tgaggttaaa ccagtttgca ttcccctaat gtggaaaaag taagaggact actcagcact 120
gtttgaagat tgcctcttct acagcttctg agaattgtgt tatttcactt gccaagtgaa 180
ggaccccctc cccaacatgc cccagcccac ccctaagcat ggtcccttgt caccaggcaa 240
ccaggaaact gctacttgtg gacctcacca gagaccagga gggtttggtt agctcacagg 300
acttcccca ccccagaaga ttagcatccc atactagact catactcaac tcaactaggc 360
tcatactcaa ttgatggtta ttagacaatt ccatttcttt ctggttatta taaacagaaa 420
atctttcctc ttctcattac cagtaaaggc tcttggtatc tttctgttgg aatgatttct 480
atgaacttgt cttattttaa tggtgggttt tttttctggt                        520

<210> 389
<211> 365
<212> DNA
<213> Homo sapiens

<400> 389
cgttgcccca gtttgacaga aggaaaggcg gagcttattc aaagtctaga gggagtggag 60
gagttaaggc tggatttcag atctgcctgg ttccagccgc agtgtgccct ctgctccccc 120
aacgactttc caaataatct caccagcgcc ttccagctca ggcgtcctag aagcgtcttg 180
aagcctatgg ccagctgtct ttgtgttccc tctcaccgc ctgtcctcac agctgagact 240
cccaggaaac cttcagacta ccttcctctg ccttcagcaa ggggcgttgc ccacattctc 300
tgagggtcag tggaagaacc tagactccca ttgctagagg tagaaagggg aagggtgctg 360
gggag                                                              365

<210> 390
<211> 221
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(221)
<223> n = A,T,C or G

<400> 390
tgcctctcca tcctggcccc gacttctctg tcaggaaagt ggggatggac cccatctgca 60
tacacggntt ctcatgggtg tggaacatct ctgcttgcgg tttcaggaag gcctctggct 120
gctctangag tctgancnga ntcgttgccc cantntgaca naaggaaagg cggagcttat 180
tcaaagtcta gagggagtgg aggagttaag ctggatttc a                      221

<210> 391
<211> 325
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(325)
<223> n = A,T,C or G

<400> 391
tggagcaggt cccgaggcct ccctagagcc tggggccgac tctgtgncga tgcangcttt 60
ctctcgcgcc cagcctggag ctgctcctgg catctaccaa caatcagncg aggcgagcag 120
tagccaggc actgctgcca acagccagtc cnnataccat catgtnaccc ggtgngctct 180
naanttngat ntccanagcc ctacccatcn tagttctgct ctcccaccgg ntaccagccc 240
cactgcccag gaatcctaca gccagtaccc tgtcccgacg tctctaccta ccagtacgat 300
```

136

```
gagacctccg gctactacta tgacc                                     325
```

<210> 392
<211> 277
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(277)
<223> n = A,T,C or G

<400> 392
```
atattgttta actccttcct ttatatcttt taacattttc atggngaaag gttcacatct 60
agtctcactt nggcnagngn ctcctacttg agtctcttcc ccggcctgnn ccagtngnaa 120
antaccanga accgncatgn cttaanaacn ncctggtttn tgggttnntc aatgactgca 180
tgcagtgcac caccctgtcc actacgtgat gctgtaggat taaagtctca cagtgggcgg 240
ctgaggatac agcgccgcgt cctgtgttgc tggggaa                        277
```

<210> 393
<211> 566
<212> DNA
<213> Homo sapiens

<400> 393
```
actagtccag tgtggtggaa ttcgcggccg cgtcgacgga caggtcagct gtctggctca 60
gtgatctaca ttctgaagtt gtctgaaaat gtcttcatga ttaaattcag cctaaacgtt 120
ttgccgggaa cactgcagag acaatgctgt gagtttccaa ccttagccca tctgcgggca 180
gagaaggtct agtttgtcca tcagcattat catgatatca ggactggtta cttggttaag 240
gaggggtcta ggagatctgt ccctttttaga gacaccttac ttataatgaa gtatttggga 300
gggtggtttt caaaagtaga aatgtcctgt attccgatga tcatcctgta aacattttat 360
catttattaa tcatccctgc ctgtgtctat tattatattc atatctctac gctggaaact 420
ttctgcctca atgtttactg tgcctttgtt tttgctagtt tgtgttgttg aaaaaaaaaa 480
cattctctgc ctgagtttta attttttgtcc aaagttattt taatctatac aattaaaagc 540
ttttgcctat caaaaaaaaa aaaaaa                                    566
```

<210> 394
<211> 384
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(384)
<223> n = A,T,C or G

<400> 394
```
gaacatacat gtcccggcac ctgagctgca gtctgacatc atcgccatca cgggcctcgc 60
tgcaaattng gaccgggcca aggctggact gctggagcgt gtgaaggagc tacaggccna 120
gcaggaggac cgggctttaa ggagttttaa gctgagtgtc actgtagacc ccaaatacca 180
tcccaagatt atcgggagaa aggggggcagt aattacccaa atccggttgg agcatgacgt 240
gaacatccag tttcctgata aggacgatgg gaaccagccc caggaccaaa ttaccatcac 300
agggtacgaa aagaacacag aagctgccag ggatgctata ctgagaattg tgggtgaact 360
tgagcagatg gtttctgagg acgt                                      384
```

<210> 395
<211> 399
<212> DNA

137

<213> Homo sapiens

<400> 395
ggcaaaactg tgtgacctca ataagacctc gcagatccaa ggtcaagtat cagaagtgac 60
tctgaccttg gactccaaga cctacatcaa cagcctggct atattagatg atgagccagt 120
tatcagaggt ttcatcattg cggaaattgt ggagtctaag gaaatcatgg cctctgaagt 180
attcacgtct ttccagtacc ctgagttctc tatagagttg cctaacacag gcagaattgg 240
ccagctactt gtctgcaatt gtatcttcaa gaataccctg gccatccctt tgactgacgt 300
caagttctct ttggaaagcc tgggcatctc ctcactacag acctctgacc atgggacggt 360
gcagcctggt gagaccatcc aatcccaaat aaaatgcac   399

<210> 396
<211> 403
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(403)
<223> n = A,T,C or G

<400> 396
tggagttntc agtgcaaaca agccataaag cttcagtagc aaaattactgt ctcacagaaa 60
gacattttca acttctgctc cagctgctga taaaacaaat catgtgttta gcttgactcc 120
agacaaggac aacctgttcc ttcataactc tctagagaaa aaaaggagtt gttagtagat 180
actaaaaaaa gtggatgaat aatctggata ttttttcctaa aaagattcct tgaaacacat 240
taggaaaatg gagggcctta tgatcagaat gctagaatta gtccattgtg ctgaagcagg 300
gtttagggga gggagtgagg gataaaagaa ggaaaaaaag aagagtgaga aaacctattt 360
atcaaagcag gtgctatcac tcaatgttag gccctgctct ttt   403

<210> 397
<211> 100
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(100)
<223> n = A,T,C or G

<400> 397
actagtncag tgtggtggaa ttcgcggccg cgtcgaccta naanccatct ctatagcaaa 60
tccatccccg ctcctggttg gtnacagaat gactgacaaa   100

<210> 398
<211> 278
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(278)
<223> n = A,T,C or G

<400> 398
gcggccgcgt cgacagcagt tccgccagcg ctcgcccctg ggtgggggatg tgctgcacgc 60
ccacctggac atctggaagt cagcggcctg gatgaaagag cggacttcac ctggggcgat 120
tcactactgt gcctcgacca gtgaggagag ctggaccgac agcgaggtgg actcatcatg 180

138

```
ctccgggcag cccatccacc tgtggcagtt cctcaaggag ttgctactca agccccacag 240
ctatggccgc ttcattangt ggctcaacaa ggagaagg                        278
```

<210> 399
<211> 298
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(298)
<223> n = A,T,C or G

<400> 399
```
acggaggtgg aggaagcgnc cctgggatcg anaggatggg tcctgncatt gaccncctcn 60
ggggtgccng catggagcgc atgggcgcgg gcctgggcca cggcatggat cgcgtgggct 120
ccgagatcga gcgcatgggc ctggtcatgg accgcatggg ctccgtggag cgcatgggct 180
ccggcattga gcgcatgggc ccgctggggcc tcgaccacat ggcctccanc attgancgca 240
tgggccagac catggagcgc attggctctg gcgtggagcn catgggtgcc ggcatggg   298
```

<210> 400
<211> 548
<212> DNA
<213> Homo sapiens

<400> 400
```
acatcaacta cttcctcatt ttaaggtatg gcagttccct tcatcccctt ttcctgcctt 60
gtacatgtac atgtatgaaa tttccttctc ttaccgaact ctctccacac atcacaaggt 120
caaagaacca cacgcttaga agggtaagag ggcaccctat gaaatgaaat ggtgatttct 180
tgagtctctt ttttccacgt ttaaggggcc atggcaggac ttagagttgc gagttaagac 240
tgcagagggc tagagaatta tttcatacag gctttgaggc cacccatgtc acttatcccg 300
tataccctct caccatcccc ttgtctactc tgatgccccc aagatgcaac tgggcagcta 360
gttggcccca taattctggg cctttgttgt ttgttttaat tacttgggca tcccaggaag 420
ctttccagtg atctcctacc atgggccccc ctcctgggat caagcccctc ccaggccctg 480
tccccagccc ctcctgcccc agcccacccg cttgccttgg tgctcagccc tcccattggg 540
agcaggtt                                                          548
```

<210> 401
<211> 355
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(355)
<223> n = A,T,C or G

<400> 401
```
actgtttcca tgttatgttt ctacacattg ctacctcagt gctcctggaa acttagcttt 60
tgatgtctcc aagtagtcca ccttcattta actctttgaa actgtatcat ctttgccaag 120
taagagtggt ggcctatttc agctgctttg acaaaatgac tggctcctga cttaacgttc 180
tataaatgaa tgtgctgaag caaagtgccc atggtggcgg cgaagaagan aaagatgtgt 240
tttgttttgg actctctgtg gtcccttcca atgctgnggg tttccaacca ggggaagggt 300
cccttttgca ttgccaagtg ccataaccat gagcactact ctaccatggn tctgc      355
```

<210> 402
<211> 407
<212> DNA

139

<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(407)
<223> n = A,T,C or G

<400> 402
atggggcaag ctggataaag aaccaagacc cactggagta tgctgtcttc aagaaaccca 60
tctcacatgc ggtggcatac ataggctcaa aataaaggaa tggagaaaaa tatttcaagc 120
aaatggaaaa cagaaaaaag caggtgttgc actcctactt tctgacaaaa cagactatgc 180
gaataaagat aaaaaagaga aggacattac aaaggtggtc ctgacctttg ataaatctca 240
ttgcttgata ccaacctggg ctgttttaat tgcccaaacc aaaaggataa tttgctgagg 300
ttgtggagct tctcccctgc agagagtccc tgatctccca aaatttggtt gagatgtaag 360
gntgattttg ctgacaactc ctttttctgaa gttttactca tttccaa   407

<210> 403
<211> 303
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(303)
<223> n = A,T,C or G

<400> 403
cagtatttat agccnaactg aaaagctagt agcaggcaag tctcaaatcc aggcaccaaa 60
tcctaagcaa gagccatggc atggtgaaaa tgcaaaagga gagtctggcc aatctacaaa 120
tagagaacaa gacctactca gtcatgaaca aaaaggcaga caccaacatg gatctcatgg 180
gggattggat attgtaatta tagagcagga agatgacagt gatcgtcatt ggcacaaca 240
tcttaacaac gaccgaaacc cattatttac ataaacctcc attcggtaac catgttgaaa 300
gga   303

<210> 404
<211> 225
<212> DNA
<213> Homo sapiens

<400> 404
aagtgtaact tttaaaaatt tagtggattt tgaaaattct tagaggaaag taaaggaaaa 60
attgttaatg cactcattta cctttacatg gtgaaagttc tctcttgatc ctacaaacag 120
acattttcca ctcgtgtttc catagttgtt aagtgtatca gatgtgttgg gcatgtgaat 180
ctccaagtgc ctgtgtaata aataaagtat ctttatttca ttcat   225

<210> 405
<211> 334
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(334)
<223> n = A,T,C or G

<400> 405
gagctgttat actgtgagtt ctactaggaa atcatcaaat ctgagggttg tctggaggac 60
ttcaatacac ctcccccat agtgaatcag cttccagggg gtccagtccc tctccttact 120

140

```
tcatccccat cccatgccaa aggaagaccc tccctccttg gctcacagcc ttctctaggc 180
ttcccagtgc ctccaggaca gagtgggtta tgttttcagc tccatccttg ctgtgagtgt 240
ctggtgcggt tgtgcctcca gcttctgctc agtgcttcat ggacagtgtc cagcccatgt 300
cactctccac tctctcannd tggatcccac ccct                           334
```

<210> 406
<211> 216
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(216)
<223> n = A,T,C or G

<400> 406
```
tttcatacct aatgagggag ttganatnac atnnaaccag gaaatgcatg gatctcaang 60
gaaacaaaca cccaataaac tcggagtggc agactgacaa ctgtgagaca tgcacttgct 120
acnaaacaca aatttnatgt tgcacccttg tttctacacc tgtgggttat gacaaagaca 180
actgccaaag aatnttcaag aaggaggact gccant                          216
```

<210> 407
<211> 413
<212> DNA
<213> Homo sapiens

<400> 407
```
gctgacttgc tagtatcatc tgcattcatt gaagcacaag aacttcatgc cttgactcat 60
gtaaatgcaa taggattaaa aaataaattt gatatcacat ggaaacagac aaaaaatatt 120
gtacaacatt gcacccagtg tcagattcta cacctggcca ctcaggaagc aagagttaat 180
cccagaggtc tatgtcctaa tgtgttatgg caaatggatg tcatgcacgt accttcattt 240
ggaaaattgt catttgtcca tgtgacagtt gatacttatt cacatttcat atgggcaacc 300
tgccagacag gagaaagtct tcccatgtta aaagacattt attatcttgt tttcctgtca 360
tgggagttcc agaaaaagtt aaaacagaca atgggccagg ttctgtagta aag        413
```

<210> 408
<211> 183
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(183)
<223> n = A,T,C or G

<400> 408
```
ggagctngcc ctcaattcct ccatntctat gttancatat ttaatgtctt ttgnnattaa 60
tncttaacta gttaatcctt aaagggctan ntaatcctta actagtccct ccattgtgag 120
cattatcctt ccagtattcn ccttctnttt tatttactcc ttcctggcta cccatgtact 180
ntt                                                             183
```

<210> 409
<211> 250
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature

141

```
<222> (1)...(250)
<223> n = A,T,C or G

<400> 409
cccacgcatg ataagctctt tatttctgta agtcctgcta ggaaatcatc aaatctgacg 60
gtggtttggg ggacctgaac aaacctcctg taattaatca gctttcagtt tctcccccta 120
gtccctcctt caacaacata ggaggatcct ccccttcttt ctgctcacgg ccttatctag 180
gcttcccagt gcccccagga cagcgtgggc tatgtttaca gcgcntcctt gctggggggg 240
ggccntatgc                                                       250


<210> 410
<211> 306
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(306)
<223> n = A,T,C or G

<400> 410
ggctggtttg caagaatgaa atgaatgatt ctacagctag gacttaacct tgaaatggaa 60
agtcttgcaa tcccatttgc aggatccgtc tgtgcacatg cctctgtaga gagcagcatt 120
cccagggacc ttggaaacag ttggcactgt aaggtgcttg ctccccaaga cacatcctaa 180
aaggtgttgt aatggtgaaa accgcttcct tctttattgc cccttcttat ttatgtgaac 240
nactggttgg cttttttttgn atctttttta aactggaaag ttcaattgng aaaatgaata 300
tcntgc                                                           306


<210> 411
<211> 261
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(261)
<223> n = A,T,C or G

<400> 411
agagatattn cttaggtnaa agttcataga gttcccatga actatatgac tggccacaca 60
ggatcttttg tatttaagga ttctgagatt ttgcttgagc aggattagat aaggctgttc 120
tttaaatgtc tgaaatggaa cagatttcaa aaaaaaaccc cacaatctag ggtgggaaca 180
aggaaggaaa gatgtgaata ggctgatggg caaaaaacca atttacccat cagttccagc 240
cttctctcaa ggngaggcaa a                                           261


<210> 412
<211> 241
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(241)
<223> n = A,T,C or G

<400> 412
gttcaatgtt acctgacatt tctacaacac cccactcacc gatgtattcg ttgcccagtg 60
ggaacatacc agcctgaatt tggaaaaaat aattgtgttt cttgcccagg aaatactacg 120
```

142

```
actgactttg atggctccac aaacataacc cagtgtaaaa acagaagatg tggaggggag 180
ctgggagatt tcactgggta cattgaattc ccaaactacc cangcaatta cccagccaac 240
a                                                                 241
```

```
<210> 413
<211> 231
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(231)
<223> n = A,T,C or G

<400> 413
aactcttaca atccaagtga ctcatctgtg tgcttgaatc ctttccactg tctcatctcc 60
ctcatccaag tttctagtac cttctctttg ttgtgaagga taatcaaact gaacaacaaa 120
aagtttactc tcctcatttg gaacctaaaa actctcttct tcctgggtct gagggctcca 180
agaatccttg aatcanttct cagatcattg gggacaccan atcaggaacc t          231
```

```
<210> 414
<211> 234
<212> DNA
<213> Homo sapiens

<400> 414
actgtccatg aagcactgag cagaagctgg aggcacaacg caccagacac tcacagcaag 60
gatggagctg aaaacataac ccactctgtc ctggaggcac tgggaagcct agagaaggct 120
gtgagccaag gagggagggt cttcctttgg catgggatgg ggatgaagta aggagaggga 180
ctggacccccc tggaagctga ttcactatgg ggggaggtgt attgaagtcc tcca        234
```

```
<210> 415
<211> 217
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(217)
<223> n = A,T,C or G

<400> 415
gcataggatt aagactgagt atcttttcta cattctttta actttctaag gggcacttct 60
caaaacacag accaggtagc aaatctccac tgctctaagg ntctcaccac cactttctca 120
cacctagcaa tagtagaatt cagtcctact tctgaggcca gaagaatggt tcagaaaaat 180
antggattat aaaaaataac aattaagaaa aataatc                          217
```

```
<210> 416
<211> 213
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(213)
<223> n = A,T,C or G

<400> 416
```

143

```
atgcatatnt aaagganact gcctcgcttt tagaagacat ctggnctgct ctctgcatga 60
ggcacagcag taaagctctt tgattcccag aatcaagaac tctcccttc agactattac 120
cgaatgcaag gtggttaatt gaaggccact aattgatgct caaatagaag gatattgact 180
atattggaac agatggagtc tctactacaa aag                                213
```

<210> 417
<211> 303
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(303)
<223> n = A,T,C or G

<400> 417
```
nagtcttcag gcccatcagg gaagttcaca ctggagagaa gtcatacata tgtactgtat 60
gtgggaaagg ctttactctg agttcaaatc ttcaagccca tcagagagtc cacactggag 120
agaagccata caaatgcaat gagtgtggga agagcttcag gagggattcc cattatcaag 180
ttcatctagt ggtccacaca ggagagaaac cctataaatg tgagatatgt gggaagggct 240
tcantcaaag ttcgtatctt caaatccatc ngaaggncca cagtatanan aaacctttta 300
agt                                                                 303
```

<210> 418
<211> 328
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(328)
<223> n = A,T,C or G

<400> 418
```
tttttggcgg tggtggggca gggacgggac angagtctca ctctgttgcc caggctggag 60
tgcacaggca tgatctcggc tcactacaac ccctgcctcc catgtccaag cgattcttgt 120
gcctcagcct tccctgtagc tagaattaca ggcacatgcc accacaccca gctagttttt 180
gtatttttag tagagacagg gtttcaccat gttggccagg ctggtctcaa actcctnacc 240
tcagnggtca ggctggtctc aaactcctga cctcaagtga tctgcccacc tcagcctccc 300
aaagtgctan gattacaggc cgtgagcc                                      328
```

<210> 419
<211> 389
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(389)
<223> n = A,T,C or G

<400> 419
```
cctcctcaag acggcctgtg gtccgcctcc cggcaaccaa gaagcctgca gtgccatatg 60
acccctgagc catggactgg agcctgaaag gcagcgtaca ccctgctcct gatcttgctg 120
cttgtttcct ctctgtggct ccattcatag cacagttgtt gcactgaggc ttgtgcaggc 180
cgagcaaggc caagctggct caaagagcaa ccagtcaact ctgccacggt gtgccaggca 240
ccggttctcc agccaccaac ctcactcgct cccgcaaatg gcacatcagt tcttctaccc 300
taaaggtagg accaaagggc atctgctttt ctgaagtcct ctgctctatc agccatcacg 360
```

144

```
tggcagccac tcnggctgtg tcgacgcgg                                    389
```

```
<210> 420
<211> 408
<212> DNA
<213> Homo sapiens
```

```
<400> 420
gttcctccta actcctgcca gaaacagctc tcctcaacat gagagctgca cccctcctcc 60
tggccagggc agcaagcctt agccttggct tcttgtttct gcttttttc tggctagacc 120
gaagtgtact agccaaggag ttgaagtttg tgactttggt gtttcggcat ggagaccgaa 180
gtcccattga cacctttccc actgacccca taaaggaatc ctcatggcca caaggatttg 240
gccaactcac ccagctgggc atggagcagc attatgaact tggagagtat ataagaaaga 300
gatatagaaa attcttgaat gagtcctata aacatgaaca ggtttatatt cgaagcacag 360
acgttgaccg gactttgatg aagtgctatg acaaacctgg caagcccg                408
```

```
<210> 421
<211> 352
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> misc_feature
<222> (1)...(352)
<223> n = A,T,C or G
```

```
<400> 421
gctcaaaaat cttttttactg atnggcatgg ctacacaatc attgactatt acggaggcca 60
gaggagaatg aggcctggcc tgggagccct gtgcctacta naagcacatt agattatcca 120
ttcactgaca gaacaggtct tttttgggtc cttcttctcc accacnatat acttgcagtc 180
ctccttcttg aagattcttt ggcagttgtc tttgtcataa cccacaggtg tagaaacaag 240
ggtgcaacat gaaatttctg tttcgtagca agtgcatgtc tcacaagttg gcangtctgc 300
cactccgagt ttattgggtg tttgtttcct ttgagatcca tgcatttcct gg            352
```

```
<210> 422
<211> 337
<212> DNA
<213> Homo sapiens
```

```
<400> 422
atgccaccat gctggcaatg cagcgggcgg tcgaaggcct gcatatccag cccaagctgg 60
cgatgatcga cggcaaccgt tgcccgaagt tgccgatgcc agccgaagcg gtggtcaagg 120
gcgatagcaa ggtgccggcg atcgcggcgg cgtcaatcct ggccaaggtc agccgtgatc 180
gtgaaatggc agctgtcgaa ttgatctacc cgggttatgg catcggcggg cataagggct 240
atccgacacc ggtgcacctg gaagccttgc agcggctggg gccgacgccg attcaccgac 300
gcttcttccg ccggtacggc tggcctatga aaattat                            337
```

```
<210> 423
<211> 310
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> misc_feature
<222> (1)...(310)
<223> n = A,T,C or G
```

```
<400> 423
```

145

```
gctcaaaaat cttttactg atatggcatg gctacacaat cattgactat tagaggccag 60
aggagaatga ggcctggcct gggagccctg tgcctactan aagcncatta gattatccat 120
tcactgacag aacaggtctt ttttgggtcc ttcttctcca ccacgatata cttgcagtcc 180
tccttcttga agattctttg gcagttgtct ttgtcataac ccacaggtgt anaaacaagg 240
gtgcaacatg aaatttctgt ttcgtagcaa gtgcatgtct cacagttgtc aagtctgccc 300
tccgagttta                                                         310

<210> 424
<211> 370
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(370).
<223> n = A,T,C or G

<400> 424
gctcaaaaat cttttactg ataggcatgg ctacacaatc attgactatt agaggccaga 60
ggagaatgag gcctggcctg ggagccctgt gcctactaga agcacattag attatccatt 120
cactgacaga acaggtcttt tttgggtcct tcttctccac cacgatatac ttgcagtcct 180
ccttcttgaa gattctttgg cagttgtctt tgtcataacc cacaggtgta gaaacatcct 240
ggttgaatct cctggaactc cctcattagg tatgaaatag catgatgcat tgcataaagt 300
cacgaaggtg gcaaagatca caacgctgcc cagganaaca ttcattgtga taagcaggac 360
tccgtcgacg                                                         370

<210> 425
<211> 216
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(216)
<223> n = A,T,C or G

<400> 425
aattgctatn ntttattttg ccactcaaaa taattaccaa aaaaaaaaaa tnttaaatga 60
taacaacnca acatcaaggn aaananaaca ggaatggntg actntgcata aatnggccga 120
anattatcca ttatnttaag ggttgacttc aggntacagc acacagacaa acatgcccag 180
gaggntntca ggaccgctcg atgtnttntg aggagg                           216

<210> 426
<211> 596
<212> DNA
<213> Homo sapiens

<400> 426
cttccagtga ggataaccct gttgccccgg gccgaggttc tccattaggc tctgattgat 60
tggcagtcag tgatggaagg gtgttctgat cattccgact gccccaaggg tcgctggcca 120
gctctctgtt ttgctgagtt ggcagtagga cctaatttgt taattaagag tagatggtga 180
gctgtccttg tattttgatt aacctaatgg ccttcccagc acgactcgga ttcagctgga 240
gacatcacgg caacttttaa tgaaatgatt tgaagggcca ttaagaggca cttcccgtta 300
ttaggcagtt catctgcact gataacttct tggcagctga gctggtcgga gctgtggccc 360
aaacgcacac ttggcttttg gttttgagat acaactctta atcttttagt catgcttgag 420
ggtggatggc cttttcagct ttaacccaat ttgcactgcc ttggaagtgt agccaggaga 480
atacactcat atactcgtgg gcttagaggc cacagcagat gtcattggtc tactgcctga 540
gtcccgctgg tcccatccca ggaccttcca tcggcgagta cctgggagcc cgtgct 596
```

146

```
<210> 427
<211> 107
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(107)
<223> n = A,T,C or G

<400> 427
gaagaattca agttaggttt attcaaaggg cttacngaga atcctanacc caggncccag 60
cccgggagca gccttanaga gctcctgttt gactgcccgg ctcagng               107

<210> 428
<211> 38
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(38)
<223> n = A,T,C or G

<400> 428
gaacttccna anaangactt tattcactat tttacatt                          38

<210> 429
<211> 544
<212> DNA
<213> Homo sapiens

<400> 429
ctttgctgga cggaataaaa gtggacgcaa gcatgacctc ctgatgaggg cgctgcattt 60
attgaagagc ggctgcagcc ctgcggttca gattaaaatc cgagaattgt atagacgccg 120
atatccacga actcttgaag gactttctga tttatccaca atcaaatcat cggttttcag 180
tttggatggt ggctcatcac ctgtagaacc tgacttggcc gtggctggaa tccactcgtt 240
gccttccact tcagttacac ctcactcacc atcctctcct gttggttctg tgctgcttca 300
agatactaag cccacatttg agatgcagca gccatctccc ccaattcctc ctgtccatcc 360
tgatgtgcag ttaaaaaatc tgccctttta tgatgtcctt gatgttctca tcaagcccac 420
gagtttagtt caaagcagta ttcagcgatt tcaagagaag ttttttattt ttgctttgac 480
acctcaacaa gttagagaga tatgcatatc cagggatttt ttgccaggtg gtaggagaga 540
ttat                                                              544

<210> 430
<211> 507
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(507)
<223> n = A,T,C or G

<400> 430
cttatcncaa tggggctccc aaacttggct gtgcagtgga aactccgggg gaattttgaa 60
gaacactgac acccatcttc caccccgaca ctctgattta attgggctgc agtgagaaca 120
```

```
gagcatcaat ttaaaaagct gcccagaatg ttntcctggg cagcgttgtg atctttgccn 180
ccttcgtgac tttatgcaat gcatcatgct atttcatacc taatgaggga gttccaggag 240
attcaaccag gatgtttcta cncctgtggg ttatgacaaa gacaactgcc aaagaatntt 300
caagaaggag gactgcaagt atatcgtggt ggagaagaag gacccaaaaa agacctgttc 360
tgtcagtgaa tggataatct aatgtgcttc tagtaggcac agggctccca ggccaggcct 420
cattctcctc tggcctctaa tagtcaatga ttgtgtagcc atgcctatca gtaaaaagat 480
ttttgagcaa aaaaaaaaaa aaaaaaa                                     507
```

```
<210> 431
<211> 392
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(392)
<223> n = A,T,C or G

<400> 431
gaaaattcag aatggataaa aacaaatgaa gtacaaaata tttcagattt acatagcgat 60
aaacaagaaa gcacttatca ggaggactta caaatggaag tacactctan aaccatcatc 120
tatcatggct aaatgtgaga ttagcacagc tgtattattt gtacattgca aacacctaga 180
aagagatggg aaacaaaatc ccaggagttt tgtgtgtgga gtcctgggtt ttccaacaga 240
catcattcca gcattctgag attagggnga ttggggatca ttctggagtt ggaatgttca 300
acaaaagtga tgttgttagg taaaatgtac aacttctgga tctatgcaga cattgaaggt 360
gcaatgagtc tggcttttac tctgctgttt ct                              392
```

```
<210> 432
<211> 387
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(387)
<223> n = A,T,C or G

<400> 432
ggtatccnta cataatcaaa tatagctgta gtacatgttt tcattggngt agattaccac 60
aaatgcaagg caacatgtgt agatctcttg tcttattctt ttgtctataa tactgtattg 120
ngtagtccaa gctctcggna gtccagccac tgngaaacat gctcccttta gattaacctc 180
gtggacnctn ttgttgnatt gtctgaactg tagngccctg tattttgctt ctgtctgnga 240
attctgttgc ttctggggca tttccttgng atgcagagga ccaccacaca gatgacagca 300
atctgaattg ntccaatcac agctgcgatt aagacatact gaaatcgtac aggaccggga 360
acaacgtata gaacactgga gtccttt                                     387
```

```
<210> 433
<211> 281
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(281)
<223> n = A,T,C or G

<400> 433
ttcaactagc anagaanact gcttcagggn gtgtaaaatg aaaggcttcc acgcagttat 60
```

148

```
ctgattaaag aacactaaga gagggacaag gctagaagcc gcaggatgtc tacactatag 120
caggcnctat ttgggttggc tggaggagct gtggaaaaca tggagagatt ggcgctggag 180
atcgccgtgg ctattcctcn ttgntattac accagngagg ntctctgtnt gcccactggt 240
tnnaaaaccg ntatacaata atgatagaat aggacacaca t                     281
```

```
<210> 434
<211> 484
<212> DNA
<213> Homo sapiens
```

```
<400> 434
ttttaaaata agcatttagt gctcagtccc tactgagtac tctttctctc ccctcctctg 60
aatttaattc tttcaacttg caatttgcaa ggattacaca tttcactgtg atgtatattg 120
tgttgcaaaa aaaaaaaagt gtctttgttt aaaattactt ggtttgtgaa tccatcttgc 180
ttttccccca ttggaactag tcattaaccc atctctgaac tggtagaaaa acatctgaag 240
agctagtcta tcagcatctg acaggtgaat tggatggttc tcagaaccat ttcacccaga 300
cagcctgttt ctatcctgtt taataaatta gtttgggttc tctacatgca taacaaaccc 360
tgctccaatc tgtcacataa aagtctgtga cttgaagttt agtcagcacc cccaccaaac 420
tttattttc tatgtgtttt ttgcaacata tgagtgtttt gaaaataaag tacccatgtc 480
ttta                                                             484
```

```
<210> 435
<211> 424
<212> DNA
<213> Homo sapiens
```

```
<400> 435
gcgccgctca gagcaggtca ctttctgcct tccacgtcct ccttcaagga agccccatgt 60
gggtagcttt caatatcgca ggttcttact cctctgcctc tataagctca aacccaccaa 120
cgatcgggca agtaaacccc ctccctcgcc gacttcggaa ctggcgagag ttcagcgcag 180
atgggcctgt ggggagggg caagatagat gaggggagc ggcatggtgc ggggtgaccc 240
cttggagaga ggaaaaaggc cacaagaggg gctgccaccg ccactaacgg agatggccct 300
ggtagagacc tttgggggtc tggaacctct ggactcccca tgctctaact cccacactct 360
gctatcagaa acttaaactt gaggattttc tctgtttttc actcgcaata aattcagagc 420
aaac                                                             424
```

```
<210> 436
<211> 667
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> misc_feature
<222> (1)...(667)
<223> n = A,T,C or G
```

```
<400> 436
accttgggaa nactctcaca atataaaggg tcgtagactt tactccaaat tccaaaaagg 60
tcctggccat gtaatcctga aagtttccc aaggtagcta taaaatcctt ataagggtgc 120
agcctcttct ggaattcctc tgatttcaaa gtctcactct caagttcttg aaaacgaggg 180
cagttcctga aaggcaggta tagcaactga tcttcagaaa gaggaactgt gtgcaccggg 240
atgggctgcc agagtaggat aggattccag atgctgacac cttctggggg aaacagggct 300
gccaggtttg tcatagcact catcaaagtc cggtcaacgt ctgtgcttcg aatataaacc 360
tgttcatgtt tataggactc attcaagaat tttctatatc tcttttcttat atactctcca 420
agttcataat gctgctccat gcccagctgg gtgagttggc caaatccttg tggccatgag 480
gattccttta tggggtcagt gggaaaggtg tcaatgggac ttcggtctcc atgccgaaac 540
accaaagtca caaacttcaa ctccttggct agtacacttc ggtctagcca gaaaaaaagc 600
agaaacaaga agccaaggct aaggcttgct gccctgccag gaggagggt gcagctctca 660
```

149

```
tgttgag                                                        667

<210> 437
<211> 693
<212> DNA
<213> Homo sapiens

<400> 437
ctacgtctca accctcattt ttaggtaagg aatcttaagt ccaaagatat taagtgactc 60
acacagccag gtaaggaaag ctggattggc acactaggac tctaccatac cgggtttgt 120
taaagctcag gttaggaggc tgataagctt ggaaggaact tcagacagct ttttcagatc 180
ataaaagata attcttagcc catgttcttc tccagagcag acctgaaatg acagcacagc 240
aggtactcct ctattttcac ccctcttgct tctactctct ggcagtcaga cctgtgggag 300
gccatgggag aaagcagctc tctggatgtt tgtacagatc atggactatt ctctgtggac 360
catttctcca ggttacccta ggtgtcacta ttggggggac agccagcatc tttagctttc 420
atttgagttt ctgtctgtct tcagtagagg aaacttttgc tcttcacact tcacatctga 480
acacctaact gctgttgctc ctgaggtggt gaaagacaga tatagagctt acagtattta 540
tcctatttct aggcactgag ggctgtgggg taccttgtgg tgccaaaaca gatcctgttt 600
taaggacatg ttgcttcaga gatgtctgta actatctggg ggctctgttg gctctttacc 660
ctgcatcatg tgctctcttg gctgaaaatg acc                           693

<210> 438
<211> 360
<212> DNA
<213> Homo sapiens

<400> 438
ctgcttatca caatgaatgt tctcctgggc agcgttgtga tctttgccac cttcgtgact 60
ttatgcaatg catcatgcta tttcatacct aatgagggag ttccaggaga ttcaaccagg 120
atgtttctac acctgtgggt tatgacaaag acaactgcca aagaatcttc aagaaggagg 180
actgcaagta tatctggtgg agaagaagga cccaaaaaag acctgttctg tcagtgaatg 240
gataatctaa tgtgcttcta gtaggcacag ggctcccagg ccaggcctca ttctcctctg 300
gcctctaata gtcaataatt gtgtagccat gcctatcagt aaaaagattt ttgagcaaac 360

<210> 439
<211> 431
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(431)
<223> n = A,T,C or G

<400> 439
gttcctnnta actcctgcca gaaacagctc tcctcaacat gagagctgca cccctcctcc 60
tggccagggc agcaagcctt agccttggct tcttgtttct gcttttttc tggctagacc 120
gaagtgtact agccaaggag ttgaagtttg tgactttggt gtttcggcat ggagaccgaa 180
gtcccattga cacctttccc actgaccca taaaggaatc ctcatggcca caaggatttg 240
gccaactcac ccagctgggc atggagcagc attatgaact tggagagtat ataagaaaga 300
gatatagaaa attcttgaat gagtcctata aacatgaaca ggtttatatt cgaagcacag 360
acgttgaccg gactttgatg agtgctatga caaacctggc agcccgtcga cgcggccgcg 420
aatttagtag t                                                   431

<210> 440
<211> 523
<212> DNA
<213> Homo sapiens
```

150

<400> 440
agagataaag cttaggtcaa agttcataga gttcccatga actatatgac tggccacaca 60
ggatctttg tatttaagga ttctgagatt ttgcttgagc aggattagat aaggctgttc 120
tttaaatgtc tgaaatggaa cagatttcaa aaaaaaaccc cacaatctag ggtgggaaca 180
aggaaggaaa gatgtgaata ggctgatggg caaaaaacca atttacccat cagttccagc 240
cttctctcaa ggagaggcaa agaaaggaga tacagtggag acatctggaa agttttctcc 300
actggaaaac tgctactatc tgttttttata tttctgttaa aatatatgag gctacagaac 360
taaaaattaa aacctctttg tgtcccttgg tcctggaaca tttatgttcc ttttaaagaa 420
acaaaaatca aactttacag aaagatttga tgtatgtaat acatatagca gctcttgaag 480
tatatatatc atagcaaata agtcatctga tgagaacaag cta   523

<210> 441
<211> 430
<212> DNA
<213> Homo sapiens

<400> 441
gttcctccta actcctgcca gaaacagctc tcctcaacat gagagctgca cccctcctcc 60
tggccagggc agcaagcctt agccttggct tcttgtttct gcttttttttc tggctagacc 120
gaagtgtact agccaaggag ttgaagtttg tgactttggt gtttcggcat ggagaccgaa 180
gtcccattga caccttttccc actgacccca taaaggaatc ctcatggcca caaggatttg 240
gccaactcac ccagctgggc atggagcagc attatgaact tggagagtat ataagaaaga 300
gatatagaaa attcttgaat gagtcctata aacatgaaca ggtttatatt cgaagcacag 360
acgttgaccg gactttgatg agtgctatga caaacctggc agcccgtcga cgcggccgcg 420
aatttagtag   430

<210> 442
<211> 362
<212> DNA
<213> Homo sapiens

<400> 442
ctaaggaatt agtagtgttc ccatcacttg tttggagtgt gctattctaa aagattttga 60
tttcctggaa tgacaattat attttaactt tggtggggga aagagttata ggaccacagt 120
cttcacttct gatacttgta aattaatctt ttattgcact tgttttgacc attaagctat 180
atgtttagaa atggtcattt tacggaaaaa ttagaaaaat tctgataata gtgcagaata 240
aatgaattaa tgttttactt aatttatatt gaactgtcaa tgacaaataa aaattctttt 300
tgattatttt ttgttttcat ttaccagaat aaaaactaag aattaaaagt ttgattacag 360
tc   362

<210> 443
<211> 624
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(624)
<223> n = A,T,C or G

<400> 443
tttttttttt gcaacacaat atacatcaca gtgaaatgtg taatccttgc aaattgcaag 60
ttgaaagaat taaattcaga ggaggggaga gaaagagtac tcagtaggga ctgagcacta 120
aatgcttatt ttaaaagaaa tgtaaagagc agaaagcaat tcaggctacc ctgccttttg 180
tgctggctag tactccggtc ggtgtcagca gcacgtggca ttgaacattg caatgtggag 240
cccaaaccac agaaaatggg gtgaaattgg ccaactttct attaacttgg cttcctgttt 300
tataaaatat tgtgaataat atcacctact tcaaagggca gttatgaggc ttaaatgaac 360

151

```
taacgcctac aaaacactta aacatagata acataggtgc aagtactatg tatctggtac 420
atggtaaaca tccttattat taaagtcaac gctaaaatga atgtgtgtgc atatgctaat 480
agtacagaga gagggcactt aaaccaacta agggcctgga gggaaggttt cctggaaaga 540
ngatgcttgt gctgggtcca aatcttggtc tactatgacc ttggccaaat tatttaaact 600
ttgtccctat ctgctaaaca gatc                                        624
```

```
<210> 444
<211> 425
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> misc_feature
<222> (1)...(425)
<223> n = A,T,C or G
```

```
<400> 444
gcacatcatt nntcttgcat tctttgagaa taagaagatc agtaaatagt tcagaagtgg 60
gaagctttgt ccaggcctgt gtgtgaaccc aatgttttgc ttagaaatag aacaagtaag 120
ttcattgcta tagcataaca caaaatttgc ataagtggtg gtcagcaaat ccttgaatgc 180
tgcttaatgt gagaggttgg taaaatcctt tgtgcaacac tctaactccc tgaatgtttt 240
gctgtgctgg gacctgtgca tgccagacaa ggccaagctg gctgaaagag caaccagcca 300
cctctgcaat ctgccacctc ctgctggcag gatttgtttt tgcatcctgt gaagagccaa 360
ggaggcacca gggcataagt gagtagactt atggtcgacg cggccgcgaa tttagtagta 420
gtaga                                                             425
```

```
<210> 445
<211> 414
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> misc_feature
<222> (1)...(414)
<223> n = A,T,C or G
```

```
<400> 445
catgtttatg nttttggatt actttgggca cctagtgttt ctaaatcgtc tatcattctt 60
ttctgttttt caaaagcaga gatggccaga gtctcaacaa actgtatctt caagtctttg 120
tgaaattctt tgcatgtggc agattattgg atgtagtttc ctttaactag catataaatc 180
tggtgtgttt cagataaatg aacagcaaaa tgtggtggaa ttaccatttg gaacattgtg 240
aatgaaaaat tgtgtctcta gattatgtaa caaataacta tttcctaacc attgatcttt 300
ggatttttat aatcctactc acaaatgact aggcttctcc tcttgtattt tgaagcagtg 360
tgggtgctgg attgataaaa aaaaaaaaag tcgacgcggc cgcgaattta gtag        414
```

```
<210> 446
<211> 631
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> misc_feature
<222> (1)...(631)
<223> n = A,T,C or G
```

```
<400> 446
acaaattaga anaaagtgcc agagaacacc acataccttg tccggaacat tacaatggct 60
tctgcatgca tgggaagtgt gagcattcta tcaatatgca ggagccatct tgcaggtgtg 120
```

152

```
atgctggtta tactggacaa cactgtgaaa aaaaggacta cagtgttcta tacgttgttc 180
ccggtcctgt acgatttcag tatgtcttaa tcgcagctgt gattggaaca attcagattg 240
ctgtcatctg tgtggtggtc ctctgcatca caagggccaa actttaggta atagcattgg 300
actgagattt gtaaactttc caaccttcca ggaaatgccc cagaagcaac agaattcaca 360
gacagaagca aaatacaggg cactacagtt cagacaatac aacaagagcg tccacgaggt 420
taatctaaag ggagcatgtt tcacagtggc tggactaccg agagcttgga ctacacaata 480
cagtattata gacaaaagaa taagacaaga gatctacaca tgttgccttg catttgtggt 540
aatctacacc aatgaaaaca tgtactacag ctatatttga ttatgtatgg atatatttga 600
aatagtatac attgtcttga tgttttttct g                                631
```

<210> 447
<211> 585
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(585)
<223> n = A,T,C or G

<400> 447
```
ccttgggaaa antntcacaa tataaagggt cgtagacttt actccaaatt ccaaaaaggt 60
cctggccatg taatcctgaa agtttttccca aggtagctat aaaatcctta taagggtgca 120
gcctcttctg gaattcctct gatttcaaag tctcactctc aagttcttga aaacgagggc 180
agttcctgaa aggcaggtat agcaactgat cttcagaaag aggaactgtg tgcaccggga 240
tgggctgcca gagtgaggata ggattccaga tgctgacacc ttctggggga aacagggctg 300
ccaggtttgt catagcactc atcaaagtcc ggtcaacgtc tgtgcttcga atataaacct 360
gttcatgttt ataggactca ttcaagaatt ttctatatct ctttcttata tactctccaa 420
gttcataatg ctgctccatg cccagctggg tgagttggcc aaatccttgt ggccatgagg 480
attcctttat ggggtcagtg ggaaaggtgt caatgggact tcggtctcca tgccgaaaca 540
ccaaagtcac aaacttcaac tccttggcta gtacacttcg gtcta               585
```

<210> 448
<211> 93
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(93)
<223> n = A,T,C or G

<400> 448
```
tgctcgtggg tcattctgan nnccgaactg accntgccag ccctgccgan gggccnccat 60
ggctccctag tgccctggag aggangggggc tag                            93
```

<210> 449
<211> 706
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(706)
<223> n = A,T,C or G

<400> 449
```
ccaagttcat gctntgtgct ggacgctgga cagggggcaa aagcnnttgc tcgtgggtca 60
```

153

```
ttctgancac cgaactgacc atgccagccc tgccgatggt cctccatggc tccctagtgc 120
cctggagagg aggtgtctag tcagagagta gtcctggaag gtggcctctg ngaggagcca 180
cggggacagc atcctgcaga tggtcgggcg cgtcccattc gccattcagg ctgcgcaact 240
gttgggaagg gcgatcggtg cgggcctctt cgctattacg ccagctggcg aaaggggat 300
.gtgctgcaag gcgattaagt tgggtaacgc cagggttttc ccagtcncga cgttgtaaaa 360
cgacggccag tgaattgaat ttaggtgacn ctatagaaga gctatgacgt cgcatgcacg 420
cgtacgtaag cttggatcct ctagagcggc cgcctactac tactaaattc gcggccgcgt 480
cgacgtggga tccncactga gagagtggag agtgacatgt gctggacnct gtccatgaag 540
cactgagcag aagctggagg cacaacgcnc cagacactca cagctactca ggaggctgag 600
aacaggttga acctgggagg tggaggttgc aatgagctga gatcaggccn ctgcncccca 660
gcatggatga cagagtgaaa ctccatctta aaaaaaaaaa aaaaaa         706
```

```
<210> 450
<211> 493
<212> DNA
<213> Homo sapiens
```

```
<400> 450
gagacggagt gtcactctgt tgcccaggct ggagtgcagc aagacactgt ctaagaaaaa 60
acagttttaa aaggtaaaac aacataaaaa gaaatatcct atagtggaaa taagagagtc 120
aaatgaggct gagaacttta caaagggatc ttacagacat gtcgccaata tcactgcatg 180
agcctaagta taagaacaac ctttggggag aaaccatcat ttgacagtga ggtacaattc 240
caagtcaggt agtgaaatgg gtggaattaa actcaaatta atcctgccag ctgaaacgca 300
agagacactg tcagagagtt aaaaagtgag ttctatccat gaggtgattc cacagtcttc 360
tcaagtcaac acatctgtga actcacagac caagttctta aaccactgtt caaactctgc 420
tacacatcag aatcacctgg agagctttac aaactcccat tgccgagggt cgacgcggcc 480
gcgaatttag tag                                          493
```

```
<210> 451
<211> 501
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> misc_feature
<222> (1)...(501)
<223> n = A,T,C or G
```

```
<400> 451
gggcgcgtcc cattcgccat tcaggctgcg caactgttgg gaagggcgat cggtgcgggc 60
ctcttcgcta ttacgccagc tggcgaaagg gggatgtgct gcaaggcgat taagttgggt 120
aacgccaggg ttttcccagt cncgacgttg taaaacgacg ccagtgaat tgaatttagg 180
tgacnctata gaagagctat gacgtcgcat gcacgcgtac gtaagcttgg atcctctaga 240
gcggccgcct actactacta aattcgcggc cgcgtcgacg tgggatccnc actgagagag 300
tggagagtga catgtgctgg acnctgtcca tgaagcactg agcagaagct ggaggcacaa 360
cgcnccagac actcacagct actcaggagg ctgagaacag gttgaacctg ggaggtggag 420
gttgcaatga gctgagatca ggccnctgcn ccccagcatg gatgacagag tgaaactcca 480
tcttaaaaaa aaaaaaaaaa a                                  501
```

```
<210> 452
<211> 51.
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> misc_feature
<222> (1)...(51)
<223> n = A,T,C or G
```

154

```
<400> 452
agacggtttc accnttacaa cnccttttag gatgggnntt ggggagcaag c          51

<210> 453
<211> 317
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(317)
<223> n = A,T,C or G

<400> 453
tacatcttgc tttttcccca ttggaactag tcattaaccc atctctgaac tggtagaaaa 60
acatctgaag agctagtcta tcagcatctg gcaagtgaat tggatggttc tcagaaccat 120
ttcacccana cagcctgttt ctatcctgtt taataaatta gtttgggttc tctacatgca 180
taacaaaccc tgctccaatc tgtcacataa aagtctgtga cttgaagttt antcagcacc 240
cccaccaaac tttatttttc tatgtgtttt ttgcaacata tgagtgtttt gaaaataagg 300
tacccatgtc tttatta                                                317

<210> 454
<211> 231
<212> DNA
<213> Homo sapiens

<400> 454
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taagccacgc cacgctcttg aaggagtctt gaattctcct ctgctcactc agtagaacca 120
agaagaccaa attcttctgc atcccagctt gcaaacaaaa ttgttcttct aggtctccac 180
ccttcctttt tcagtgttcc aaagctcctc acaatttcat gaacaacagc t           231

<210> 455
<211> 231
<212> DNA
<213> Homo sapiens

<400> 455
taccaaagag ggcataataa tcagtctcac agtagggttc accatcctcc aagtgaaaaa 60
cattgttccg aatgggcttt ccacaggcta cacacacaaa acaggaaaca tgccaagttt 120
gtttcaacgc attgatgact tctccaagga tcttcctttg gcatcgacca cattcagggg 180
caaagaattt ctcatagcac agctcacaat acagggctcc tttctcctct a           231

<210> 456
<211> 231
<212> DNA
<213> Homo sapiens

<400> 456
ttggcaggta cccttacaaa gaagacacca taccttatgc gttattaggt ggaataatca 60
ttccattcag tattatcgtt attattcttg gagaaaccct gtctgtttac tgtaaccttt 120
tgcactcaaa ttcctttatc aggaataact acatagccac tatttacaaa gccattggaa 180
ccttttttatt tggtgcagct gctagtcagt ccctgactga cattgccaag t           231

<210> 457
<211> 231
<212> DNA
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<213> Homo sapiens

<220>
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<222> (1)...(231)
<223> n = A,T,C or G

<400> 457
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tatttgattt tattagcaat ctctttcaga agacccttga gatcattaag ctttgtatcc  180
agttgtctaa atcgatgcct catttcctct gaggtgtcgc tggcttttgt g           231

<210> 458
<211> 231
<212> DNA
<213> Homo sapiens

<400> 458
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acaccctaac cttgggtaac agcatttgga attatcattt gggatgagta gaatttccaa  180
ggtcctgggt taggcatttt ggggggccag accccaggag aagaagattc t           231

<210> 459
<211> 231
<212> DNA
<213> Homo sapiens

<400> 459
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ccttcgcgaa acctgtggtg gcccaccagt cctaacggga caggacagag agacagagca  120
gccctgcact gttttccctc caccacagcc atcctgtccc tcattggctc tgtgctttcc  180
actatacaca gtcaccgtcc caatgagaaa caagaaggag caccctccac a           231

<210> 460
<211> 231
<212> DNA
<213> Homo sapiens

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gcaggtataa catgctgcaa caacagatgt gactaggaac ggccggtgac atggggaggg   60
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cccacctccc cacacgcaca cggccagcct ggagcccaca gaagggtcct cctgcagcca  180
gtggagcttg gtccagcctc cagtccaccc ctaccaggct taaggataga a           231

<210> 461
<211> 231
<212> DNA
<213> Homo sapiens

<400> 461
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gcgtgtgctc cagaagagtg tgtgcatgcc agaggggaaa caggcgcctg tgtgtcctgg  120
gtggggttca gtgaggagtg ggaaattggt tcagcagaac caagccgttg ggtgaataag  180
aggggggattc catggcactg atagagccct atagtttcag agctgggaat t          231

<210> 462
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156

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<211> 231
<212> DNA
<213> Homo sapiens

<400> 462
aggtaccctc attgtagcca tgggaaaatt gatgttcagt ggggatcagt gaattaaatg 60
gggtcatgca agtataaaaa ttaaaaaaaa aagacttcat gcccaatctc atatgatgtg 120
gaagaactgt tagagagacc aacagggtag tgggttagag atttccagag tcttacattt 180
tctagaggag gtatttaatt tcttctcact catccagtgt tgtatttagg a     .       231

<210> 463
<211> 231
<212> DNA
<213> Homo sapiens              ¢

<400> 463
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actgagtaga caggtgtcct cttggcatgg taagtcttaa gtcccctccc agatctgtga 120
catttgacag gtgtcttttc ctctggacct cggtgtcccc atctgagtga gaaaaggcag 180
tggggaggtg gatcttccag tcgaagcggt atagaagccc gtgtgaaaag c         231

<210> 464
<211> 231
<212> DNA
<213> Homo sapiens

<400> 464
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aaggacatca catatgaaga atgtttaagt tggaggtggc aacgtgaatt gcaaacaggg 120
cctgcttcag tgactgtgtg cctgtagtcc cagctactcg ggagtctgtg tgaggccagg 180
ggtgccagcg caccagctag atgctctgta acttctaggc cccattttcc c         231

<210> 465
<211> 231
<212> DNA
<213> Homo sapiens

<400> 465
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gtggcaaatt agcaacaaat tctgacatca tatttatggt ttctgtatct ttgttgatga 120
aggatggcac aatttttgct tgtgttcata atatactcag attagttcag ctccatcaga 180
taaactggag acatgcagga cattagggta gtgttgtagc tctggtaatg a         231

<210> 466
<211> 231
<212> DNA
<213> Homo sapiens

<400> 466
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cctgtgcaat caaatattgt ggagaattcc ctagctggag aagtcacaaa gactataggc 180
aataatggag accagtccca caagatgaca accagtcgtt gtgtgcggct g         231

<210> 467
<211> 311
<212> DNA
<213> Homo sapiens
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157

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<400> 467
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tgtgccttaa cagaaggtct tgagattcta agtgggaatc atttcagtga ctgtcatgtg 180
gcatgggtct ctgcccaagc tcgtaatgag actatagcaa ggcggctgtg ggacgtcagt 240
tgtgacctgc tgggcctccc aatagactaa caggcagtgc cagttggacc caagagaaga 300
ctgcagcaga c                                                      311

<210> 468
<211> 3112
<212> DNA
<213> Homo sapiens

<400> 468
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tggaaggcac tggatgcctg atgatgaagt ggactttcaa actggggcac tactgaaacg 180
atgggatggc cagagacaca ggagatgagt tggagcaagc tcaataacaa agtggttcaa 240
cgaggacttg gaattgcatg gagctggagc tgaagtttag cccaattgtt tactagttga 300
gtgaatgtgg atgattggat gatcatttct catctctgag cctcaggttc cccatccata 360
aaatggggata cacagtatga tctataaagt gggatatagt atgatctact tcactgggtt 420
atttgaagga tgaattgaga taatttattt caggtgccta gaacaatgcc cagattagta 480
catttggtgg aactgagaaa tggcataaca ccaaatttaa tatatgtcag atgttactat 540
gattatcatt caatctcata gtttttgtcat ggcccaattt atcctcactt gtgcctcaac 600
aaattgaact gttaacaaag gaatctctgg tcctgggtaa tggctgagca ccactgagca 660
tttccattcc agttggcttc ttgggtttgc tagctgcatc actagtcatc ttaaataaat 720
gaagttttaa catttctcca gtgattttt tatctcacct ttgaagatac tatgttatgt 780
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gatctgtgaa caggctggga agcatctcaa gatctttcca gggttatact tactagcaca 2160
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ctttgtttga tttttttttcc agtataaagt taaaatgctt agccttgtac tgaggctgta 2460
tacagccaca gcctctcccc atccctccag ccttatctgt catcaccatc aacccctccc 2520
atgcacctaa acaaaatcta acttgtaatt ccttgaacat gtcaggcata cattattcct 2580
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158

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tctgcctgag aagctcttcc ttgtctctta aatctagaat gatgtaaagt tttgaataag 2640
ttgactatct tacttcatgc aaagaaggga cacatatgag attcatcatc acatgagaca 2700
gcaaatacta aaagtgtaat ttgattataa gagtttagat aaatatatga aatgcaagag 2760
ccacagaggg aatgtttatg gggcacgttt gtaagcctgg gatgtgaagc aaaggcaggg 2820
aacctcatag tatcttatat aaatatacttc atttctctat ctctatcaca atatccaaca 2880
agcttttcac agaattcatg cagtgcaaat ccccaaaggt aacctttatc catttcatgg 2940
tgagtgcgct ttagaatttt ggcaaatcat actggtcact tatctcaact ttgagatgtg 3000
tttgtccttg tagttaattg aaagaaatag ggcactcttg tgagccactt tagggttcac 3060
tcctggcaat aaagaattta caaagagcaa aaaaaaaaaa aaaaaaaaa aa         3112
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<210> 469
<211> 2229
<212> DNA
<213> Homo sapiens
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<400> 469
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tgatttgcca aaattctaaa gcgcactcac catgaaatgg ataaaggtta cctttgggga 180
tttgcactgc atgaattctg tgaaaagctt gttggatatt gtgatagaga tagagaaatg 240
aagtatatta tataagatac tatgaggttc cctgcctttg cttcacatcc caggcttaca 300
aacgtgcccc ataaacattc cctctgtggc tcttgcattt catatattta tctaaactct 360
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ccttctttgc atgaagtaag atagtcaact tattcaaaac tttacatcat tctagattta 480
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ttacaagtta gattttgttt aggtgcatgg gaggggttca tggtgatgac agataaggct 600
ggagggatgg ggagaggctg tggctgtata cagcctcagt gcaaggctaa gcattttaac 660
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gcacaaagt gggaaatgaa tttcagtatg ggcaaagaca ctgaggatga tgttgattag 900
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cagtgtagaa aggtcacagt acagatctgg gaactaaata ttaaaaatga gtgtggctgg 1140
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ttttgagggt tagaaatatg aaatgatttg gttatgaacg cacagtttag gcagcaggtg 1260
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cacagtattc catttgttt gttgcatgtc ttgtgaagcc atcaagattt tctcgtctgt 1380
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ggtcacctga ggtcaggagt tcaagaccag cctggccaat atggtgaaac cccatctcta 2160
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aatggaatt                                                      2229
```

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<210> 470
<211> 2426
<212> DNA
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159

<213> Homo sapiens

<400> 470
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caaaattcta aagcgcactc accatgaaat ggataaaggt tacctttggg gatttgcact 180
gcatgaattc tgtgaaaagc ttgttggata ttgtgataga gatagagaaa tgaagtatat 240
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ccataaacat tccctctgtg gctcttgcat ttcatatatt tatctaaact cttataatca 360
aattcacatt ttagtatttg ctgtctcatg tgatgatgaa tctcatatgt gtcccttctt 420
tgcatgaagt aagatagtca acttattcaa aactttacat cattctagat ttaagagaca 480
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tccgagcatc acaaacaccc tctctgtttc ttcactgggc acagaatttt aatacttatt 1920
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gggtgacggt tttgcccaac acaatg   2426

<210> 471
<211> 812
<212> DNA
<213> Homo sapiens

<400> 471
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aaatattaaa aatgagtgtg gctggatata tggagaatgt tgggcccaga aggaaccgta 120
gagatcagat attacaacag ctttgttttg agggttagaa atatgaaatg atttggttat 180
gaacgcacag tttaggcagc agggccagaa tcctgaccct ctgccccgtg gttatctcct 240
ccccagcttg gctgcctcat gtcatcacag tattccattt tgtttgttgc atgtcttgtg 300
aagccatcaa gattttctcg tctgtttttc tctcattggt aatgctcact ttgtgacttc 360
atttcaaatc tgtaatcccg ttcaaataaa tatccacaac aggatctgtt ttcctgccca 420

160

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tcctttaagg aacacatcaa ttcattttct aatgtccttc cctcacaagc gggaccaggc 480
acagggccgag gctcatcgat gacccaagat ggcggccggg catttctccc agggatctct 540
gtgcttcctt ttgtgcttcc tgtgtgtgtg gatatttaaa ggggctggaa atgtgcaaaa 600
acatgtcact acttagacat tatattgtca tcttgctgtt tctagtgatg ttaattatct 660
ccatttcagc agatgtgtgg cctcagatgg taaagtcagc agcctttctt atttctcacc 720
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cacaaatctc ccctctgttt ttctgatgcc ag                              812
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<210> 472
<211> 515
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(515)
<223> n = A,T,C or G

<400> 472
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gttccagaat tattggtcct tgcagcccgg tgaatctcag caagaggaac caccaactga 180
caatcaggat attgaacctg gacaagagag agaaggaaca cctccgatcg aagaacgtaa 240
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cattgaaaat gtgactgaaa atttgaaaat tctctcaata aagtttgagt tttctctgaa 480
gaaaaaaaaa naaaaaaaaa aaanaaaaan aaaaa                           515
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<210> 473
<211> 5829
<212> DNA
<213> Homo sapiens

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161

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162

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<220>

163

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164

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<212> PRT
<213> Homo sapiens

165

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            20   25   30
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        35   40   45
His His His Thr His Glu His Thr Asp Thr Leu Pro Tyr Gly His Trp
    50   55   60
His Thr His Cys His Thr Val Thr Trp Thr His Leu His Thr Ile Thr
65   70   75   80
Pro Pro His Thr Leu Pro Val Asp Thr Arg Thr His Arg His Cys His
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Thr Asp Thr Gln Asn Thr Val Thr Arg Arg His His His Ala Asp Thr
            100   105   110
Pro Pro Leu Trp Cys Arg Leu Asn Tyr Pro Ala Gly Gly Thr Ala Val
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<210> 478
<211> 143
<212> PRT
<213> Homo sapiens

<400> 478
Met Tyr Arg His Thr Glu Thr Leu Pro His Gly Asp Thr Val Thr Gln
                5   10   15
Ser His Gly His Thr Gly Ile Val Thr Trp Thr Asp Thr Gln Thr Tyr
            20   25   30
Gly Glu Ile Thr Trp Thr His His His Thr Ile Thr Gly Thr Gln Thr
        35   40   45
His Gly Asp Ile Thr Thr Trp Thr His Cys His Thr Thr Thr Gly Thr
    50   55   60
Arg Asp Ile Thr Leu Ser His Gly His Thr Ile Thr His Met Asn Thr
65   70   75   80
Pro Thr His Cys His Met Asp Thr Gly Thr His Thr Ala Thr Leu Ser
                85   90   95
His Gly His Thr Ser Thr Pro Ser His His His Thr His Cys Leu Trp
            100   105   110
Thr Gln Gly His Thr Asp Thr Val Thr Gln Ile His Lys Thr Leu Ser
        115   120   125
His Gly Asp Ile Thr Met Gln Ile His His His Ser Gly Ala Val
    130   135   140

<210> 479
<211> 222
<212> PRT
<213> Homo sapiens

<400> 479
Met Tyr Arg His Thr Glu Thr Leu Pro His Gly Asp Thr Val Thr Gln
                5   10   15
Ser His Glu His Thr Gly Ile Val Thr Trp Thr Asp Thr Gln Thr Tyr
            20   25   30

166

```
Gly Glu Ile Thr Leu Thr His His His Thr Ile Thr Gly Thr Gln Thr
        35                      40                      45
His Gly Asp Ile Thr Thr Trp Thr His Cys His Thr Thr Thr Gly Thr
        50                      55                      60
Arg Asp Ile Thr Leu Ser His Gly His Thr Ile Thr His Met Asn Thr
65                      70                      75                      80
Pro Thr His Cys His Met Asp Thr Ala Thr His Thr Ala Thr Leu Ser
                85                      90                      95
His Gly His Thr Ser Ile Pro Ser His His His Thr His Cys His Val
            100                     105                     110
Asp Thr Arg Thr His Arg His Cys His Thr Asp Thr Gln Asn Thr Val
            115                     120                     125
Thr Arg Arg His His His Ala Asp Thr Pro Pro His Gly His Ser Thr
        130                     135                     140
Arg His Ser Ala Thr Gln Ile His His His Thr Glu Met Arg Thr His
145                     150                     155                     160
Cys His Thr Asp Thr Thr Thr Ser Leu Pro His Phe His Val Ser Ala
                165                     170                     175
Gly Gly Val Gly Pro Thr Thr Leu Gly Ser Asn Arg Glu Ile Thr Trp
            180                     185                     190
Thr Tyr Ser Glu Gly Lys Ile Phe Phe Tyr Phe Leu Gly Asn Gln Ala
        195                     200                     205
Arg Leu Cys Leu Lys Lys Arg Lys Lys Lys Gln Tyr Thr Val
        210                     215                     220
```

```
<210> 480
<211> 144
<212> PRT
<213> Homo sapiens

<400> 480
Met Glu Pro Tyr Arg Gly Asn Glu Gln Pro Ser Gln Glu Gln Gly Val
                5                       10                      15
Cys Cys Leu Trp Gly Leu Gln Ser Leu Pro Gln Gly Ser Tyr Val Thr
            20                      25                      30
Val Gly Phe Leu Val Val Lys Arg Gln Thr Ile Gly Arg Leu Glu Arg
        35                      40                      45
Asp Phe Met Phe Lys Cys Arg Lys Gln Pro Gly Leu Pro Pro Ser Gly
        50                      55                      60
Leu Cys Leu Leu Trp Pro Trp Pro Asn Leu Glu Phe Gly Arg Arg Gln
65                      70                      75                      80
Asp Arg Leu Thr Trp Ser Ser Val Ser Val Ala Gly Val Cys Ala Cys
                85                      90                      95
Arg Ala Arg Pro Gly Trp Leu Gly Glu Gln Pro Ala Thr Ser Ala Gly
            100                     105                     110
Val Arg Leu Glu Gln Val Glu Gln Pro Pro Ala His Pro Leu Gln Glu
        115                     120                     125
Ala Gly Val Ala Arg Phe Pro Arg Pro Glu Trp Val Pro Pro Asn Gly
        130                     135                     140
```

```
<210> 481
<211> 167
<212> PRT
<213> Homo sapiens

<400> 481
```

```
Met His Gly Pro Gln Val Leu Ala Arg Cys Ser Glu Cys Ala Cys Pro
                5                   10                  15
Ala Leu Ala Ala Thr Ser Ala Gly Val Arg Leu Glu Gly Val Asp Arg
            20                  25                  30
Pro Pro Thr Leu Pro Ser Gln Gly Ser Gly Trp Pro Cys Ser His Ser
        35                  40                  45
Leu Ser Gly Cys His Leu Met Ala Asp Gly Ala Lys Ala Leu Gly Lys
    50                  55                  60
Ala Asp Gly Pro Trp Pro Tyr Leu Phe Val Arg Arg Thr Asp Val Pro
 65                  70                  75                  80
Cys Pro Ala Ala Ser Glu Val Gly Gly Cys Ala Pro Ser Ser Trp Arg
                85                  90                  95
Ala Leu Ala Glu Val Thr Gly Cys Ser Leu Gly Pro Leu Gly Leu Ala
            100                 105                 110
Gln His Ala Gln Ala Ser Val Leu Leu Cys Tyr Lys Trp Ser His
        115                 120                 125
Ile Gly Glu Thr Ser Ser His Leu Arg Ser Lys Val Tyr Ala Ala Phe
    130                 135                 140
Gly Gly Ser Ser Pro Cys Leu Lys Gly Leu Met Ser Leu Trp Ala Ser
145                 150                 155                 160
Trp Leu Ser Arg Gly Arg Pro
                165
```

<210> 482
<211> 143
<212> PRT
<213> Homo sapiens

<400> 482
```
Met Glu Pro Tyr Arg Gly Asn Lys Lys Gln Val Gln Glu Lys Gly Val
                5                   10                  15
Pro Cys Leu Trp Gly Ser Ser Pro Cys Leu Arg Cys His Met Ala Leu
            20                  25                  30
Arg Ala Ser Trp Leu Pro Gly Gly Gly Pro Gln Ala Ile Leu Gly Arg
        35                  40                  45
Thr Leu Cys Ser Ser Ala Glu Ser Ser Gln Asp Cys His Pro Gly Gly
    50                  55                  60
Pro Ser Ile Ala Leu Ala Lys Pro Cys Arg Gly Val Trp Leu Leu Phe
 65                  70                  75                  80
Glu Pro Ala Trp Pro Pro Trp His Ala Arg Ala Pro Gly Ala Gly Thr
                85                  90                  95
Leu Leu Arg Val Cys Leu Ser Cys Leu Gly Cys His Leu Cys Gly Gly
            100                 105                 110
Ala Ser Gly Gly Gly Gly Pro Ala Thr Asn Leu Thr Gln Ser Arg Lys
        115                 120                 125
Trp Met Ala Met Phe Pro Gln Pro Glu Trp Leu Pro Pro Asp Gly
    130                 135                 140
```

<210> 483
<211> 143
<212> PRT
<213> Homo sapiens

<400> 483
```
Met Glu Thr Gln Arg Gly Asn Lys Gln Arg Ala Gln Glu Gln Gly Val
                5                   10                  15
Cys Cys Leu Trp Gly Ser Ser Pro Cys Leu Gly Ser Tyr Gly Thr Ala
```

168

```
              20                    25                    30
Gly Phe Leu Val Ala Lys Arg Arg Thr Thr Gly Leu Leu Glu Glu Asp
         35                    40                    45
Phe Thr Phe Lys Cys Arg Lys Gln Pro Lys Leu Pro Ser Met Arg Leu
     50                    55                    60
Ser Leu Leu Trp Pro Trp Arg Asp Leu Lys Phe Val Pro Arg Gln Asp
65          .        70                    75                    80
Lys Leu Thr Arg Ser Ser Val Ser Val Ala Gly Ala Tyr Ala Cys Arg
                 85                    90                    95
Ala Gly Pro Gly Trp Leu Lys Glu Gln Pro Ala Thr Ser Ala Arg Val
            100                   105                   110
Arg Leu Val Gln Ala Glu His Pro Pro Pro His Pro Leu Glu Glu Val
         115              .    120                   125
Gly Met Ala Arg Phe Pro Gln Pro Glu Cys Leu Pro Pro Tyr Cys
   130                   135                   ·140
```

```
        <210> 484
        <211> 30
        <212> PRT
        <213> Homo Sapien

        <400> 484
Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe
 1               5                    10                   15
Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile
            20                    25                    30

        <210> 485
        <211> 31
        <212> DNA
        <213> Artificial Sequence

        <220>
        <223> Made in a lab

        <400> 485
gggaagctta tcacctatgt gccgcctctg c                                    31

        <210> 486
        <211> 27
        <212> DNA
        <213> Artificial Sequence

        <220> ·
        <223> Made in a lab

        <400> 486
gcgaattctc acgctgagta tttggcc                                         27

        <210> 487
        <211> 36
        <212> DNA
        <213> Artificial Sequence

        <220>
        <223> Made in a lab

        <400> 487
```

169

```
cccgaattct tagctgccca tccgaacgcc ttcatc                              36

    <210> 488
    <211> 33
    <212> DNA
    <213> Artificial Sequence

    <220>
    <223> Made in a lab

    <400> 488
gggaagcttc ttccccggct gcaccagctg tgc                                 33

    <210> 489
    <211> 19
    <212> PRT
    <213> Artificial Sequence

    <220>
    <223> Made in a lab

    <400> 489
Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg Ala Val Tyr Leu Ala
1               5                   10                  15
Ser Val Ala


    <210> 490
    <211> 20
    <212> PRT
    <213> Artificial Sequence

    <220>
    <223> Made in a lab

    <400> 490
Tyr Leu Ala Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala Thr Cys
1               5                   10                  15
Leu Ser His Ser
            20

    <210> 491
    <211> 20
    <212> PRT
    <213> Artificial Sequence

    <220>
    <223> Made in a lab

    <400> 491
Thr Cys Leu Ser His Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu
1               5                   10                  15
Thr Gly Phe Thr
            20

    <210> 492
    <211> 20
    <212> PRT
```

170

<210> 492 (not shown; continued)

<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 492
Ala Leu Thr Gly Phe Thr Phe Ser Ala Leu Gln Ile Leu Pro Tyr Thr
1   5   10   15
Leu Ala Ser Leu
        20

<210> 493
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 493
Tyr Thr Leu Ala Ser Leu Tyr His Arg Glu Lys Gln Val Phe Leu Pro
1   5   10   15
Lys Tyr Arg Gly
        20

<210> 494
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 494
Leu Pro Lys Tyr Arg Gly Asp Thr Gly Gly Ala Ser Ser Glu Asp Ser
1   5   10   15
Leu Met Ile Ser
        20

<210> 495
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 495
Asp Ser Leu Met Thr Ser Phe Leu Pro Gly Pro Lys Pro Gly Ala Pro
1   5   10   15
Phe Pro Asn Gly
        20

<210> 496
<211> 21
<212> PRT
<213> Artificial Sequence

```
        <220>
        <223> Made in a lab

        <400> 496
Ala Pro Phe Pro Asn Gly His Val Gly Ala Gly Gly Ser Gly Leu Leu
1               5                   10                  15
Pro Pro Pro Pro Ala
            20

        <210> 497
        <211> 20
        <212> PRT
        <213> Artificial Sequence

        <220>
        <223> Made in a lab

        <400> 497
Leu Leu Pro Pro Pro Pro Ala Leu Cys Gly Ala Ser Ala Cys Asp Val
1               5                   10                  15
Ser Val Arg Val
            20

        <210> 498
        <211> 20
        <212> PRT
        <213> Artificial Sequence

        <220>
        <223> Made in a lab

        <400> 498
Asp Val Ser Val Arg Val Val Val Gly Glu Pro Thr Glu Ala Arg Val
1               5                   10                  15
Val Pro Gly Arg
            20

        <210> 499
        <211> 20
        <212> PRT
        <213> Artificial Sequence

        <220>
        <223> Made in a lab

        <400> 499
Arg Val Val Pro Gly Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp
1               5                   10                  15
Ser Ala Phe Leu
            20

        <210> 500
        <211> 20
        <212> PRT
        <213> Artificial Sequence

        <220>
```

172

<400> 500
Leu Asp Ser Ala Phe Leu Leu Ser Gln Val Ala Pro Ser Leu Phe Met
1   5   10   15
Gly Ser Ile Val
            20

<210> 501
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 501
Phe Met Gly Ser Ile Val Gln Leu Ser Gln Ser Val Thr Ala Tyr Met
1   5   10   15
Val Ser Ala Ala
            20

<210> 502
<211> 414
<212> DNA
<213> Homo Sapien

<220>
<221> misc_feature
<222> (1)...(414)
<223> n=A,T,C or G

<400> 502
caccatggag acaggcctgc gctggctttt cctggtcgct gtgctcaaag gtgtccaatg   60
tcagtcggtg gaggagtccg ggggtcgcct ggtcacgcct gggacacctt tgacantcac   120
ctgtagagtt tttggaatng acctcagtag caatgcaatg agctgggtcc gccaggctcc   180
agggaagggg ctggaatgga tcggagccat tgataattgt ccacantacg cgacctgggc   240
gaaaggccga ttnatnattt ccaaaacctn gaccacggtg gatttgaaaa tgaccagtcc   300
gacaaccgag gacacggcca cctatttttg tggcagaatg aatactggta atagtggttg   360
gaagaatatt tggggcccag gcaccctggt caccgtntcc tcagggcaac ctaa   414

<210> 503
<211> 379
<212> DNA
<213> Homo Sapien

<220>
<221> misc_feature
<222> (1)...(379)
<223> n=A,T,C or G

<400> 503
atncgatggt gcttggtcaa aggtgtccag tgtcagtcgg tggaggagtc cggggggtcgc   60
ctggtcacgc ctgggacacc cctgacactc acctgcaccg tntctggatt ngacatcagt   120
agctatggag tgagctgggt ccgccaggct ccagggaagg ggctggnata catcggatca   180
ttagtagtag tggtacattt tacgcgagct gggcgaaagg ccgattcacc atttccaaaa   240
cctngaccac ggtggatttg aaaatcacca gtttgacaac cgaggacacg gccacctatt   300
tntgtgccag agggggggttt aattataaag acatttgggg cccaggcacc ctggtcaccg   360

173

tntccttagg gcaacctaa   379

```
        <210> 504
        <211> 19
        <212> PRT
        <213> Artificial Sequence

        <220>
        <223> Made in a lab


        <400> 504
Gly Phe Thr Asn Tyr Thr Asp Phe Glu Asp Ser Pro Tyr Phe Lys Glu
1               5               10              15
Asn Ser Ala


        <210> 505
        <211> 20
        <212> PRT
        <213> Artificial Sequence

        <220>
        <223> Made in a lab

        <400> 505
Lys Glu Asn Ser Ala Phe Pro Pro Phe Cys Cys Asn Asp Asn Val Thr
1               5               10              15
Asn Thr Ala Asn
            20

        <210> 506
        <211> 407
        <212> DNA
        <213> Homo Sapien

        <400> 506
atggagacag gcctgcgctg gcttctcctg gtcgctgcgc tcaaaggtgt ccagtgtcag   60
tcgctggagg agtccggggg tcgcctggtc acgcctggga cacccctgac actcacctgc  120
accgtctctg gattctccct cagtagcaat gcaatgatct gggtccgcca ggctccaggg  180
aagggctgg aatacatcgg atacattagt tatggtgta gcgcatacta cgcgagctgg   240
gtgaaaggcc gattcaccat ctccaaaacc tcgaccacgg tggatctgag aatgaccagt  300
ctgacaaccg aggacacggc cacctatttc tgtgccagaa atagtgattt tagtggtatg  360
ttgtggggcc caggcaccct ggtcaccgtc tcctcaggc aacctaa                 407

        <210> 507
        <211> 422
        <212> DNA
        <213> Homo Sapien

        <400> 507
atggagacag gcctgcgctg gcttctcctg gtcgctgtgc tcaaaggtgt ccagtgtcag   60
tcggtggagg agtccggggg tcgcctggtc acgcctggga cacccctgac actcacctgt  120
acagtctctg gattctccct cagcaactac gacctgaact gggtccgcca ggctccaggg  180
aagggctgg aatggatcgg gatcattaat tatgttggta ggacggacta cgcgaactgg   240
gcaaaaggcc ggttcaccat ctccaaaacc tcgaccaccg tggatctcaa gatcgccagt  300
ccgacaaccg aggacacggc cacctatttc tgtgccagag ggtggaagtg cgatgagtct  360
ggtccgtgct tgcgcatctg gggcccaggc accctggtca ccgtctcctt agggcaacct  420
```

174

aa   422

```
    <210> 508
    <211> 411
    <212> DNA
    <213> Homo Sapien

    <220>
    <221> misc_feature
    <222> (1)...(411)
    <223> n=A,T,C or G

    <400> 508
atggagacag gcctcgctgg cttctcctgg tcgctgtgct caaaggtgtc cagtgtcagt    60
cggtggagga gtccgggggt cgcctggtca cgcctgggac acccctgaca ctcacctgca   120
cagtctctgg aatcgacctc agtagctact gcatgagctg ggtccgccag gctccaggga   180
aggggctgga atggatcgga atcattggta ctcctggtga cacatactac gcgaggtggg   240
cgaaaggccg attcaccatc tccaaaacct cgaccacggt gcatntgaaa atcnccagtc   300
cgacaaccga ggacacggcc acctatttct gtgccagaga tcttcgggat ggtagtagta   360
ctggttatta taaaatctgg ggcccaggca ccctggtcac cgtctccttg g           411

    <210> 509
    <211> 15
    <212> PRT
    <213> Artificial Sequence

    <220>
    <223> Made in a lab

    <400> 509
Leu Cys Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser
1               5                   10                  15

    <210> 510
    <211> 15
    <212> PRT
    <213> Artificial Sequence

    <220>
    <223> Made in a lab

    <400> 510
Pro Glu Tyr Asn Arg Pro Leu Leu Ala Asn Asp Leu Met Leu Ile
1               5                   10                  15

    <210> 511
    <211> 15
    <212> PRT
    <213> Artificial Sequence

    <220>
    <223> Made in a lab

    <400> 511

Tyr His Pro Ser Met Phe Cys Ala Gly Gly Gly Gln Asp Gln Lys
1               5                   10                  15
```

175

```
        <210> 512
        <211> 15
        <212> PRT
        <213> Artificial Sequence

        <220>
        <223> Made in a lab

        <400> 512
Asp Ser Gly Gly Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu
1               5               10              15

        <210> 513
        <211> 15
        <212> PRT
        <213> Artificial Sequence

        <220>
        <223> Made in a lab

        <400> 513
Ala Pro Cys Gly Gln Val Gly Val Pro Asx Val Tyr Thr Asn Leu
1               5               10              15

        <210> 514
        <211> 15
        <212> PRT
        <213> Artificial Sequence

        <220>
        <223> Made in a lab

        <400> 514
Leu Cys Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser
1               5               10              15

        <210> 515
        <211> 15
        <212> PRT
        <213> Artificial Sequence

        <220>
        <223> Made in a lab

        <400> 515
Met Val Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg
1               5               10              15

        <210> 516
        <211> 15
        <212> PRT
        <213> Artificial Sequence

        <220>
        <223> Made in a lab

        <400> 516
Val Ser Glu Ser Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln
```

176

```
1                  5                    10                    15
```

```
          <210> 517
          <211> 15
          <212> PRT
          <213> Artificial Sequence

          <220>
          <223> Made in a lab

          <400> 517
Glu Val Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met
1                  5                    10                    15

          <210> 518
          <211> 15
          <212> PRT
          <213> Artificial Sequence

          <220>
          <223> Made in a lab

          <400> 518
Arg Ala Glu Pro Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly
1                  5                    10                    15

          <210> 519
          <211> 17
          <212> PRT
          <213> Artificial Sequence

          <220>
          <223> Made in a lab

          <400> 519
Arg Ala Glu Pro Gly Thr Glu Ala Arg Arg Asn Tyr Asp Glu Gly Cys
1                  5                    10                    15
Gly

          <210> 520
          <211> 25
          <212> PRT
          <213> Artificial Sequence

          <220>
          <223> Made in a lab

          <400> 520
Val Gly Glu Gly Leu Tyr Gln Gly Val Pro Arg Ala Glu Pro Gly Thr
1                  5                    10                    15
Glu Ala Arg Arg His Tyr Asp Glu Gly
          20                    25

          <210> 521
          <211> 21
          <212> PRT
          <213> Artificial Sequence
```

```
        <220>
        <223> Made in a lab

        <400> 521
Ala Pro Phe Pro Asn Gly His Val Gly Ala Gly Gly Ser Gly Leu Leu
1               5                   10                  15
Pro Pro Pro Pro Ala
            20


        <210> 522
        <211> 20
        <212> PRT
        <213> Artificial Sequence

        <220>
        <223> Made in a lab

        <400> 522
Leu Leu Val Val Pro Ala Ile Lys Lys Asp Tyr Gly Ser Gln Glu Asp
1               5                   10                  15
Phe Thr Gln Val
            20


        <210> 523
        <211> 254
        <212> PRT
        <213> Artificial Sequence

        <220>
        <223> Made in a lab

        <220>
        <221> VARIANT
        <222> (1)...(254)
        <223> Xaa = any amino acid

        <400> 523
Met Ala Thr Ala Gly Asn Pro Trp Gly Trp Phe Leu Gly Tyr Leu Ile
1               5                   10                  15
Leu Gly Val Ala Gly Ser Leu Val Ser Gly Ser Cys Ser Gln Ile Ile
            20                  25                  30
Asn Gly Glu Asp Cys Ser Pro His Ser Gln Pro Trp Gln Ala Ala Leu
        35                  40                  45
Val Met Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln
    50                  55                  60
Trp Val Leu Ser Ala Thr His Cys Phe Gln Asn Ser Tyr Thr Ile Gly
65                  70                  75                  80
Leu Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met
                85                  90                  95
Val Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro Leu
            100                 105                 110
Leu Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu
        115                 120                 125
Ser Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala
    130                 135                 140
Gly Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly Arg
145                 150                 155                 160
```

```
            Met Pro Thr Val Leu Gln Cys Val Asn Val Ser Val Val Ser Glu Glu
                         165                 170                 175
            Val Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe Cys
                     180                 185                 190
            Ala Gly Gly Gly Gln Xaa Gln Xaa Asp Ser Cys Asn Gly Asp Ser Gly
                     195                 200                 205
            Gly Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe Gly
                210             215                 220
            Lys Ala Pro Cys Gly Gln Val Gly Val Pro Gly Val Tyr Thr Asn Leu
            225             230                 235                 240
            Cys Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser
                         245                 250
```

<210> 524
<211> 765
<212> DNA
<213> Homo sapien

<400> 524

```
atggccacag caggaaatcc ctggggctgg ttcctggggt acctcatcct tggtgtcgca   60
ggatcgctcg tctctggtag ctgcagccaa atcataaacg gcgaggactg cagcccgcac  120
tcgcagccct ggcaggcggc actggtcatg gaaaacgaat tgttctgctc gggcgtcctg  180
gtgcatccgc agtgggtgct gtcagccgca cactgtttcc agaactccta caccatcggg  240
ctgggcctgc acagtcttga ggccgaccaa gagccaggga gccagatggt ggaggccagc  300
ctctccgtac ggcacccaga gtacaacaga cccttgctcg ctaacgacct catgctcatc  360
aagttggacg aatccgtgtc cgagtctgac accatccgga gcatcagcat tgcttcgcag  420
tgccctaccg cggggaactc ttgcctcgtt tctggctggg gtctgctggc gaacggcaga  480
atgcctaccg tgctgcagtg cgtgaacgtg tcggtggtgt ctgaggaggt ctgcagtaag  540
ctctatgacc cgctgtacca ccccagcatg ttctgcgccg gcggagggca agaccagaag  600
gactcctgca cggtgactc tggggggccc ctgatctgca cgggtactt gcagggcctt  660
gtgtctttcg gaaaagcccc gtgtggccaa gttggcgtgc caggtgtcta caccaacctc  720
tgcaaattca ctgagtggat agagaaaacc gtccaggcca gttaa              765
```

<210> 525
<211> 254
<212> PRT
<213> Homo sapien

<400> 525

```
            Met Ala Thr Ala Gly Asn Pro Trp Gly Trp Phe Leu Gly Tyr Leu Ile
            1               5                   10                  15
            Leu Gly Val Ala Gly Ser Leu Val Ser Gly Ser Cys Ser Gln Ile Ile
                        20                  25                  30
            Asn Gly Glu Asp Cys Ser Pro His Ser Gln Pro Trp Gln Ala Ala Leu
                    35                  40                  45
            Val Met Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln
                50                  55                  60
            Trp Val Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly
            65                  70                  75                  80
            Leu Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met
                        85                  90                  95
            Val Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro Leu
                    100                 105                 110
            Leu Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu
                    115                 120                 125
            Ser Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala
                130                 135                 140
            Gly Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly Arg
```

```
145                    150                    155                    160
Met Pro Thr Val Leu Gln Cys Val Asn Val Ser Val Val Ser Glu Glu
                165                    170                    175
Val Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe Cys
            180                    185                    190
Ala Gly Gly Gly Gln Asp Gln Lys Asp Ser Cys Asn Gly Asp Ser Gly
        195                    200                    205
Gly Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe Gly
    210                    215                    220
Lys Ala Pro Cys Gly Gln Val Gly Val Pro Gly Val Tyr Thr Asn Leu
225                    230                    235                    240
Cys Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser
            245                    250
```

<210> 526
<211> 963
<212> DNA
<213> Homo sapiens

<400> 526
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aactgcatcg tggtcttcat cgtaaggacg gaacgcagcc tgcacgctcc gatgtacctc 180
tttctctgca tgcttgcagc cattgacctg gcctatcca catccaccat gcctaagatc 240
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gcccagattg gcatcgtggc tgtggtccgc ggatccctct ttttttttccc actgcctctg 480
ctgatcaagc ggctggcctt ctgccactcc aatgtcctct cgcactccta ttgtgtccac 540
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gtgtcacaca ttggtgtggt actcgccttc tatgtgccac ttattggcct ctcagttgta 780
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tga                                                                963
```

<210> 527
<211> 320
<212> PRT
<213> Homo sapiens

<400> 527
```
Met Ser Ser Cys Asn Phe Thr His Ala Thr Phe Val Leu Ile Gly Ile
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Pro Gly Leu Glu Lys Ala His Phe Trp Val Gly Phe Pro Leu Leu Ser
            20                    25                    30
Met Tyr Val Val Ala Met Phe Gly Asn Cys Ile Val Val Phe Ile Val
        35                    40                    45
Arg Thr Glu Arg Ser Leu His Ala Pro Met Tyr Leu Phe Leu Cys Met
    50                    55                    60
Leu Ala Ala Ile Asp Leu Ala Leu Ser Thr Ser Thr Met Pro Lys Ile
65                    70                    75                    80
Leu Ala Leu Phe Trp Phe Asp Ser Arg Glu Ile Ser Phe Glu Ala Cys
            85                    90                    95
Leu Thr Gln Met Phe Phe Ile His Ala Leu Ser Ala Ile Glu Ser Thr
            100                    105                    110
```

180

```
Ile Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys His Pro
        115                 120                 125
Leu Arg His Ala Ala Val Leu Asn Asn Thr Val Thr Ala Gln Ile Gly
        130                 135                 140
Ile Val Ala Val Val Arg Gly Ser Leu Phe Phe Phe Pro Leu Pro Leu
145                 150                 155                 160
Leu Ile Lys Arg Leu Ala Phe Cys His Ser Asn Val Leu Ser His Ser
                165                 170                 175
Tyr Cys Val His Gln Asp Val Met Lys Leu Ala Tyr Ala Asp Thr Leu
                180                 185                 190
Pro Asn Val Val Tyr Gly Leu Thr Ala Ile Leu Leu Val Met Gly Val
            195                 200                 205
Asp Val Met Phe Ile Ser Leu Ser Tyr Phe Leu Ile Ile Arg Thr Val
        210                 215                 220
Leu Gln Leu Pro Ser Lys Ser Glu Arg Ala Lys Ala Phe Gly Thr Cys
225                 230                 235                 240
Val Ser His Ile Gly Val Val Leu Ala Phe Tyr Val Pro Leu Ile Gly
                245                 250                 255
Leu Ser Val Val His Arg Phe Gly Asn Ser Leu His Pro Ile Val Arg
            260                 265                 270
Val Val Met Gly Asp Ile Tyr Leu Leu Leu Pro Pro Val Ile Asn Pro
        275                 280                 285
Ile Ile Tyr Gly Ala Lys Thr Lys Gln Ile Arg Thr Arg Val Leu Ala
    290                 295                 300
Met Phe Lys Ile Ser Cys Asp Lys Asp Leu Gln Ala Val Gly Gly Lys
305                 310                 315                 320
```

```
        <210> 528
        <211> 20
        <212> DNA
        <213> Homo Sapien

        <400> 528
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        <210> 529
        <211> 20
        <212> DNA
        <213> Homo Sapien

        <400> 529
    atcacctatg tgccgcctct                                          20

<210> 530
<211> 1852
<212> DNA
<213> Homo sapiens

<400> 530
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aaaaccacct atgacaagcc cacagccaac ataatactaa atggggaaaa gttagaagca 120
tttcctctga gaactgcaac aataaataca aggatgctgg attttgtcaa atgccttttc 180
tgtgtctgtt gagatgctta tgtgactttg cttttaattc tgtttatgtg attatcacat 240
ttattgactt gcctgtgtta gaccggaaga gctggggtgt ttctcaggag ccaccgtgtg 300
ctgcggcagc ttcgggataa cttgaggctg catcactggg gaagaaacac aytcctgtcc 360
gtggcgctga tggctgagga cagagcttca gtgtggcttc tctgcgactg gcttcttcgg 420
ggagttcttc cttcatagtt catccatatg gctccagagg aaaattatat tattttgtta 480
tggatgaaga gtattacgtt gtgcagatat actgcagtgt cttcatctct tgatgtgtga 540
```

```
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gctttctcca ccttgctgga agtgacctgc tgtccagaag tttgatggct gaggagtata 720
ccatcgtgca tgcatctttc atttcctgca tttcttcctc cctggatgga caggggagc 780
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agccagagct agaagattta tggctattga agaagaatga agaacacgga agtactcatg 1800
tgggattccc agaaaacctg actaacggtg ccgctgctgg caatggtgat ga         1852
```

```
<210> 531
<211> 879
<212> DNA
<213> Homo sapiens
```

```
<400> 531
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tgcaagtggt gctgccactg cttcccctgc tgcaggggga gcggcaagag caacgtggtc 180
gcttggggag actacgatga cagcgccttc atggatccca ggtaccacgt ccatggagaa 240
gatctggaca agctccacag agctgcctgg tggggtaaag tccccagaaa ggatctcatc 300
gtcatgctca gggacacgga tgtgaacaag agggacaagc aaaagaggac tgctctacat 360
ctggcctctg ccaatgggaa ttcagaagta gtaaaactcg tgctggacag acgatgtcaa 420
cttaatgtcc ttgacaacaa aaagaggaca gctctgacaa aggccgtaca atgccaggaa 480
gatgaatgtg cgttaatgtt gctggaacat ggcactgatc caaatattcc agatgagtat 540
ggaaatacca ctctacacta tgctgtctac aatgaagata aattaatggc caaagcactg 600
ctcttatacg gtgctgatat cgaatcaaaa acaagcatg gcctcacacc actgctactt 660
ggtatacatg agcaaaaaca gcaagtggtg aaatttttaa tcaagaaaaa agcgaattta 720
aatgcgctga tagatatgg aagaactgct ctcatacttg ctgtatgttg tggatcagca 780
agtatagtca gccctctact tgagcaaaat gttgatgtat cttctcaaga tctggaaaga 840
cggccagaga gtatgctgtt tctagtcatc atcatgtaa                        879
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```
<210> 532
<211> 292
<212> PRT
<213> Homo sapiens
```

```
<400> 532
Met His Leu Ser Phe Pro Ala Phe Leu Pro Pro Trp Met Asp Arg Gly
                  5                   10                  15
Ser Gly Lys Ser Asn Val Gly Thr Ser Gly Asp His Asn Asp Ser Ser
              20                  25                  30
Val Lys Thr Leu Gly Ser Lys Arg Cys Lys Trp Cys Cys His Cys Phe
          35                  40                  45
Pro Cys Cys Arg Gly Ser Gly Lys Ser Asn Val Val Ala Trp Gly Asp
```

```
        50                    55                    60
Tyr Asp Asp Ser Ala Phe Met Asp Pro Arg Tyr His Val His Gly Glu
65                    70                    75                    80
Asp Leu Asp Lys Leu His Arg Ala Ala Trp Trp Gly Lys Val Pro Arg
                85                    90                    95
Lys Asp Leu Ile Val Met Leu Arg Asp.Thr Asp Val Asn Lys Arg Asp
            100                   105                   110
Lys Gln Lys Arg Thr Ala Leu His Leu Ala Ser Ala Asn Gly Asn Ser
            115                   120                   125
Glu Val Val Lys Leu Val Leu Asp Arg Arg Cys Gln Leu Asn Val Leu
            130                   135                   140
Asp Asn Lys Lys Arg Thr Ala Leu Thr Lys Ala Val Gln Cys Gln Glu
145                   150                   155                   160
Asp Glu Cys Ala Leu Met Leu Leu Glu His Gly Thr Asp Pro Asn Ile
                165                   170                   175
Pro Asp Glu Tyr Gly Asn Thr Thr Leu His Tyr Ala Val Tyr Asn Glu
            180                   185                   190
Asp Lys Leu Met Ala Lys Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu
            195                   200                   205
Ser Lys Asn Lys His Gly Leu Thr Pro Leu Leu Leu Gly Ile His Glu
            210                   215                   220
Gln Lys Gln Gln Val Val Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu
225                   230                   235                   240
Asn Ala Leu Asp Arg Tyr Gly Arg Thr Ala Leu Ile Leu Ala Val Cys
                245                   250                   255
Cys Gly Ser Ala Ser Ile Val Ser Pro Leu Leu Glu Gln Asn Val Asp
        260                   265                   270·
Val Ser Ser Gln Asp Leu Glu Arg Arg Pro Glu Ser Met Leu.Phe Leu
        275                   280                 - 285
Val Ile Ile Met
        290
```

<210> 533
<211> 801
<212> DNA
<213> Homo sapiens

<400> 533
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tatgccactg cacgattctt ggttgccaag aggccaacca caggccatct tgagaaggag 180
tttatgttcc actgcagaaa gcagccagga tcaccatcca ggggacttgg tcttctgtgg 240
ccctggccag acatagaatt tgtgccaagg caggacaagc tcactcagag cagcgtgtta 300
gtacctcaaa tctgtgcgtg ccagacaagg ccaaactggc tcaatgagca accagccacc 360
tctgcagggg tgcgtctgga ggaggtggac cagccaccaa ccttacccag tcaaggaagt 420
ggatggccat gttcccacag cctgagtggc tgccacctga tggctgatat agcaaaggcc 480
ttaggaaaag cagatggccc ttggccctac cttttttgtta gaagaactga tgttccatgt 540
cctgcagcga gtgaggttgg tggctgtgcc cccagctcct ggcacaccct cgcagaggtg 600
actggttgct ctttgagccc tcttagcctt gcccagcatg cacaagcctc agtgctacta 660
ctgtgctaca aatggagcca tagggggaa acgagcagcc atctcaggag caaggtgtat 720
gctgcctttg ggggctccag tccttgcctc aagggtctta tgtcactgtg ggcttcttgg 780
ttgccaagag gcagaccata g                                          801
```

<210> 534
<211> 266
<212> PRT
<213> Homo sapiens

183

<400> 534

Met	Tyr	Lys	Leu	Gln	Cys	Asn	Asn	Cys	Ala	Thr	Asn	Gly	Ala	Thr	Glu
				5				10						15	

Arg Lys Gln Ala Ala Gly Ser Gly Ala Gly Tyr Ala Leu Pro Ser Ala
            20   25   30

Leu Gln Ser Met Pro Gln Gly Ser Tyr Ala Thr Ala Arg Phe Leu Val
        35   40   45

Ala Lys Arg Pro Thr Thr Gly His Leu Glu Lys Glu Phe Met Phe His
    50   55   60

Cys Arg Lys Gln Pro Gly Ser Pro Ser Arg Gly Leu Gly Leu Leu Trp
65 ·   70   75   80

Pro Trp Pro Asp Ile Glu Phe Val Pro Arg Gln Asp Lys Leu Thr Gln
                85   90   95

Ser Ser Val Leu Val Pro Gln Ile Cys Ala Cys Gln Thr Arg Pro Asn
            100   105   .   110

Trp Leu Asn Glu Gln Pro Ala Thr Ser Ala Gly Val Arg Leu Glu Glu
        115   120   125

Val Asp Gln Pro Pro Thr Leu Pro Ser Gln Gly Ser Gly Trp Pro Cys
    130   135   140

Ser His Ser Leu Ser Gly Cys His Leu Met Ala Asp Ile Ala Lys Ala
145   150   155   160

Leu Gly Lys Ala Asp Gly Pro Trp Pro Tyr Leu Phe Val Arg Arg Thr
                165   170   175

Asp Val Pro Cys Pro Ala Ala Ser Glu Val Gly Gly Cys Ala Pro Ser
            180   .   185   190

Ser Trp His Thr Leu Ala Glu Val Thr Gly Cys Ser Leu Ser Pro Leu
        · 195   200   205

Ser Leu Ala Gln His Ala Gln Ala Ser Val Leu Leu Leu Cys Tyr Lys
    210   215   220

Trp Ser His Ile Gly Glu Thr Ser Ser His Leu Arg Ser Lys Val Tyr
225   230   235   240

Ala Ala Phe Gly Gly Ser Ser Pro Cys Leu Lys Gly Leu Met Ser Leu
            245   250   255

Trp Ala Ser Trp Leu Pro Arg Gly Arg Pro
            260   265

<210> 535
<211> 6082
<212> DNA
<213> Homo sapiens

<400> 535
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cggagcccgc ggccactgcc gcctgatcag cgcgaccccg gccccgcgcc gccccgcccg 180
gcaagatgct gcccgtgtac caggaggtga agcccaaccc gctgcaggac gcgaacctct 240
gctcacgcgt gttcttctgg tggctcaatc ccttgtttaa aattggccat aaacggagat 300
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agttgcaagg gttctgggat aaagaagttt taagagctga gaatgacgca cagaagcctt 420
ctttaacaag agcaatcata aagtgttact ggaaatctta tttagttttg ggaatttta 480
cgttaattga ggaaagtgcc aaagtaatcc agcccatatt tttgggaaaa attattaatt 540
attttgaaaa ttatgatccc atggattctg tggctttgaa cacagcgtac gcctatgcca 600
cggtgctgac tttttgcacg ctcattttgg ctatactgca tcacttatat ttttatcacg 660
ttcagtgtgc tgggatgagg ttacgagtag ccatgtgcca tatgatttat cggaaggcac 720
ttcgtcttag taacatggcc atggggaaga caaccacagg ccagatagtc aatctgctgt 780
ccaatgatgt gaacaagttt gatcaggtga cagtgttctt acacttcctg tgggcaggac 840
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184

```
cactgcaggc gatcgcagtg actgccctac tctggatgga gataggaata tcgtgccttg 900
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tgaatttggc ttcgtttttc agtgcaagca aaatcatcgt gtttgtgacc ttcaccacct 1200
acgtgctcct cggcagtgtg atcacagcca gccgcgtgtt cgtggcagtg acgctgtatg 1260
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gagtgataat ctttgccact gtgaacttca cca ... (line continues)
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ttatacatac aagatgctag ttcatttgaa tatttctccc aacttatcca aggatctcca 4320
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185

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<210> 536
<211> 6140
<212> DNA
<213> Homo sapiens

<220>
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<400> 536
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ctgcccttgc aaagctgttt tgggaagttg ttctcatcac tgaggagtaa aactgcaact 960
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186

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187

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<210> 537
<211> 1228
<212> PRT
<213> Homo sapiens

<400> 537

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                5                  10                 15
Asn Leu Cys Ser Arg Val Phe Phe Trp Trp Leu Asn Pro Leu Phe Lys
            20                 25                 30
Ile Gly His Lys Arg Arg Leu Glu Glu Asp Asp Met Tyr Ser Val Leu
        35                 40                 45
Pro Glu Asp Arg Ser Gln His Leu Gly Glu Glu Leu Gln Gly Phe Trp
    50                 55                 60
Asp Lys Glu Val Leu Arg Ala Glu Asn Asp Ala Gln Lys Pro Ser Leu
65                 70                 75                 80
Thr Arg Ala Ile Ile Lys Cys Tyr Trp Lys Ser Tyr Leu Val Leu Gly
                85                 90                 95
Ile Phe Thr Leu Ile Glu Glu Ser Ala Lys Val Ile Gln Pro Ile Phe
            100                105                110
Leu Gly Lys Ile Ile Asn Tyr Phe Glu Asn Tyr Asp Pro Met Asp Ser
        115                120                125
Val Ala Leu Asn Thr Ala Tyr Ala Tyr Ala Thr Val Leu Thr Phe Cys
    130                135                140
Thr Leu Ile Leu Ala Ile Leu His His Leu Tyr Phe Tyr His Val Gln
145                150                155                160
Cys Ala Gly Met Arg Leu Arg Val Ala Met Cys His Met Ile Tyr Arg
                165                170                175
```

188

```
Lys Ala Leu Arg Leu Ser Asn Met Ala Met Gly Lys Thr Thr Thr Gly
            180                     185                 190
Gln Ile Val Asn Leu Leu Ser Asn Asp Val Asn Lys Phe Asp Gln Val
            195                     200                 205
Thr Val Phe Leu His Phe Leu Trp Ala Gly Pro Leu Gln Ala Ile Ala
        210                 215                     220
Val Thr Ala Leu Leu Trp Met Glu Ile Gly Ile Ser Cys Leu Ala Gly
225                     230                 235                 240
Met Ala Val Leu Ile Ile Leu Leu Pro Leu Gln Ser Cys Phe Gly Lys
                245                 250                 255
Leu Phe Ser Ser Leu Arg Ser Lys Thr Ala Thr Phe Thr Asp Ala Arg
            260                 265                     270
Ile Arg Thr Met Asn Glu Val Ile Thr Gly Ile Arg Ile Ile Lys Met
        275                 280                     285
Tyr Ala Trp Glu Lys Ser Phe Ser Asn Leu Ile Thr Asn Leu Arg Lys
        290                 295                 300
Lys Glu Ile Ser Lys Ile Leu Arg Ser Ser Cys Leu Arg Gly Met Asn
305                 310                 315                     320
Leu Ala Ser Phe Phe Ser Ala Ser Lys Ile Ile Val Phe Val Thr Phe
                325                 330                 335
Thr Thr Tyr Val Leu Leu Gly Ser Val Ile Thr Ala Ser Arg Val Phe
            340                 345                     350
Val Ala Val Thr Leu Tyr Gly Ala Val Arg Leu Thr Val Thr Leu Phe
        355                 360                     365
Phe Pro Ser Ala Ile Glu Arg Val Ser Glu Ala Ile Val Ser Ile Arg
    370                 375                 380
Arg Ile Gln Thr Phe Leu Leu Leu Asp Glu Ile Ser Gln Arg Asn Arg
385                 390                 395                     400
Gln Leu Pro Ser Asp Gly Lys Lys Met Val His Val Gln Asp Phe Thr
                405                 410                 415
Ala Phe Trp Asp Lys Ala Ser Glu Thr Pro Thr Leu Gln Gly Leu Ser
            420                 425                 430
Phe Thr Val Arg Pro Gly Glu Leu Leu Ala Val Val Gly Pro Val Gly
    435                 440                 445
Ala Gly Lys Ser Ser Leu Leu Ser Ala Val Leu Gly Glu Leu Ala Pro
    450                 455                 460
Ser His Gly Leu Val Ser Val His Gly Arg Ile Ala Tyr Val Ser Gln
465                 470                 475                     480
Gln Pro Trp Val Phe Ser Gly Thr Leu Arg Ser Asn Ile Leu Phe Gly
                485                 490                 495
Lys Lys Tyr Glu Lys Glu Arg Tyr Glu Lys Val Ile Lys Ala Cys Ala
            500                 505                 510
Leu Lys Lys Asp Leu Gln Leu Leu Glu Asp Gly Asp Leu Thr Val Ile
        515                 520                 525
Gly Asp Arg Gly Thr Thr Leu Ser Gly Gly Gln Lys Ala Arg Val Asn
        530                 535                 540
Leu Ala Arg Ala Val Tyr Gln Asp Ala Asp Ile Tyr Leu Leu Asp Asp
545                 550                 555                 560
Pro Leu Ser Ala Val Asp Ala Glu Val Ser Arg His Leu Phe Glu Leu
                565                 570                 575
Cys Ile Cys Gln Ile Leu His Glu Lys Ile Thr Ile Leu Val Thr His
            580                 585                 590
Gln Leu Gln Tyr Leu Lys Ala Ala Ser Gln Ile Leu Ile Leu Lys Asp
        595                 600                 605
Gly Lys Met Val Gln Lys Gly Thr Tyr Thr Glu Phe Leu Lys Ser Gly
    610                 615                 620
Ile Asp Phe Gly Ser Leu Leu Lys Lys Asp Asn Glu Glu Ser Glu Gln
625                 630                 635                     640
```

189

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Pro Pro Val Pro Gly Thr Pro Thr Leu Arg Asn Arg Thr Phe Ser Glu
            645             650             655
Ser Ser Val Trp Ser Gln Gln Ser Ser Arg Pro Ser Leu Lys Asp Gly
            660             665             670
Ala Leu Glu Ser Gln Asp Thr Glu Asn Val Pro Val Thr Leu Ser Glu
        675             680             685
Glu Asn Arg Ser Glu Gly Lys Val Gly Phe Gln Ala Tyr Lys Asn Tyr
    690             695             700
Phe Arg Ala Gly Ala His Trp Ile Val Phe Ile Phe Leu Ile Leu Leu
705             710             715             720
Asn Thr Ala Ala Gln Val Ala Tyr Val Leu Gln Asp Trp Trp Leu Ser
            725             730             735
Tyr Trp Ala Asn Lys Gln Ser Met Leu Asn Val Thr Val Asn Gly Gly
            740             745             750
Gly Asn Val Thr Glu Lys Leu Asp Leu Asn Trp Tyr Leu Gly Ile Tyr
        755         .       760             765
Ser Gly Leu Thr Val Ala Thr Val Leu Phe Gly Ile Ala Arg Ser Leu
    770             775             780
Leu Val Phe Tyr Val Leu Val Asn Ser Ser Gln Thr Leu His Asn Lys
785             790             795             800
Met Phe Glu Ser Ile Leu Lys Ala Pro Val Leu Phe Phe Asp Arg Asn
            805             810             815
Pro Ile Gly Arg Ile Leu Asn Arg Phe Ser Lys Asp Ile Gly His Leu
        820             825             830
Asp Asp Leu Leu Pro Leu Thr Phe Leu Asp Phe Ile Gln Thr Leu Leu
        835             840             845
Gln Val Val Gly Val Val Ser Val Ala Val Ala Val Ile Pro Trp Ile
    850             855             860
Ala Ile Pro Leu Val Pro Leu Gly Ile Ile Phe Ile Phe Leu Arg Arg
865             870             875             880
Tyr Phe Leu Glu Thr Ser Arg Asp Val Lys Arg Leu Glu Ser Thr Thr
            885             890             895
Arg Ser Pro Val Phe Ser His Leu Ser Ser Ser Leu Gln Gly Leu Trp
    .       900             905             910
Thr Ile Arg Ala Tyr Lys Ala Glu Glu Arg Cys Gln Glu Leu Phe Asp
    915             920             925
Ala His Gln Asp Leu His Ser Glu Ala Trp Phe Leu Phe Leu Thr Thr
    930             935             940
Ser Arg Trp Phe Ala Val Arg Leu Asp Ala Ile Cys Ala Met Phe Val
945             950             955             960
Ile Ile Val Ala Phe Gly Ser Leu Ile Leu Ala Lys Thr Leu Asp Ala
            965             970             975
Gly Gln Val Gly Leu Ala Leu Ser Tyr Ala Leu Thr Leu Met Gly Met
            980             985             990
Phe Gln Trp Cys Val Arg Gln Ser Ala Glu Val Glu Asn Met Met Ile
    995             1000            1005
Ser Val Glu Arg Val Ile Glu Tyr Thr Asp Leu Glu Lys Glu Ala Pro
    1010            1015            1020
Trp Glu Tyr Gln Lys Arg Pro Pro Pro Ala Trp Pro His Glu Gly Val
1025            1030            1035            1040
Ile Ile Phe Asp Asn Val Asn Phe Met Tyr Ser Pro Gly Gly Pro Leu
            1045            1050            1055
Val Leu Lys His Leu Thr Ala Leu Ile Lys Ser Gln Glu Lys Val Gly
            1060            1065            1070
Ile Val Gly Arg Thr Gly Ala Gly Lys Ser Ser Leu Ile Ser Ala Leu
        1075            1080            1085
Phe Arg Leu Ser Glu Pro Glu Gly Lys Ile Trp Ile Asp Lys Ile Leu
    1090            1095            1100
```

190

```
Thr Thr Glu Ile Gly Leu His Asp Leu Arg Lys Lys Met Ser Ile Ile
1105               1110               1115               1120
Pro Gln Glu Pro Val Leu Phe Thr Gly Thr Met Arg Lys Asn Leu Asp
              1125               1130               1135
Pro Phe Asn Glu His Thr Asp Glu Glu Leu Trp Asn Ala Leu Gln Glu
          1140               1145               1150
Val Gln Leu Lys Glu Thr Ile Glu Asp Leu Pro Gly Lys Met Asp Thr
          1155               1160               1165
Glu Leu Ala Glu Ser Gly Ser Asn Phe Ser Val Gly Gln Arg Gln Leu
          1170               1175               1180
Val Cys Leu Ala Arg Ala Ile Leu Arg Lys Asn Gln Ile Leu Ile Ile
1185               1190               1195               1200
Asp Glu Ala Thr Ala Asn Val Asp Pro Arg Thr Asp Glu Leu Ile Gln
              1205               1210               1215
Lys Lys Ser Gly Arg Asn Leu Pro Thr Ala Pro Cys
              1220               1225
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<210> 538
<211> 1261
<212> PRT
<213> Homo sapiens

<400> 538
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Leu Gln Gly Phe Trp Asp Lys Glu Val Leu Arg Ala Glu Asn Asp Ala
              20                  25                  30
Gln Lys Pro Ser Leu Thr Arg Ala Ile Ile Lys Cys Tyr Trp Lys Ser
          35                  40                  45
Tyr Leu Val Leu Gly Ile Phe Thr Leu Ile Glu Glu Ser Ala Lys Val
      50                  55                  60
Ile Gln Pro Ile Phe Leu Gly Lys Ile Ile Asn Tyr Phe Glu Asn Tyr
65                  70                  75                  80
Asp Pro Met Asp Ser Val Ala Leu Asn Thr Ala Tyr Ala Tyr Ala Thr
              85                  90                  95
Val Leu Thr Phe Cys Thr Leu Ile Leu Ala Ile Leu His His Leu Tyr
          100                 105                 110
Phe Tyr His Val Gln Cys Ala Gly Met Arg Leu Arg Val Ala Met Cys
          115                 120                 125
His Met Ile Tyr Arg Lys Ala Leu Arg Leu Ser Asn Met Ala Met Gly
      130                 135                 140
Lys Thr Thr Thr Gly Gln Ile Val Asn Leu Leu Ser Asn Asp Val Asn
145                 150                 155                 160
Lys Phe Asp Gln Val Thr Val Phe Leu His Phe Leu Trp Ala Gly Pro
              165                 170                 175
Leu Gln Ala Ile Ala Val Thr Ala Leu Leu Trp Met Glu Ile Gly Ile
          180                 185                 190
Ser Cys Leu Ala Gly Met Ala Val Leu Ile Ile Leu Leu Pro Leu Gln
      195                 200                 205
Ser Cys Phe Gly Lys Leu Phe Ser Ser Leu Arg Ser Lys Thr Ala Thr
      210                 215                 220
Phe Thr Asp Ala Arg Ile Arg Thr Met Asn Glu Val Ile Thr Gly Ile
225                 230                 235                 240
Arg Ile Ile Lys Met Tyr Ala Trp Glu Lys Ser Phe Ser Asn Leu Ile
              245                 250                 255
Thr Asn Leu Arg Lys Lys Glu Ile Ser Lys Ile Leu Arg Ser Ser Cys
          260                 265                 270
Leu Arg Gly Met Asn Leu Ala Ser Phe Phe Ser Ala Ser Lys Ile Ile
```

191

```
         275                    280                    285
Val Phe Val Thr Phe Thr Thr Tyr Val Leu Leu Gly Ser Val Ile Thr
    290                    295                    300
Ala Ser Arg Val Phe Val Ala Val Thr Leu Tyr Gly Ala Val Arg Leu
305                    310                    315                    320
Thr Val Thr Leu Phe Phe Pro Ser Ala Ile Glu Arg Val Ser Glu Ala
             325                    330                    335
Ile Val Ser Ile Arg Arg Ile Gln Thr Phe Leu Leu Leu Asp Glu Ile
             340                    345                    350
Ser Gln Arg Asn Arg Gln Leu Pro Ser Asp Gly Lys Lys Met Val His
             355                    360                    365
Val Gln Asp Phe Thr Ala Phe Trp Asp Lys Ala Ser Glu Thr Pro Thr
    370                    375                    380
Leu Gln Gly Leu Ser Phe Thr Val Arg Pro Gly Glu Leu Leu Ala Val
385                    390                    395                    400
Val Gly Pro Val Gly Ala Gly Lys Ser Ser Leu Leu Ser Ala Val Leu
             405                    410                    415
Gly Glu Leu Ala Pro Ser His Gly Leu Val Ser Val His Gly Arg Ile
             420                    425                    430
Ala Tyr Val Ser Gln Gln Pro Trp Val Phe Ser Gly Thr Leu Arg Ser
             435                    440                    445
Asn Ile Leu Phe Gly Lys Lys Tyr Glu Lys Glu Arg Tyr Glu Lys Val
    450                    455                    460
Ile Lys Ala Cys Ala Leu Lys Lys Asp Leu Gln Leu Leu Glu Asp Gly
465                    470                    475                    480
Asp Leu Thr Val Ile Gly Asp Arg Gly Thr Thr Leu Ser Gly Gly Gln
             485                    490                    495
Lys Ala Arg Val Asn Leu Ala Arg Ala Val Tyr Gln Asp Ala Asp Ile
             500                    505                    510
Tyr Leu Leu Asp Asp Pro Leu Ser Ala Val Asp Ala Glu Val Ser Arg
             515                    520                    525
His Leu Phe Glu Leu Cys Ile Cys Gln Ile Leu His Glu Lys Ile Thr
    530                    535                    540
Ile Leu Val Thr His Gln Leu Gln Tyr Leu Lys Ala Ala Ser Gln Ile
545                    550                    555                    560
Leu Ile Leu Lys Asp Gly Lys Met Val Gln Lys Gly Thr Tyr Thr Glu
             565                    570                    575
Phe Leu Lys Ser Gly Ile Asp Phe Gly Ser Leu Leu Lys Lys Asp Asn
             580                    585                    590
Glu Glu Ser Glu Gln Pro Pro Val Pro Gly Thr Pro Thr Leu Arg Asn
             595                    600                    605
Arg Thr Phe Ser Glu Ser Ser Val Trp Ser Gln Gln Ser Ser Arg Pro
    610                    615                    620
Ser Leu Lys Asp Gly Ala Leu Glu Ser Gln Asp Thr Glu Asn Val Pro
625                    630                    635                    640
Val Thr Leu Ser Glu Glu Asn Arg Ser Glu Gly Lys Val Gly Phe Gln
             645                    650                    655
Ala Tyr Lys Asn Tyr Phe Arg Ala Gly Ala His Trp Ile Val Phe Ile
             660                    665                    670
Phe Leu Ile Leu Leu Asn Thr Ala Ala Gln Val Ala Tyr Val Leu Gln
             675                    680                    685
Asp Trp Trp Leu Ser Tyr Trp Ala Asn Lys Gln Ser Met Leu Asn Val
    690                    695                    700
Thr Val Asn Gly Gly Gly Asn Val Thr Glu Lys Leu Asp Leu Asn Trp
705                    710                    715                    720
Tyr Leu Gly Ile Tyr Ser Gly Leu Thr Val Ala Thr Val Leu Phe Gly
             725                    730                    735
Ile Ala Arg Ser Leu Leu Val Phe Tyr Val Leu Val Asn Ser Ser Gln
```

192

```
                 740                745                750
Thr Leu His Asn Lys Met Phe Glu Ser Ile Leu Lys Ala Pro Val Leu
        755                760                765
Phe Phe Asp Arg Asn Pro Ile Gly Arg Ile Leu Asn Arg Phe Ser Lys
    770                775                780
Asp Ile Gly His Leu Asp Asp Leu Leu Pro Leu Thr Phe Leu Asp Phe
785                790                795                800
Ile Gln Thr Leu Leu Gln Val Val Gly Val Val Ser Val Ala Val Ala
            805                810                815
Val Ile Pro Trp Ile Ala Ile Pro Leu Val Pro Leu Gly Ile Ile Phe
        820                825                830
Ile Phe Leu Arg Arg Tyr Phe Leu Glu Thr Ser Arg Asp Val Lys Arg
        835                840                845
Leu Glu Ser Thr Thr Arg Ser Pro Val Phe Ser His Leu Ser Ser Ser
    850                855                860
Leu Gln Gly Leu Trp Thr Ile Arg Ala Tyr Lys Ala Glu Glu Arg Cys
865                870                875                880
Gln Glu Leu Phe Asp Ala His Gln Asp Leu His Ser Glu Ala Trp Phe
            885                890                895
Leu Phe Leu Thr Thr Ser Arg Trp Phe Ala Val Arg Leu Asp Ala Ile
            900                905                910
Cys Ala Met Phe Val Ile Ile Val Ala Phe Gly Ser Leu Ile Leu Ala
        915                920                925
-Lys Thr Leu Asp Ala Gly Gln Val Gly Leu Ala Leu Ser Tyr Ala Leu
    930                935                940
Thr Leu Met Gly Met Phe Gln Trp Cys Val Arg Gln Ser Ala Glu Val
945                950                955                960
Glu Asn Met Met Ile Ser Val Glu Arg Val Ile Glu Tyr Thr Asp Leu
            965                970                975
Glu Lys Glu Ala Pro Trp Glu Tyr Gln Lys Arg Pro Pro Pro Ala Trp
        980.                985                990
Pro His Glu Gly Val Ile Ile Phe Asp Asn Val Asn Phe Met Tyr Ser
        995                1000                1005
Pro Gly Gly Pro Leu Val Leu Lys His Leu Thr Ala Leu Ile Lys Ser
    1010                1015                1020
Gln Glu Lys Val Gly Ile Val Gly Arg Thr Gly Ala Gly Lys Ser Ser
1025                1030                1035                1040
Leu Ile Ser Ala Leu Phe Arg Leu Ser Glu Pro Glu Gly Lys Ile Trp
            1045                1050                1055
Ile Asp Lys Ile Leu Thr Thr Glu Ile Gly Leu His Asp Leu Arg Lys
            1060                1065                1070
Lys Met Ser Ile Ile Pro Gln Glu Pro Val Leu Phe Thr Gly Thr Met
    1075                1080                1085
Arg Lys Asn Leu Asp Pro Phe Asn Glu His Thr Asp Glu Glu Leu Trp
    1090                1095                1100
Asn Ala Leu Gln Glu Val Gln Leu Lys Glu Thr Ile Glu Asp Leu Pro
1105                1110                1115                1120
Gly Lys Met Asp Thr Glu Leu Ala Glu Ser Gly Ser Asn Phe Ser Val
            1125                1130                1135
Gly Gln Arg Gln Leu Val Cys Leu Ala Arg Ala Ile Leu Arg Lys Asn
            1140                1145                1150
Gln Ile Leu Ile Ile Asp Glu Ala Thr Ala Asn Val Asp Pro Arg Thr
    1155                1160                1165
Asp Glu Leu Ile Gln Lys Lys Ile Arg Glu Lys Phe Ala His Cys Thr
    1170                1175                1180
Val Leu Thr Ile Ala His Arg Leu Asn Thr Ile Ile Asp Ser Asp Lys
1185                1190                1195                1200
Ile Met Val Leu Asp Ser Gly Arg Leu Lys Glu Tyr Asp Glu Pro Tyr
```

```
                    1205              1210              1215
Val Leu Leu Gln Asn Lys Glu Ser Leu Phe Tyr Lys Met Val Gln Gln
            1220              1225              1230
Leu Gly Lys Ala Glu Ala Ala Ala Leu Thr Glu Thr Ala Lys Gln Arg
        1235              1240              1245
Trp Gly Phe Thr Met Leu Ala Arg Leu Val Ser Asn Ser
    1250              1255              1260
```

<210> 539
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 539
```
Cys Leu Ser His Ser Val Ala Val Val Thr
 1               5               10
```

<210> 540
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 540
```
Ala Val Val Thr Ala Ser Ala Ala Leu
 1               5
```

<210> 541
<211> 14
<212> PRT
<213> Homo sapiens

<400> 541
```
Leu Ala Gly Leu Leu Cys Pro Asp Pro Arg Pro Leu Glu Leu
                5               10
```

<210> 542
<211> 15
<212> PRT
<213> Homo sapiens

<400> 542
```
Thr Gln Val Val Phe Asp Lys Ser Asp Leu Ala Lys Tyr Ser Ala
                5               10              15
```

<210> 543
<211> 12
<212> PRT
<213> Homo sapiens

<400> 543
```
Phe Met Gly Ser Ile Val Gln Leu Ser Gln Ser Val
                5               10
```

194

```
<210> 544
<211> 18
<212> PRT
<213> Homo sapiens

<400> 544
Thr Tyr Val Pro Pro Leu Leu Leu Glu Val Gly Val Glu Glu Lys Phe
                 5                  10                  15
Met Thr


<210> 545
<211> 18
<212> PRT
<213> Homo sapiens

<400> 545
Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg Ala Val Tyr Leu Ala
                 5                  10                  15
Ser Val


<210> 546
<211> 29
<212> PRT
<213> Homo sapiens

<400> 546
Phe Val Gly Glu Gly Leu Tyr Gln Gly Val Pro Arg Ala Glu Pro Gly
                 5                  10                  15
Thr Glu Ala Arg Arg His Tyr Asp Glu Gly Val Arg Met
            20                  25


<210> 547
<211> 58
<212> PRT
<213> Homo sapiens

<400> 547
Val Ala Glu Glu Ala Ala Leu Gly Pro Thr Glu Pro Ala Glu Gly Leu
                 5                  10                  15
Ser Ala Pro Ser Leu Ser Pro His Cys Cys Pro Cys Arg Ala Arg Leu
            20                  25                  30
Ala Phe Arg Asn Leu Gly Ala Leu Leu Pro Arg Leu His Gln Leu Cys
        35                  40                  45
Cys Arg Met Pro Arg Thr Leu Arg Arg Leu
    50                  55


<210> 548
<211> 18
<212> PRT
<213> Homo sapiens

<400> 548
Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu Gly Thr Gln Glu
```

195

```
                    5              10              15
Glu Cys
```

```
<210> 549
<211> 18
<212> PRT
<213> Homo sapiens

<400> 549
Leu Glu Ala Leu Leu Ser Asp Leu Phe Arg Asp Pro Asp His Cys Arg
                    5              10              15
Gln Ala
```

```
<210> 550
<211> 14
<212> PRT
<213> Homo sapiens

<400> 550
Ser Asp His Trp Arg Gly Arg Tyr Gly Arg Arg Arg Pro Phe
                    5              10
```

```
<210> 551
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 551
Phe Asp Lys Ser Asp Leu Ala Lys Tyr Ser Ala
                    5              10
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```
<210> 552
<211> 2577
<212> DNA
<213> Homo sapiens

<400> 552
agcatatgta acatgacctg tgcttcagtg ttcttttgtg atcaaaaatt ccttactttt 60
agtttttat ctatggtaga accacccaga gcagggtcc tcaactccca ggccacagac 120
tcataccagt ccacggacta ttatgaacca caccacacag gaggaggtga gcactaggca 180
agccaaggaa gcttcacctg tacttacagc cacacgccat ggctcatatt acagcctgaa 240
ctctgcctcc actcagatca gtgataacat tagaaactca ttggagcacg aaccctgttg 300
tgaactgcct atccgaagga tctaggttgt gtgcttcgta tgagaatcta atgccagatg 360
atctatcatt gtctcacttt gcccccagat aagaccatct agttgcagaa aaataagctc 420
agagcttcca ctgattctac attatggata tgtgccgccg aagcaagcac aaagccctac 480
ttttacacat gcctagtgat gcttcatgga caaggcttgg ctctgttgag tccaactaac 540
ctacctgaga ttctgagatt tctcttcaat ggcttcctgt gagctagagt ttgaaaatat 600
cttaaaatct tgagctagag atggaagtag cttggacgat tttcattatc atgtaaatcg 660
ggtcactcaa ggggccaacc acagctggga gccactgctc aggggaaggt tcatatggga 720
ctttctactg cccaaggttc tatacaggat ataaaggtgc ctcacagtat agatctggta 780
gcaaagaaga agaaacaaac actgatctct ttctgccacc cctctgaccc tttggaactc 840
ctctgaccct ttagaacaag cctacctaat atctgctaga gaaaagacca caacggcct 900
caaaggatct cttaccatga aggtctcagc taattcttgg ctaagatgtg ggttccacat 960
```

```
taggttctga atatgggggg aagggtcaat ttgctcattt tgtgtgtgga taaagtcagg 1020
atgcccaggg gccagagcag ggggctgctg ctttgggaac aatggctgag catataacca 1080
taggtatggg aacaaaaaac atcaaagtca ctgtatcaat tgccatgaag actcgaggga 1140
cctgaatcta ccgattcatc ttaaggcagc aggaccagtt tgagtggcaa caatgcagca 1200
gcagaatcaa tggaaacaac agaatgattg caatgtcctt ttttttctcc tccttctgac 1260
ttgataaaag ggaccgtctt ccttggattt agtgaacccc tttggttcct gaaaaattca 1320
aggagtatct aggacatagt ccccagaaga cagtacaaga ctttctgata aactggacat 1380
ttcaagrccc aaataactaa tcagaaaaat caaagatgtg atactatttt ttatcccatg 1440
cataggtgct acacttggat caaatgaaca atgttgggat ctytatggat aaaggtctta 1500
aaagtcctga gataaagaat cctgcaccca ctggtacttc taacttgtct tgttttttgt 1560
ctgwtttctg gctgatgcag gggactaact cactgccacg cgaaaactac ctgaactgaa 1620
ctatgacatc tcacctgata tgtaagatgt aactgttata attattttaa acctcaattt 1680
agcattaact agccttttaa tgtaaacact tacacattat gaygactaga aacagcatac 1740
tctctggccg tctgtccaga tagatcttga gaagatacat caatgttttg ctcaagtaga 1800
aggctgacta tacttgccga tccacaacat acagcaagta tgagagcagt tctaaaatga 1860
cagagatagg aacagtaata aagttattkt aaaagctaat ttgatatact·ttaccaattt 1920
aacatcttgc ctgtccgtgc agaatcaaac atttacatgc actaaaagac ataagcatct 1980
tcagtgctca agtgttcatc tttgtaaaat accaccaagt ttaaaaggaa gggacaaaaa 2040
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ttgatggaca agaaacaata ttagggccac ttatctgaaa tgaacaaaga tttaagtgaa 2160
gatttcatca cagcttccct agactgatat gctgtaatag aaaatcagct aggggggtaaa 2220
ataaataaga gctctctgca tgctgaaagc aagtaagatt aataataatg gtaagaatag 2280
tagtcacagg agtttcagtt aatgatgcca ataagcatgt gctaggcact gaattaaatg 2340
ccacatatat ctttcttatg cgcagcaaac tttgaaggat atattctcct actttttcata 2400
tatgacaaca tatttggtgg taaataacgt tcccaaggtc acacacctag caagtaagaa 2460
agttaggaat taaacccagt attgtgtgaa tctaaagcct aactttttc tctttatcac 2520
ccacctacgg cttgtcttca ttaaaggaaa agtgtatcca cttaaaaaaa aaaaaaa    2577
```

```
<210> 553
<211> 58
<212> PRT
<213> Homo sapiens

<400> 553
Ser Ile Cys Asn Met Thr Cys Ala Ser Val Phe Phe Cys Asp Gln Lys
                  5                   10                  15
Phe Leu Thr Phe Ser Phe Leu Ser Met Val Glu Pro Pro Arg Ala Gly
               20                  25                  30
Val Leu Asn Ser Gln Ala Thr Asp Ser Tyr Gln Ser Thr Asp Tyr Tyr
            35                  40                  45
Glu Pro His His Thr Gly Gly Gly Glu His
         50                  55
```

```
<210> 554
<211> 59
<212> PRT
<213> Homo sapiens

<400> 554
Leu Gln Lys Asn Lys Leu Arg Ala Ser Thr Asp Ser Thr Leu Trp Ile
                  5                   10                  15
Cys Ala Ala Glu Ala Ser Thr Lys Pro Tyr Phe Tyr Thr Cys Leu Val
               20                  25                  30
Met Leu His Gly Gln Gly Leu Ala Leu Leu Ser Pro Thr Asn Leu Pro
            35                  40                  45
Glu Ile Leu Arg Phe Leu Phe Asn Gly Phe Leu ·
         50                  55
```

197

<210> 555
<211> 71
<212> PRT
<213> Homo sapiens

<400> 555
Leu Gly Arg Phe Ser Leu Ser Cys Lys Ser Gly His Ser Arg Gly Gln
                  5   10   15
Pro Gln Leu Gly Ala Thr Ala Gln Gly Lys Val His Met Gly Leu Ser
              20   25   30
Thr Ala Gln Gly Ser Ile Gln Asp Ile Lys Val Pro His Ser Ile Asp
          35   40   45
Leu Val Ala Lys Lys Lys Lys Gln Thr Leu Ile Ser Phe Cys His Pro
      50   55   60
Ser Asp Pro Leu Glu Leu Leu
 65   70

<210> 556
<211> 81
<212> PRT
<213> Homo sapiens

<400> 556
Asn His Pro Glu Gln Gly Ser Ser Thr Pro Arg Pro Gln Thr His Thr
                  5   10   15
Ser Pro Arg Thr Ile Met Asn His Thr Thr Gln Glu Glu Val Ser Thr
              20   25   30
Arg Gln Ala Lys Glu Ala Ser Pro Val Leu Thr Ala Thr Arg His Gly
          35   40   45
Ser Tyr Tyr Ser Leu Asn Ser Ala Ser Thr Gln Ile Ser Asp Asn Ile
      50   55   60
Arg Asn Ser Leu Glu His Glu Pro Cys Cys Glu Leu Pro Ile Arg Arg
 65   70   75   80
Ile

<210> 557
<211> 54
<212> PRT
<213> Homo sapiens

<400> 557
Ser Leu Ser Ala Thr Pro Leu Thr Leu Trp Asn Ser Ser Asp Pro Leu
                  5   10   15
Glu Gln Ala Tyr Leu Ile Ser Ala Arg Glu Lys Thr Asn Asn Gly Leu
              20   25   30
Lys Gly Ser Leu Thr Met Lys Val Ser Ala Asn Ser Trp Leu Arg Cys
          35   40   45
Gly Phe His Ile Arg Phe
      50

<210> 558
<211> 77
<212> PRT
<213> Homo sapiens

198

```
<220>
<221> VARIANT
<222> (1)...(77)
<223> Xaa = Any amino acid

<400> 558
Asn Asp Arg Asp Arg Asn Ser Asn Lys Val Ile Xaa Lys Ala Asn Leu
                5                   10                  15
Ile Tyr Phe Thr Asn Leu Thr Ser Cys Leu Ser Val Gln Asn Gln Thr
            20                  25                  30
Phe Thr Cys Thr Lys Arg His Lys His Leu Gln Cys Ser Ser Val His
        35                  40                  45
Leu Cys Lys Ile Pro Pro Arg Leu Lys Gly Arg Asp Lys Lys Lys Lys
    50                  55                  60
Pro Ser Tyr Leu Ser Gly Val Leu His Ser Arg Ser Tyr
65                  70                  75


<210> 559
<211> 50
<212> PRT
<213> Homo sapiens

<400> 559
Thr Leu Pro Pro Leu Arg Ser Val Ile Thr Leu Glu Thr His Trp Ser
                5                   10                  15
Thr Asn Pro Val Val Asn Cys Leu Ser Glu Gly Ser Arg Leu Cys Ala
            20                  25                  30
Ser Tyr Glu Asn Leu Met Pro Asp Asp Leu Ser Leu Ser His Phe Ala
        35                  40                  45
Pro Arg
    50


<210> 560
<211> 56
<212> PRT
<213> Homo sapiens

<400> 560
Ile Gly Ser Leu Lys Gly Pro Thr Thr Ala Gly Ser His Cys Ser Gly
                5                   10                  15
Glu Gly Ser Tyr Gly Thr Phe Tyr Cys Pro Arg Phe Tyr Thr Gly Tyr
            20                  25                  30
Lys Gly Ala Ser Gln Tyr Arg Ser Gly Ser Lys Glu Glu Glu Thr Asn
        35                  40                  45
Thr Asp Leu Phe Leu Pro Pro Leu
    50                  55


<210> 561
<211> 57
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
```

```
<222> (1)...(57)
<223> Xaa = Any amino acid

<400> 561
Val Leu His Leu Asp Gln Met Asn Asn Val Gly Ile Xaa Met Asp Lys
                  5                  10                  15
Gly Leu Lys Ser Pro Glu Ile Lys Asn Pro Ala Pro Thr Gly Thr Ser
              20                  25                  30
Asn Leu Ser Cys Phe Leu Ser Xaa Phe Trp Leu Met Gln Gly Thr Asn
          35                  40                  45
Ser Leu Pro Arg Glu Asn Tyr Leu Asn
      50                  55


<210> 562
<211> 59
<212> PRT
<213> Homo sapiens


<220>
<221> VARIANT
<222> (1)...(59)
<223> Xaa = Any amino acid

<400> 562
Asp Leu Tyr Pro Xaa Arg Ser Gln His Cys Ser Phe Asp Pro Ser Val
                  5                  10                  15
Ala Pro Met His Gly Ile Lys Asn Ser Ile Thr Ser Leu Ile Phe Leu
              20                  25                  30
Ile Ser Tyr Leu Xaa Leu Glu Met Ser Ser Leu Ser Glu Ser Leu Val
          35                  40                  45
Leu Ser Ser Gly Asp Tyr Val Leu Asp Thr Pro
      50                  55



<210> 563
<211> 79
<212> PRT
<213> Homo sapiens


<400> 563
Cys Phe Leu Phe Pro Tyr Leu Trp Leu Tyr Ala Gln Pro Leu Phe Pro
                  5                  10                  15
Lys Gln Gln Pro Pro Ala Leu Ala Pro Gly His Pro Asp Phe Ile His
              20                  25                  30
Thr Gln Asn Glu Gln Ile Asp Pro Ser Pro His Ile Gln Asn Leu Met
          35                  40                  45
Trp Asn Pro His Leu Ser Gln Glu Leu Ala Glu Thr Phe Met Val Arg
      50                  55                  60
Asp Pro Leu Arg Pro Leu Leu Val Phe Ser Leu Ala Asp Ile Arg
  65                  70                  75


<210> 564
<211> 64
<212> PRT
<213> Homo sapiens

<400> 564
```

200

```
Ala Cys Ser Lys Gly Ser Glu Glu Phe Gln Arg Val Arg Gly Val Ala
                  5                   10                      15
Glu Arg Asp Gln Cys Leu Phe Leu Leu Leu Cys Tyr Gln Ile Tyr Thr
              20                  25                  30
Val Arg His Leu Tyr Ile Leu Tyr Arg Thr Leu Gly Ser Arg Lys Ser
          35                  40                  45
His Met Asn Leu Pro Leu Ser Ser Gly Ser Gln Leu Trp Leu Ala Pro
      50                  55                  60
```

```
<210> 565
<211> 57
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (1)...(57)
<223> Xaa = Any amino acid

<400> 565
```
```
Leu Tyr Tyr Cys Ser Tyr Leu Cys His Phe Arg Thr Ala Leu Ile Leu
                  5                   10                      15
Ala Val Cys Cys Gly Ser Ala Ser Ile Val Ser Leu Leu Leu Glu Gln
              20                  25                  30
Asn Ile Asp Val Ser Ser Gln Asp Leu Ser Gly Gln Thr Ala Arg Glu
          35                  40                  45
Tyr Ala Val Ser Ser Xaa His Asn Val
      50                  55
```

```
<210> 566
<211> 55
<212> PRT
<213> Homo sapiens

<400> 566
```
```
Ile Leu Leu Glu Phe Phe Arg Asn Gln Arg Gly Ser Leu Asn Pro Arg
                  5                   10                      15
Lys Thr Val Pro Phe Ile Lys Ser Glu Gly Gly Glu Lys Lys Gly His
              20                  25                  30
Cys Asn His Ser Val Val Ser Ile Asp Ser Ala Ala Ala Leu Leu Pro
          35                  40                  45
Leu Lys Leu Val Leu Leu Pro
      50                  55
```

```
<210> 567
<211> 51
<212> PRT
<213> Homo sapiens

<400> 567
```
```
Tyr Ser Asp Phe Asp Val Phe Cys Ser His Thr Tyr Gly Tyr Met Leu
                  5                   10                      15
Ser His Cys Ser Gln Ser Ser Ser Pro Leu Leu Trp Pro Leu Gly Ile
              20                  25                  30
Leu Thr Leu Ser Thr His Lys Met Ser Lys Leu Thr Leu Pro Pro Ile
```

201

```
          35              40              45
Phe Arg Thr
    50


<210> 568
<211> 75
<212> PRT
<213> Homo sapiens

<400> 568
Lys Val Gly Glu Tyr Ile Leu Gln Ser Leu Leu Arg Ile Arg Lys Ile
                  5                  10                  15
Tyr Val Ala Phe Asn Ser Val Pro Ser Thr Cys Leu Leu Ala Ser Leu
              20                  25                  30
Thr Glu Thr Pro Val Thr Thr Ile Leu Thr Ile Ile Ile Asn Leu Thr
          35                  40                  45
Cys Phe Gln His Ala Glu Ser Ser Tyr Leu Phe Tyr Pro Leu Ala Asp
      50                  55                  60
Phe Leu Leu Gln His Ile Ser Leu Gly Lys Leu
65                  70                  75


<210> 569
<211> 4809
<212> DNA
<213> Homo sapiens

<400> 569
gcatccagag tggtggactg gttacaggct atgaacctac actgatgcgg caccaccacc 60
cagagtccac rggttatgtt ggttcacatt tactcttgct gtggtatggt ctataggttt 120
ggacagatgt ccgataatcc tttttacatt ttggcatcct tgggtagctc gtcttgtagg 180
aatggacttg cttcaaagtg gaggcaggca gatccttcag acgggtatat ggagccctgt 240
tttcagttgc ttttctaatt ctctcttatc gtttacctca aaatcttcct gaggtctcgc 300
ttccttttaa aatccttgtc tactttgcag catcactctg acactcccat tgattcctca 360
gcacctactg actacacggt taggagtgca agggtagaat tcatgtttta ttcatctttg 420
ggtctgtagc acccagcaaa gtgctcagta aatgcgcagt aattgatttg acctctgaac 480
aaatacacac tgtactaaga atctacacac cgaaagacaa aaacaagaca aatttgagtg 540
ctacaggtgt cacgcttggc atcacacatg tgcctgtgta ttcctctagg tggttaccag 600
gagctctgcc actgcatgtc cactagtgac gggttcgctc caccacccca gctgggtagc 660
cgctgctctc acataagggg tccaattaaa attgccagga ataaattccc ccggactttg 720
acttctcaag agctaagaag gtttgctgag tattctggca tgatgtttgg tgatcaaaca 780
actgctggcc aaaaatgatg agtatttccc cctcttgctg aagatgtgct ccatacaata 840
gtccatcaca ttcatcattc atcagtctgg aagtgtgcag aacaacatgt aatagataat 900
atgattggct gcacacttcc agactgatga atgatgaatg tgatggacta ttgtatggag 960
cacatcttca gcaagagggg gaaatactca tcattttatc tattacatgt tgttctggtt 1020
tttttttttt tccaatgtcc agcctaaact ataaagtact ttgagaacgc acagtgagcc 1080
ataagcttgc caataaagag tcctctgtgg tatggaactg gcttatttca tacacaatct 1140
gcaaacaatg agggcactat tggaaacata ctgtgctgca cagagcattt acaccgctta 1200
tctttaatct tccccagcaa tccttgcttt gtgcgcattt atgatccttg ctctcagaag 1260
tccacatact tttccccaac cgtaacaaat tatttaactc atctaatgta tgtatgtccg 1320
cgcagtctga aaacagtaat tgtccttggg aagaagtgag tttaagagag ctctagggca 1380
ctcatcacaa ctccagccct gccctccatg tggtagcagc tctttggact ggggctaagt 1440
gcttattctt gtgcttcatt cctggtaagc tcaatttctt taccttagga taactttgct 1500
ggaaaagggc tcagattcag ccgaccattg tggcctctgt ggctgtcaca gcttgtccct 1560
gacatgctat gatgttgggt ccccttctca tcccttgggg atttcttctg ctggcccaca 1620
gccagaacaa ctaggccttt tactccacca tcccttgtt ttcttttgtt tcgttggtaa 1680
aaatcaatcc ttctaccatc catgcatagc aatttctaaa aactgaattt caagagcagt 1740
atctgaagaa acaaacatga tttggtcctt ttagtaaaca gaataaattt taataaatca 1800
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actttgaaat agttgtaaga gttaagaaaa agcacaaaac tgagatcatc agagcagctt 1860
ggcctcaaag gacaggcagc aggattctac agggtttgag ccttcctaag tgaagctgtt 1920
tcctgcaggc tccctgctcc aagctcctag ctaacagccc cttctcccac gattggcaac 1980
aaagagcaaa aataactttg tacttgatgc tgagtcagtg taaaaagcca taaaaaattc 2040
cctctaaatg tcaaaatgtt tgcctccttt gaggcttctc tcctcctact gggtctggat 2100
aaattagcac tgggcttata ttgagtcaca gatctgggcc ctgccacaga gagcttcctc 2160
ctagtgtgtg atgcttttc tccaaactat tgatacaaaa tgcactggaa tagaaatcaa 2220
cagaaactgg tcaaaggtgt ggcatacaca ttctcatgta gatgtaaagc tgtgcttaga 2280
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taaattacaa aaaccctcca catttcttca tggattgtat tagtccatgt tctccagaga 2400
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ggtgccagct tgaggatgct gggcaagtcc cgagccgtct gccttcctag taccacagtt 4440
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ttcagaactg gaaaaatgct ttaaatttgg ctttgtcatg attattaaaa cactctgtac 4740
attttttatt attgaaatta acacattgcc tacttttttaa aaattggaaa aagaaaaaaa 4800
aaaaaaaaa                                                          4809
```

<210> 570
<211> 951
<212> DNA
<213> Homo sapiens

<400> 570

```
aaaattgaat attgagatac cattctttag tgttaccttt tttacccaca tgtgtttctg 60
aaaatattgg aattttattc atcttaaaaa ttggacccgg cctttatttac catctttaat 120
ccattttagt actatggggtg agtacatgga attgaagtct ggcttaaatc ttcagaaagt 180
tatatatcta ttttatttta ttttttttgag acagagtctc gctgtgtcac ccaggctgga 240
gtgcggtgcc acaatcttgg ctcactgcaa cctctgagtc ccaggttcaa gcgatactca 300
tgcctcggcc tcctgagtag ctgggactac aggcgtgcac caccacatct ggctaatctt 360
tttttgtatt tttagtagag acggggtttc actgtggtct ccatctcctg acctcgtgat 420
ccgcctgcct cccaaagtgc tgggattaca ggcatgagcc accgcacaca gctgggactg 480
ggtaatttat aaagaaaaga ggtttaatga ctcacagttc cgcatggctg gagaggcctc 540
aggaaactta caatcatggt ggaaggcgaa ggggaagcaa ggcacgtctt acatggtggc 600
aggagagaac gagtgagggg ggagactgcc acaaactttt tttttttgag acaagagtct 660
ggccctgttg cccaggctgg agtgcagtgg catgatctca gctcactgca acctctgcct 720
cacaggttca agcaattctc atgcctcagc ctcccgcata gctgggacca caggtatgca 780
ccaccacacc tagctaattt ttgtagtttt agtagagatg gggtctcact atgttgctca 840
ggctggtcta aaactcctgg ctccagcaa tccgcctgcc ttggcctccc aaagtgctgg 900
ggttacaggc ataagccacc acatccagcc tgccacatac ttttaaacta t       951
```

```
<210> 571
<211> 819
<212> DNA
<213> Homo sapiens
```

```
<400> 571
cagcttaaaa atggtttctt gaaatcagtg attagcattc actcaccagt accCctacta 60
aggggtaggc actggtttgt actcctggga atacaggagt acaccagaat ttatttctgc 120
ttattgcttt tgttgcaaat gccgtggctt catctgagga attctagaat tcagagggtg 180
tagccctcca ctctgctgtc ttgctatctg ctctcattgc atccgtttaa cctgcaattct 240
gaaagatgtt tctcaggttt ttccttgacg attttcttct tttctgattc tgacaatgtt 300
ttaaatcatt gtactgtggt tatcatttct ctgcatttat tttacccatc ttcctttgta 360
acttgtccta ttgtctttta atttctgcct gttcttatg gctttcaact tcataaataa 420
catgttttct caaatctctt tgtgaattcc agagagggcc aggcacggtg gctcacatct 480
gtaatcccag cactttgggg aggctgagac gggtggatca cttgaggtca ggagtttgag 540
accagcctgg ccaacatggt gaaatcccgt ttcactaaaa atacaaaaat tacccaggca 600
tggtggcggg cgcctgtaat cccaggtact cgggaggctg agggaggaga atcgcttgaa 660
cctgggaggc tgagggagga gaatcgcttg aacccgggag gcagaggttg cagtgaaccg 720
agatcatgtt gctgcactcc agcctggtca acagagcaag actctgcctc aaaaacaaac 780
aaataaacaa acaaacaaac aaaacagaga gattttgct         819
```

```
<210> 572
<211> 203
<212> DNA
<213> Homo sapiens
```

```
<400> 572
tatagaatac tcaagctatg catcaagctt ggtaccgagc tcggatccac tatttacggc 60
cgccagtgtg ctggaattcg cccttagctc ggatccacta gtccagtgtg gtggaattcc 120
attgtgttgg gcccaacaca atggagccac cacatccagc ctgccacata cttttaaact 180
atcaggtctc atgagaactc atg             203
```

```
<210> 573
<211> 132
<212> PRT
<213> Homo sapiens
```

```
<400> 573
Met Val Glu Gly Glu Gly Glu Ala Arg His Val Leu His Gly Gly Arg
              5                  10                  15
Arg Glu Arg Val Arg Gly Glu Thr Ala Thr Asn Phe Phe Phe Leu Arg
```

204

```
                20                  25                  30
Gln Glu Ser Gly Pro Val Ala Gln Ala Gly Val Gln Trp His Asp Leu
            35                  40                  45
Ser Ser Leu Gln Pro Leu Pro His Arg Phe Lys Gln Phe Ser Cys Leu
        50                  55                  60
Ser Leu Pro His Ser Trp Asp His Arg Tyr Ala Pro Pro His Leu Ala
65                  70                  75                  80
Asn Phe Cys Ser Phe Ser Arg Asp Gly Val Ser Leu Cys Cys Ser Gly
                85                  90                  95
Trp Ser Lys Thr Pro Gly Leu Gln Gln Ser Ala Cys Leu Gly Leu Pro
            100                 105                 110
Lys Cys Trp Gly Tyr Arg His Lys Pro Pro His Pro Ala Cys His Ile
            115                 120                 125
Leu Leu Asn Tyr
        130


<210> 574
<211> 62
<212> PRT
<213> Homo sapiens


<400> 574
Met Thr His Ser Ser Ala Trp Leu Glu Arg Pro Gln Glu Thr Tyr Asn
                    5                  10                  15
His Gly Gly Arg Arg Arg Gly Ser Lys Ala Arg Leu Thr Trp Trp Gln
                20                  25                  30
Glu Arg Thr Ser Glu Gly Gly Asp Cys His Lys Leu Phe Phe Phe Glu
            35                  40                  45
Thr Arg Val Trp Pro Cys Cys Pro Gly Trp Ser Ala Val Ala
        50                  55                  60


<210> 575
<211> 76
<212> PRT
<213> Homo sapiens


<400> 575
Met Val Lys Ser Arg Phe Thr Lys Asn Thr Lys Ile Thr Gln Ala Trp
                    5                  10                  15
Trp Arg Ala Pro Val Ile Pro Gly Thr Arg Glu Ala Glu Gly Gly Glu
                20                  25                  30
Ser Leu Glu Pro Gly Arg Leu Arg Glu Glu Asn Arg Leu Asn Pro Gly
            35                  40                  45
Gly Arg Gly Cys Ser Glu Pro Arg Ser Cys Cys Cys Thr Pro Ala Trp
            50                  55                  60
Ser Thr Glu Gln Asp Ser Ala Ser Lys Thr Asn Lys
65                  70                  75


<210> 576
<211> 68
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
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```
<222> (1)...(68)
<223> Xaa = Any Amino Acid

<400> 576
Met Leu Gly Lys Ser Arg Ala Val Cys Leu Pro Ser Thr Thr Val Thr
                  5                  10                  15
Thr Val Cys Tyr Leu Ala Ser Ser Ser Ala Ser Arg Glu Thr Ala Thr
                 20                  25                  30
Arg Gln Ala Pro Gly Asn Trp Lys Met Xaa Ser Lys Cys His Ala Gln
             35                  40                  45
Leu Leu Phe Thr Phe Tyr Leu Asn His Phe Tyr Gln Ile Arg Leu Asn
         50                  55                  60
Pro Gly Tyr Ser
65


<210> 577
<211> 57
<212> PRT
<213> Homo sapiens


<400> 577
Met Tyr Leu Glu Asn Ser Phe Tyr Cys Gln Met Ile Leu Leu Lys Arg
                  5                  10                  15
Cys Arg Leu Ser Lys Ile Ser Thr Gln Arg Val Val Pro Asp Gly Pro
                 20                  25                  30
Pro Ala Pro Val Pro Gly Ser Phe Pro Met Phe Pro Arg Phe Gly Phe
             35                  40                  45
Arg Leu Ala Pro Pro Ala Asp Thr Pro
         50                  55


<210> 578
<211> 51
<212> PRT
<213> Homo sapiens


<400> 578
Met Gln Leu Ile Tyr Leu Cys Phe Leu Gly Leu Leu Tyr Ile Arg His
                  5                  10                  15
His Asp Ser Gln Ser Phe Val Ile Leu Tyr Tyr Lys Lys Leu Asn Tyr
                 20                  25                  30
Tyr Phe Lys Tyr Gly Gln Ile Arg Ala Phe His Ile Ala Lys Val Tyr
             35                  40                  45
Gln Pro His
         50


<210> 579
<211> 56
<212> PRT
<213> Homo sapiens


<400> 579
Met His Phe Thr Phe Met Gln Leu Ile Tyr Leu Cys Phe Leu Gly Leu
                  5                  10                  15
Leu Tyr Ile Arg His His Asp Ser Gln Ser Phe Val Ile Leu Tyr Tyr
                 20                  25                  30
Lys Lys Leu Asn Tyr Tyr Phe Lys Tyr Gly Gln Ile Arg Ala Phe His
             35                  40                  45
Ile Ala Lys Val Tyr Gln Pro His
```

206

```
        50                          55

<210> 580
<211> 67
<212> PRT
<213> Homo sapiens

<400> 580
Met Glu Leu Arg Thr Lys Ala Leu Arg Thr Ala Gln Gln Leu Thr Ser
                    5                   10                  15
Cys Val Thr Ala Leu Lys Ala Ala Gly Pro Pro Leu Thr Phe Trp Lys
                20            25                  30
Gly Lys Trp Val Gln Cys Cys Leu Pro Leu Trp Gly Leu Leu Gly Ser
        35                  40                  45
His Ala Phe Tyr Ile Tyr Ala Val Asp Ile Phe Met Phe Pro Gly Ser
    50                  55                  60
Phe Ile His
 65


<210> 581
<211> 77
<212> PRT
<213> Homo sapiens

<400> 581
Met Leu Glu Val Lys Phe Glu Val Ser Leu Arg Pro Thr Gly Asn Glu
                5                   10                  15
Thr Ala Gly Gln Thr His Gly Thr Gln Asp Lys Gly Ser Lys Asp Ser
                20                  25                  30
Thr Ala Ala Asp Ile Leu Cys Asp Ser Leu Glu Ser Ser Arg Pro Ala
        35                  40                  45
Ala His Ile Leu Glu Gly Lys Met Gly Thr Met Leu Ser Ala Thr Leu
    50                  55                  60
Gly Pro Ser Trp Val Thr Cys Ile Leu His Leu Cys Ser
 65                  70                  75


<210> 582
<211> 51
<212> PRT
<213> Homo sapiens

<400> 582
Met Leu Phe Leu Gln Thr Ile Asp Thr Lys Cys Thr Gly Ile Glu Ile
                5                   10                  15
Asn Arg Asn Trp Ser Lys Val Trp His Thr His Ser His Val Asp Val
                20                  25                  30
Lys Leu Cys Leu Glu Phe Leu Cys Gly Val Trp Phe Gly Leu Gly Phe
        35                  40                  45
Leu Gly Val
    50


<210> 583
<211> 60
<212> PRT
<213> Homo sapiens

<400> 583
Met Ser Thr Ser Asp Gly Phe Ala Pro Pro Pro Gln Leu Gly Ser Arg
```

```
                        5                    10                   15
Cys Ser His Ile Arg Gly Pro Ile Lys Ile Ala Arg Asn Lys Phe Pro
                 20                    25                   30
Arg Thr Leu Thr Ser Gln Glu Leu Arg Arg Phe Ala Glu Tyr Ser Gly
            35                    40                   45
Met Met Phe Gly Asp Gln Thr Thr Ala Gly Gln Lys
        50                    55                   60
```

<210> 584
<211> 76
<212> PRT
<213> Homo sapiens

<400> 584
```
Met Cys Leu Cys Ile Pro Leu Gly Gly Tyr Gln Glu Leu Cys His Cys
                 5                    10                   15
Met Ser Thr Ser Asp Gly Phe Ala Pro Pro Pro Gln Leu Gly Ser Arg
            20                    25                   30
Cys Ser His Ile Arg Gly Pro Ile Lys Ile Ala Arg Asn Lys Phe Pro
        35                    40                   45
Arg Thr Leu Thr Ser Gln Glu Leu Arg Arg Phe Ala Glu Tyr Ser Gly
     50                    55                   60
Met Met Phe Gly Asp Gln Thr Thr Ala Gly Gln Lys
  65                    70                   75
```

<210> 585
<211> 50
<212> PRT
<213> Homo sapiens

<400> 585
```
Met Val Tyr Arg Phe Gly Gln Met Ser Asp Asn Pro Phe Tyr Ile Leu
                 5                    10                   15
Ala Ser Leu Gly Ser Ser Ser Cys Arg Asn Gly Leu Ala Ser Lys Trp
            20                    25                   30
Arg Gln Ala Asp Pro Ser Asp Gly Tyr Met Glu Pro Cys Phe Gln Leu
        35                    40                   45
Leu Phe
     50
```

<210> 586
<211> 60
<212> PRT
<213> Homo sapiens

<400> 586
```
Met Leu Val His Ile Tyr Ser Cys Cys Gly Met Val Tyr Arg Phe Gly
                 5                    10                   15
Gln Met Ser Asp Asn Pro Phe Tyr Ile Leu Ala Ser Leu Gly Ser Ser
            20                    25                   30
Ser Cys Arg Asn Gly Leu Ala Ser Lys Trp Arg Gln Ala Asp Pro Ser
        35                    40                   45
Asp Gly Tyr Met Glu Pro Cys Phe Gln Leu Leu Phe
     50                    55                   60
```

<210> 587
<211> 1408
<212> DNA

208

<210> Homo sapiens

<400> 587
ctggacactt tgcgagggct tttgctggct gctgctgctg cccgtcatgc tactcatcgt 60
agcccgcccg gtgaagctcg ctgctttccc tacctcctta agtgactgcc aaacgcccac 120
cggctggaat tgctctggtt atgatgacag agaaaatgat ctcttcctct gtgacaccaa 180
cacctgtaaa tttgatgggg aatgtttaag aattggagac actgtgactt gcgtctgtca 240
gttcaagtgc aacaatgact atgtgcctgt gtgtggctcc aatggggaga gctaccagaa 300
tgagtgttac ctgcgacagg ctgcatgcaa acagcagagt gagatacttg tggtgtcaga 360
aggatcatgt gccacagatg caggatcagg atctggagat ggagtccatg aaggctctgg 420
agaaactagt caaaaggaga catccacctg tgatatttgc cagtttggtg cagaatgtga 480
cgaagatgcc gaggatgtct ggtgtgtgtg taatattgac tgttctcaaa ccaacttcaa 540
tccccctctgc gcttctgatg ggaaatctta tgataatgca tgccaaatca agaagcatc 600
gtgtcagaaa caggagaaaa ttgaagtcat gtctttgggt cgatgtcaag ataacacaac 660
tacaactact aagtctgaag atgggcatta tgcaagaaca gattatgcag agaatgctaa 720
caaattagaa gaaagtgcca gagaacacca cataccttgt ccggaacatt acaatggctt 780
ctgcatgcat gggaagtgtg agcattctat caatatgcag gagccatctt gcaggtgtga 840
tgctggttat actggacaac actgtgaaaa aaaggactac agtgttctat acgttgttcc 900
cggtcctgta cgatttcagt atgtcttaat cgcagctgtg attggaacaa ttcagattgc 960
tgtcatctgt gtggtggtcc tctgcatcac aaggaaatgc cccagaagca acagaattca 1020
cagacagaag caaaatacag ggcactacag ttcagacaat acaacaagag cgtccacgag 1080
gttaatctaa agggagcatg tttcacagtg gctggactac cgagagcttg gactacacaa 1140
tacagtatta tagacaaaag aataagacaa gagatctaca catgttgcct tgcatttgtg 1200
gtaatctaca ccaatgaaaa catgtactac agctatattt gattatgtat ggatatattt 1260
gaaatagtat acattgtctt gatgtttttt ctgtaatgta aataaactat ttatatcaca 1320
caatawagtt ttttctttcc catgtatttg ttatatataa taaatactca gtgatgagaa 1380
aaaaaaaaaa aaaaaaaaaa rwmgaccc ·   1408

<210> 588
<211> 81
<212> PRT
<213> Homo sapiens

<400> 588
Met Pro Gln Lys Gln Gln Asn Ser Gln Thr Glu Ala Lys Tyr Arg Ala
                5   10   15
Leu Gln Phe Arg Gln Tyr Asn Lys Ser Val His Glu Val Asn Leu Lys
            20   25   30
Gly Ala Cys Phe Thr Val Ala Gly Leu Pro Arg Ala Trp Thr Thr Gln
        35   40   45
Tyr Ser Ile Ile Asp Lys Arg Ile Arg Gln Glu Ile Tyr Thr Cys Cys
    50   55   60
Leu Ala Phe Val Val Ile Tyr Thr Asn Glu Asn Met Tyr Tyr Ser Tyr
65   70   75   80
Ile

<210> 589
<211> 157
<212> PRT ·
<213> Homo sapiens

<400> 589
Met Thr Met Cys Leu Cys Val Ala Pro Met Gly Arg Ala Thr Arg Met
                5   10   15
Ser Val Thr Cys Asp Arg Leu His Ala Asn Ser Arg Val Arg Tyr Leu
            20   25   30
Trp Cys Gln Lys Asp His Val Pro Gln Met Gln Asp Gln Asp Leu Glu

```
          35                    40                    45
Met Glu Ser Met Lys Ala Leu Glu Lys Leu Val Lys Arg Arg His Pro
    50                    55                    60
Pro Val Ile Phe Ala Ser Leu Val Gln Asn Val Thr Lys Met Pro Arg
65                    70                    75                    80
Met Ser Gly Val Cys Val Ile Leu Thr Val Leu Lys Pro Thr Ser Ile
                  85                    90                    95
Pro Ser Ala Leu Leu Met Gly Asn Leu Met Ile Met His Ala Lys Ser
                 100                   105                   110
Lys Lys His Arg Val Arg Asn Arg Arg Lys Leu Lys Ser Cys Leu Trp
             115                   120                   125
Val Asp Val Lys Ile Thr Gln Leu Gln Leu Leu Ser Leu Lys Met Gly
         130                   135                   140
Ile Met Gln Glu Gln Ile Met Gln Arg Met Leu Thr Asn
145                   150                   155


<210> 590
<211> 347
<212> PRT
<213> Homo sapiens

<400> 590
Met Leu Leu Ile Val Ala Arg Pro Val Lys Leu Ala Ala Phe Pro Thr
                  5                    10                    15
Ser Leu Ser Asp Cys Gln Thr Pro Thr Gly Trp Asn Cys Ser Gly Tyr
             20                    25                    30
Asp Asp Arg Glu Asn Asp Leu Phe Leu Cys Asp Thr Asn Thr Cys Lys
         35                    40                    45
Phe Asp Gly Glu Cys Leu Arg Ile Gly Asp Thr Val Thr Cys Val Cys
     50                    55                    60
Gln Phe Lys Cys Asn Asn Asp Tyr Val Pro Val Cys Gly Ser Asn Gly
65                    70                    75                    80
Glu Ser Tyr Gln Asn Glu Cys Tyr Leu Arg Gln Ala Ala Cys Lys Gln
                  85                    90                    95
Gln Ser Glu Ile Leu Val Val Ser Glu Gly Ser Cys Ala Thr Asp Ala
                 100                   105                   110
Gly Ser Gly Ser Gly Asp Gly Val His Glu Gly Ser Gly Glu Thr Ser
             115                   120                   125
Gln Lys Glu Thr Ser Thr Cys Asp Ile Cys Gln Phe Gly Ala Glu Cys
         130                   135                   140
Asp Glu Asp Ala Glu Asp Val Trp Cys Val Cys Asn Ile Asp Cys Ser
145                   150                   155                   160
Gln Thr Asn Phe Asn Pro Leu Cys Ala Ser Asp Gly Lys Ser Tyr Asp
                 165                   170                   175
Asn Ala Cys Gln Ile Lys Glu Ala Ser Cys Gln Lys Gln Glu Lys Ile
                 180                   185                   190
Glu Val Met Ser Leu Gly Arg Cys Gln Asp Asn Thr Thr Thr Thr Thr
             195                   200                   205
Lys Ser Glu Asp Gly His Tyr Ala Arg Thr Asp Tyr Ala Glu Asn Ala
         210                   215                   220
Asn Lys Leu Glu Glu Ser Ala Arg Glu His His Ile Pro Cys Pro Glu
225                   230                   235                   240
His Tyr Asn Gly Phe Cys Met His Gly Lys Cys Glu His Ser Ile Asn
                 245                   250                   255
Met Gln Glu Pro Ser Cys Arg Cys Asp Ala Gly Tyr Thr Gly Gln His
                 260                   265                   270
Cys Glu Lys Lys Asp Tyr Ser Val Leu Tyr Val Val Pro Gly Pro Val
```

210

```
              275                    280                    285
Arg Phe Gln Tyr Val Leu Ile Ala Ala Val Ile Gly Thr Ile Gln Ile
      290                    295                    300
Ala Val Ile Cys Val Val Val Leu Cys Ile Thr Arg Lys Cys Pro Arg
305                    310                    315                    320
Ser Asn Arg Ile His Arg Gln Lys Gln Asn Thr Gly His Tyr Ser Ser
              325                    330                    335
Asp Asn Thr Thr Arg Ala Ser Thr Arg Leu Ile
              340                    345
```

<210> 591
<211> 565
<212> DNA
<213> Homo sapien

<400> 591
```
actaaagcaa atgaacaagc tgacttgcta gtatcatctg cattcattga agcacaagaa        60
cttcatgcct tgactcatgt aaatgcaata ggattaaaaa ataaatttga tatcacatgg       120
aaacagacaa aaaatattgt acaacattgc acccagtgtc agattctaca cctggccact       180
caggaagcaa gagttaatcc cagaggtcta tgtcctaatg tgttatggca aatggatgtc       240
atgcacgtac cttcatttgg aaaattgtca tttgtccatg tgacagttga tacttattca       300
catttcatat gggcaacctg ccagacagga gaaagtactt cccatgttaa aagacattta       360
ttatcttgtt ttcctgtcat gggagttcca gaaaaagtta aaacagacaa tgggccaggt       420
tactgtagta aagcatttca aaaattctta aatcagtgga aaattacaca tacaatagga       480
attctctata attcccaagg acaggccata attgaaggaa ctaatagaac actcaaagct       540
caattggtta aacaaaaaaa aaaaa                                             565
```

<210> 592
<211> 188
<212> PRT
<213> Homo sapien

<400> 592
```
Thr Lys Ala Asn Glu Gln Ala Asp Leu Leu Val Ser Ser Ala Phe Ile
1               5                   10                  15
Glu Ala Gln Glu Leu His Ala Leu Thr His Val Asn Ala Ile Gly Leu
              20                  25                  30
Lys Asn Lys Phe Asp Ile Thr Trp Lys Gln Thr Lys Asn Ile Val Gln
      35                  40                  45
His Cys Thr Gln Cys Gln Ile Leu His Leu Ala Thr Gln Glu Ala Arg
      50                  55                  60
Val Asn Pro Arg Gly Leu Cys Pro Asn Val Leu Trp Gln Met Asp Val
65                  70                  75                  80
Met His Val Pro Ser Phe Gly Lys Leu Ser Phe Val His Val Thr Val
              85                  90                  95
Asp Thr Tyr Ser His Phe Ile Trp Ala Thr Cys Gln Thr Gly Glu Ser
              100                 105                 110
Thr Ser His Val Lys Arg His Leu Leu Ser Cys Phe Pro Val Met Gly
      115                 120                 125
Val Pro Glu Lys Val Lys Thr Asp Asn Gly Pro Gly Tyr Cys Ser Lys
130                 135                 140
Ala Phe Gln Lys Phe Leu Asn Gln Trp Lys Ile Thr His Thr Ile Gly
145                 150                 155                 160
Ile Leu Tyr Asn Ser Gln Gly Gln Ala Ile Ile Glu Gly Thr Asn Arg
              165                 170                 175
Thr Leu Lys Ala Gln Leu Val Lys Gln Lys Lys Lys
              180                 185
```

211 .

```
<210> 593
<211> 271
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(271)
<223> n = A,T,C or G

<400> 593
actttatgtt cnagtgcana aanccncctg gattgccacc ntactctcag ggctgtgant        60
tgtgcnccca nagcaacctg ggcacgcggg gacagggggg ccnacaattg agggagcggt       120
gtccctagct ggggtctata catgncnggg naagggcngc tgagtnccat nagcaaagga       180
nctagnatnt gcgggggtgc ggcctgggcc tacccttttna agcatccntn gatccactcc      240
angaanccng gggtagncag gtttnccaac a                                       271 .

<210> 594
<211> 376
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(376)
<223> n = A,T,C or G

<400> 594
cctttggggg nggggggaac ctttaccatt gtnccccttt atttcatttg gttngggttc        60
gcgccctcnn gggccaacaa agttatcgtn nttgaagaga anattttttt ggnttngncc       120
cgattaagcg ncaaatgtgt agcaaaangc cgtgccactt gtggcgtagc tncgtcgggt       180
cgattcgacg acaaggcgtn gcgcgntanc gttagtctcn aatngacccn gtggcatgag       240
cccacgangg nttcgtgtcg tcacatggnc tctagacata acgcncnccn tttttttncag      300
aggggggntgc cgcccttagg gaggnagggg tggggacact agccaancca nantctnacc      360
ccattgaaga aaaggn                                                        376

<210> 595
<211> 242
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(242)
<223> n = A,T,C or G

<400> 595
agnctgctgn tcgtnccctn tatgtggctt catnntgagg acaaanagtng cactgaggct       60
tgngnatgcc aggcaaggnc aagctggctc aaaaagcatc cacccacctc tgnaangggt       120
atgccangag cangtgcacc agtcccaact angagncccn ggcatgntac atcttcttcc       180
accccctnaaa ntttgngcta caangnccat ttttctttttt ctcttaaggg ncncntggct      240
tc                                                                       242

<210> 596
<211> 535
<212> DNA
<213> Homo sapien
```

212

```
<220>
<221> misc_feature
<222> (1)...(535)
<223> n = A,T,C or G

<400> 596
accagttgga tactgctaaa nagatattta tgcagcctca tatgttaagt cgtatatttt      60
gaaagctttt taaatttttt ctttaagaag attttagatg cttatcactg agtaccagag     120
ggatgtaggc tgatgccctt atcaacaaag tcagggactg tggcacacaa ggattgacta     180
ctgcagacac ggccacaatg ctacctctag agggcctgaa tccccctgcc ctctctggtg     240
gggagaaggg ctggcagagc cattagcatg ggctccggcc aatcctggcc actttgacac     300
tcctggtgct gacccagggt cctggaggaa gggatgaggt gggcagtaga gatgctcagg     360
gcagtggccc ctttccatcc acactggaac tatttcagta ttttaccacc aattcagcca     420
ttcccttgtg cgctggctga acatcagccc tgctccaggt ctcagtttcc cctttgtaaa     480
gggaaagctc tggattcagg gagtgatgaa gaggtcatca tggtcttgag aattc          535

<210> 597
<211> 257
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(257)
<223> n = A,T,C or G

<400> 597
tttcnatacc caaaantacc ccatattang accanacatt tgtctnggaa aaattaccat      60
tntntaacnt ttgggccacc tgagannaaa tgggtgtaat ncatgataag atggancagn     120
attnctctta agatnngatn agaccccgtt tttcacggaa catatccaag nacccaatag     180
gnaacaagcc acgggnggag tcacaaacat atattcttta ctctcataat ccgtnncaca     240
naactnttgn acttgac                                                    257

<210> 598
<211> 222
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(222)
<223> n = A,T,C or G

<400> 598
nntggntacc gtcnaaactt nncttggtac ccgagctcgg atccactagt ccagtgtggt      60
ggaattccat tgtgttgggc tataagctgt aatagtggag ncgtgctngg ttcattgcan     120
nagnccctcc gcanncacnc ttgnnacaac ctgtgagnag gcnataaatt attcacataa     180
tcatcactgc atgaanctga ctcaaacgca tccacntaca cc                        222

<210> 599
<211> 238
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(238)
```

213

<400> 599'
```
gcatgacatc ancgatgtnt ttggnnacct ganattngct aaaactngng natgccgggn      60
atgnaggttt ggtantgatc tatgcactca catctcatgg ggacgtttca tgtggagtgn     120
tcgacaangt tgctgnancn gagaagtgat gatctcagtt gaaagggtca tgtgaataca     180
cnttacactt gaaaaagaag cacattggga atatcacgaa acgnccacca acatcctg       238
```

<210> 600
<211> 232
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(232)
<223> n = A,T,C or G

<400> 600
```
cgaactattt agactaccta ggaaaattat tttagtatca gaagaatatc aggggtgtag      60
tactcatcag agctaaatga gagcgcttta aaatgttag tttgtcttcc gccatttcta     120
cagaaagctg caatttcagg ttttcaacct aataggtgat atttaanaaa aaaaaaaagc     180
aatcgcaaat agccccactg cttttacaaa tcattttttc cccaacacaa tg            232
```

<210> 601
<211> 547
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(547)
<223> n = A,T,C or G

<400> 601
```
cattgtgttg gggaaaaaat gatttgtata agcagtgggg ctatttgcga ttgctttttt      60
ttttcttaa atatcaccta ttaggttgaa aacctgaaat tgcagctttc tgtagaaatg     120
gcggaagaca aactaacatt tttaaagcgc tctcatttag ctctgatgag tactacaccc     180
ctnatattct tctgatacta aaataatttt cctagtgtag tctaaacttt tttaaaaaga     240
catgtaatcc gcggagttag taactcaaaa cgagtgcatc tnggaagtat cgcagccgtt     300
nctggatnaa attcccagct tgctngcttg ctnagccggg gggcggtnaa aaaaacatct     360
gcagcccngg ggnaaaaacc ttcgcattgt tcttacgtgt ttacgttatt ttatttccct     420
nnagcaaggc ngggganttgg ggactcgaaa tggtacagtt gggctgggga tcgcccttgt     480
tacataaaag ncgtccagaa gagggacggt tacaggcngg ganctccaaa ggtcagtccc     540
tgccatt                                                              547
```

<210> 602
<211> 826
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(826)
<223> n = A,T,C or G

<400> 602
```
cgggggggnnt tacgtctctc tggacgcttt tattgtacca gggcgatccc agcccaactg      60
```

214

```
taccattcga gtccctactc ctgccttgct ctagggaaat aaaataacgt aaacacgtaa      120
gaacaatgcg aaagcgtttt cttccctagg ctgcagattg tcttcttcac cgcccctgct      180
tagctagcta gctagctggg aatttaatcc agaaacggct tgcgatacct cctagatgca      240
ctcgttttga gttacaaact ccgcggatta catgtctttt taaaaaagtt tagactacac      300
tagggaaaat tattttagta tcagaagaat atcaggggt gtagtactca tcagagctna      360
atgagagcgc tttaaaaatg ttagtttgtc ttccgccatt tctacagaaa gctgcaattt      420
caggttttca ncctaatagg tgatatntaa gaaaaaaaa acaatcgcan atagcccact      480
gctttacaa atcatttttc tcttctaggt atagcctgtc aggtggccta atgtattttt      540
gacatctcta ggaattttaa tagaccagaa atgggtgcca gagatatgcc tgcactaatc      600
ttaagtgggg atttatgtat ttctcaanca agtgattaaa gcaaaactag gcacgaatga      660
aatcaagatc tttaggccag aaatcatgaa nanttttana attattttan gaatctgtgg      720
cttctcttct taaaatngaa aaaaaaattg tttaaaccca naaggtctga atacccaagc      780
nccctgaacn anagaacaan gccggagcac cccctcccaa atcccc                    826
```

```
<210> 603
<211> 817
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(817)
<223> n = A,T,C or G

<400> 603
nnangacttt tgtggtntta tacaattntt ttttctattt ctatgaagag aaagccacag       60
agtcctaaaa taattctaaa actcatcatg actttcttgc ctaaaagatc ttgatttcaa      120
tcgtgcctag ttttgcttta atcacttgct tgagaaatac ataaatcccc acttaagatt      180
agtgcaggca tatctctggc acccatttct ggttctatta aaattcctag agatgtcaaa      240
aattacatta ggccacctga caggctatac ctagaagaga aaaaatgatt tgtaaaagca      300
gtggggctat ttgcgattgc ttttttttt tcttaaatat cacctattag gttgaaaacc      360
tgaaattgca gctttctgta gaaatggcgg aagacaaact aacatttta aagcgctctc      420
atttagctct gatgagtact acacccctga tattcttctg atactaaaat aattttccta      480
gtgtagtcta aactttttta aaaagacatg taatccgcgg agtttgtaac tcaaaacgag      540
tgcatctagg aggtatcgca agccgtttct ggattaaatt cccagctagc ttgcttgctt      600
agcaggggcg ggnaaanaag acatctgcag cctagggaag aaaaccttc gcattgttct      660
tacgtgttta cgttatttta tttcctanaa caaggcngaa ttgggactcg aatggttcag      720
ttggggtggg ggatcccctg gtncataaaa ngtcanaaag anggtacagg cggaacncca      780
agggtcgtcc tgcatttana ctcggaattt tggtgcc                              817
```

```
<210> 604
<211> 694
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(694)
<223> n = A,T,C or G

<400> 604
cttttcaaat cattttttnct cttctaggta tanccctgtca ggtggcctaa tgtaatttt       60
gacatctcta ngaatttaa tagaaccaga atgggtgcc agagatatgc ctgcactaat      120
cttaagtggg gatttatgta tttctcaagc aagtgattaa agcaaaacta ggcacgattg      180
aaatcaagat cttttaggca anaaagtcat gatgagtttt agaattattt taggactctg      240
tggctttctc ttcatagaaa tagaaaaaaa aattgtataa aaccacaaaa ggtcctgaat      300
agccaaagca acactganca aaaagaacan agcaggaag caacacacta ccngaattca      360
aattatacta ccagggtgta gtaaccaaaa cagcattcta ttggcataaa atagacacca      420
```

215

```
agaccaatgg ancagaataa agaaccccac aaataaatcc atatatntac cgccanctga        480
ttatcaataa cnaacaccaa gaacatatnt taagggacnt nctattcaat aantagtgct        540
ggnaaaaact gggaaatcca tatgcagaaa naatgaaact agaccctat ccctcaccat         600
acgcaaannt caacttcgga atgggattac aaaacttaag acattccaac ccaagaaact        660
atnaaancta ctattaagaa aacagatcnc nccc                                    694
```

```
<210> 605
<211> 678
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(678)
<223> n = A,T,C or G
```

```
<400> 605
taaaaatcta gactacacta ggaaattatt ttantatcag aagaatatca ggggtgtagt        60
actcatcana gctaaatgag agcgctttaa aaatgttagt ttgtcttccg ccatttctac       120
agaaagctgc aatttcaggt tttcaaccta ataggtgata tttaagaaaa aaaaaaagca       180
atcgcaaata gccccactgc ttttacaaat cattttttct cttctaggta tagcctgtca       240
ggtggcctaa tgtaattttt gacatctcta ggaattttaa tagaaccaga aatgggtgcc       300
agagatatgc ctgcactaat cttaagtggg gatttatgta tttctcaagc aagtgattaa       360
agcaaaacta ggcacgattg aaatcaanat cttttaggca agaaagtcat gatgagtttt       420
anaattattt taggactctg tggctttctc ttcatagaaa tagaaaaaa aaattgtata        480
aaaaccacaa aaggtcctga atagcccaaa gcaacactga acaaaangaa caaagcagga       540
agcaacacac taccggaatt caattatact accaaggtgt antaaccaaa acagcattct       600
attgggcata aaatagacca aagaccagtg ggaaacagaa taaagaancc caaaataaat       660
cctatattta cngcccnc                                                     678
```

```
<210> 606
<211> 263
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(263)
<223> n = A,T,C or G
```

```
<400> 606
gtggggtcng cancagccaa ctcagcttcc tttcgggctt tgttagcaga cggatcatcc        60
tctagtccac tgtgntcaaa ttccattgtg tgggggccnc tcgcctcggc canagatctg       120
agtgancana cntgtcccca ctgaggtgcc ccacagcngn ttgtnttcag cangggctna       180
caactcgacc ggcagcgnan ggctggcaga antgngcgcc tnnctcattc ctacgcngtn       240
ngccgcagga aggangacag gcc                                               263
```

```
<210> 607
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer
```

```
<400> 607
ccatgtgggt cccggttgtc tt                                                 22
```

216

```
<210> 608
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 608
gataggggtg ctcaggggtt gg                                    22

<210> 609
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 609
gctggacagg gggcaaaagc tggggcagtg aaccatgtgc                 40

<210> 610
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 610
ccttgtccag atagcccagt agctgac                               27

<210> 611
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 611
gatagagaaa accgtccagg ccagtattgt gggaggctgg gagtgc          46

<210> 612
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 612
gcacatggtt cactgcccca gcttttgccc cctgtccagc                 40

<210> 613
<211> 38
<212> DNA
```

217

<400> 613
gccgctcgag ttagaattcg gggttggcca cgatggtg   38

<400> 614
cggcgggcat atgcatcacc atcaccatca catcataaac ggcgaggact gca   53

<400> 615
gcactcccag cctcccacaa tactggcctg gacggttttc tctatc   46

<400> 616
atgcatcacc atcaccatca catcataaac ggcgaggact gcagcccgca ctcgcagccc   60
tggcaggcgg cactggtcat ggaaaacgaa ttgttctgct cgggcgtcct ggtgcatccg   120
cagtgggtgc tgtcagccgc acactgtttc cagaactcct acaccatcgg gctgggcctg   180
cacagtcttg aggccgacca agagccaggg agccagatgg tggaggccag cctctccgta   240
cggcacccag agtacaacag acccttgctc gctaacgacc tcatgctcat caagttggac   300
gaatccgtgt ccgagtctga caccatccgg agcatcagca ttgcttcgca gtgccctacc   360
gcggggaact cttgcctcgt ttctggctgg ggtctgctgg cgaacggcag aatgcctacc   420
gtgctgcagt gcgtgaacgt gtcggtggtg tctgaggagg tctgcagtaa gctctatgac   480
ccgctgtacc accccagcat gttctgcgcc ggcggagggc aagaccagaa ggactcctgc   540
aacggtgact ctggggggcc cctgatctgc aacgggtact tgcagggcct tgtgtctttc   600
ggaaaagccc cgtgtggcca agttggcgtg ccaggtgtct acaccaacct ctgcaaattc   660
actgagtgga tagagaaaac cgtccaggcc agtattgtgg gaggctggga gtgcgagaag   720
cattcccaac cctggcaggt gcttgtggcc tctcgtggca gggcagtctg cggcggtgtt   780
ctggtgcacc cccagtgggt cctcacagct gcccactgca tcaggaacaa aagcgtgatc   840
ttgctgggtc ggcacagcct gtttcatcct gaagacacag gccaggtatt tcaggtcagc   900
cacagcttcc cacacccgct ctacgatatg agcctcctga gaatcgatt cctcaggcca   960
ggtgatgact ccagccacga cctcatgctg ctccgcctgt cagagcctgc cgagctcacg   1020
gatgctgtga aggtcatgga cctgcccacc caggagccag cactggggac cacctgctac   1080
gcctcaggct ggggcagcat tgaaccagag gagttcttga ccccaaagaa acttcagtgt   1140
gtggacctcc atgttatttc caatgacgtg tgtgcgcaag ttcaccctca gaaggtgacc   1200
aagttcatgc tgtgtgctgg acgctggaca gggggcaaaa gctgggcag tgaaccatgt   1260
gccctgcccg aaaggccttc cctgtacacc aaggtggtgc attaccggaa gtggatcaag   1320

218

gacaccatcg tggccaaccc cgaattctaa   1350

<210> 617
<211> 449
<212> PRT
<213> Homo sapien

<400> 617
Met His His His His His His Ile Ile Asn Gly Glu Asp Cys Ser Pro
1   5   10   15
His Ser Gln Pro Trp Gln Ala Ala Leu Val Met Glu Asn Glu Leu Phe
            20   25   30
Cys Ser Gly Val Leu Val His Pro Gln Trp Val Leu Ser Ala Ala His
        35   40   45
Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu Gly Leu His Ser Leu Glu
    50   55   60
Ala Asp Gln Glu Pro Gly Ser Gln Met Val Glu Ala Ser Leu Ser Val
65   70   75   80
Arg His Pro Glu Tyr Asn Arg Pro Leu Leu Ala Asn Asp Leu Met Leu
                85   90   95
Ile Lys Leu Asp Glu Ser Val Ser Glu Ser Asp Thr Ile Arg Ser Ile
            100   105   110
Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly Asn Ser Cys Leu Val Ser
        115   120   125
Gly Trp Gly Leu Leu Ala Asn Gly Arg Met Pro Thr Val Leu Gln Cys
    130   135   140
Val Asn Val Ser Val Val Ser Glu Glu Val Cys Ser Lys Leu Tyr Asp
145   150   155   160
Pro Leu Tyr His Pro Ser Met Phe Cys Ala Gly Gly Gly Gln Asp Gln
                165   170   175
Lys Asp Ser Cys Asn Gly Asp Ser Gly Gly Pro Leu Ile Cys Asn Gly
            180   185   190
Tyr Leu Gln Gly Leu Val Ser Phe Gly Lys Ala Pro Cys Gly Gln Val
        195   200   205
Gly Val Pro Gly Val Tyr Thr Asn Leu Cys Lys Phe Thr Glu Trp Ile
    210   215   220
Glu Lys Thr Val Gln Ala Ser Ile Val Gly Gly Trp Glu Cys Glu Lys
225   230   235   240
His Ser Gln Pro Trp Gln Val Leu Val Ala Ser Arg Gly Arg Ala Val
                245   250   255
Cys Gly Gly Val Leu Val His Pro Gln Trp Val Leu Thr Ala Ala His
            260   265   270
Cys Ile Arg Asn Lys Ser Val Ile Leu Leu Gly Arg His Ser Leu Phe
        275   280   285
His Pro Glu Asp Thr Gly Gln Val Phe Gln Val Ser His Ser Phe Pro
    290   295   300
His Pro Leu Tyr Asp Met Ser Leu Leu Lys Asn Arg Phe Leu Arg Pro
305   310   315   320
Gly Asp Asp Ser Ser His Asp Leu Met Leu Leu Arg Leu Ser Glu Pro
                325   330   335
Ala Glu Leu Thr Asp Ala Val Lys Val Met Asp Leu Pro Thr Gln Glu
            340   345   350
Pro Ala Leu Gly Thr Thr Cys Tyr Ala Ser Gly Trp Gly Ser Ile Glu
        355   360   365
Pro Glu Glu Phe Leu Thr Pro Lys Lys Leu Gln Cys Val Asp Leu His
    370   375   380
Val Ile Ser Asn Asp Val Cys Ala Gln Val His Pro Gln Lys Val Thr
385   390   395   400

```
Lys Phe. Met Leu Cys Ala Gly Arg Trp Thr Gly Gly Lys Ser Trp Gly
             405             410             415
Ser Glu Pro Cys Ala Leu Pro Glu Arg Pro Ser Leu Tyr Thr Lys Val
             420             425             430
Val His Tyr Arg Lys Trp Ile Lys Asp Thr Ile Val Ala Asn Pro Glu
             435             440             445
Phe
```

<210> 618
<211> 385
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(385)
<223> n = A,T,C or G

<400> 618
```
ctgtgctgag aaccaaaagc tatgancact gcttttccaa atgtccataa naccaacatt    60
tttatcacta ccaccatcac ctgggagctc nttagaaagc tagtctcccg ggcaccaccc   120
tggcctactg aacctaatgt gcatttaaca agattnacgt ngaaatctgc aaagcacagg   180
ggcngataac agtaccacct gntctggttc ctanccccan gacccttaca gtctaactgg   240
gacacaaggg cttnaaatca aattgcctat cattaagata tacaanganc ntgagaaact   300
gctncactta tntattaagg ngctctaaga cttagaaacn aaangcantg ctgagangat   360
tcaaatatga ngggggncac tttnc                                         385
```

<210> 619
<211> 869
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(869)
<223> n = A,T,C or G

<400> 619
```
gatatcccgg gaattcgcgg ccgcgtcgac ctctacttgt ttagacataa atgcagtcta    60
gcattaaaga tcctttaaaa aaatgttttc ccaatggtta aaagacaagc tcaaataaat   120
gaactctcat acatatgcca aaattgatga gtagataaat atttcagtag gtagttacta   180
gctttctgtg tatgagtaaa catatgggag aaatttaaaa cactaaagta gactcaatga   240
aagcatagta tcctatgtat tcgtttttca gaaatgtcta atgaaggaag gaaacaatga   300
atgaatgccc ttattcctct tagagtgctg ggacatggtt ttgcctgaaa acttcatgtg   360
aattttatat tttgctacac attacaccca tcttagactt atacgtataa gacataaggc   420
atatcttatg tcttacatgt ataataatct aagcagaaca aaaaataacg aaatattttc   480
ttccccaaat ttttgagaca gatggatttt ccggaaagat gtgtttagct tttaatcctg   540
tggttttgtg taccacctgg cacactagag tgttgctcta attcagtgag ttgtaactct   600
gggtgaacag tggaaatact agggtacatt ttaaaaatgc taatgctcgg gcctcgctga   660
agaccaaatt aattggaatc tctgnggggng gnattgatct ttttataatc tttctanang   720
attctaatgg gcttccaggg atgaaaaccn ctgntggagc tnggaacctt cctttagttt   780
ggagaaaccc cgatgagggt ntnttaggcn ccgcctnttt ttggcctggg cttccccct    840
tatnntnttt tggaanggnc cnaattttt                                     869
```

<210> 620
<211> 339
<212> DNA

220

```
<400> 620
gngcgggcct cnccgtgctt gctctcgctg ccgacgctct ttttccacca gctgtaggan      60
aagcccgaag accactggtc ccccgggtag cccaagtacc actggtcctc ctggctcctg     120
acgctncggg tcttcctcgt ggcgtagact gccagcttcg gagacccctc agcccctccc     180
cgcttttctc caccccagga ggccatcagt agcgagctac tgcctcggcc acaacctccc     240
agcangatag cccgcggttt ccaatctgcg aaaggaggac cgccnagccc gaaatgccna     300
gcccagcnat cactgccacg ccgagccnag cgctcgtgc                            339
```

```
<400> 621
ggggngcatg gtcccnggta gccaagtaca tggtcctcct ggctcctgac gctacgggtc      60
ttcctcgtgg cgtagactgc cagcttcgga gacccctcag cccctccccg cttttctcca     120
ccccaggagg ccatcagtag cgagctactg cctcggccac aacctcccag caggatngcc     180
cgcggtttcc aatctgcgaa aggaggaccg ccnagccaga aatgccnagc cnagcgatca     240
ctgccacgcc nagccnagcg ctcgtgc                                         267
```

```
<400> 622
cttangntgt cgactgacgt catgcatgan ttaaagcaga ggtttggtga aatttatgaa      60
aaatacaaaa ttccggcttg tcctgaggaa gagccactac ttgataactc tacaagagga     120
acagatgtga aggatattcc ctttaatttg acaaataaca tacctggttg tgaggaagaa     180
gatgcatctg aaatatctgt ctcagtggta ttcgagacat ttcctgaaca aaaagaaccc     240
agtctcaaaa atatcatcca tccatactat catccgtact ctgggtccca ggaacatgtt     300
tgccagtcat cttctaagct tcatttacat gaaaataaat tagactgcga caatgataac     360
aaactaggca ttggacatat ttttagtaca gataacaact ttcataatga tgcaagcact     420
aagaaagcaa ggaacccaga agtggttacg gttgaaatga agaagacca agagtttgat      480
ttgcaaatga caaaaaatat gaaccaaaat agtgacagtg gcagtacaaa taactataaa     540
agcctgaaac ctaaattaga aaatctgagt tctttaccac cagattctga cagaacatca     600
ggaagtatat ctacatgaag aattacagca agacatgcca aaagtttaag aatgangtca     660
acacattaga aanaagantt ctgggctttg aagaaagaaa atgttccact tcataaagaa     720
ggttgaaaga agaatgggag agcccngaan ttttttgcccn gaaattttcg ggaaccctac     780
tggatgggtc nactggttgg ccatgaatga ataatggact aatcnnccaa ttcctngggga    840
agggaat                                                               847
```

221

```
<210> 623
<211> 681
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(681)
<223> n = A,T,C or G

<400> 623
aaaactgtac tcgcgcgctg catgtcgaca ctagtggatc caaagaatcg gcacgagcga      60
aaangctcan gcagcccggc tggccgccgc cgctcctccc cccaggaaag ccaangtgga     120
ngctgatgtg gctgcangag ctcgtttcac agcccctcan gtgganctgg ttgggccgcg     180
gctgccangg gcggaagtgg gtgtccccan gtctcagccc caaggctgcc cctcacaaag     240
cactggtggt ttgcctccac tgccaccttg ggctccgaac ccgctcccct gctgtggang     300
cccaccgtgg gaatccaggt ccccaggtgg actgcctgcc ttgccctcac tgcccactct     360
gcccacactt ccctgcctag anaccgggaa ggggctgtgt cggtantggt gcccacctgg     420
atgtggcagc accgactgtg ggggtggacc tggccttgcc gggtgcaaaa gtggggggccc     480
ngggaaaagc acctgaagtg gccctgaaaa atcccccctt aattttnccc caatttgggg     540
ctcnaacaaa aggaaattgc tgaagccaan ggtaccaagg tcacccctaa ggccagggtg     600
aaaaggtccc aaaattccaa tncccacccnt ttgggcttnc ctcttggaac cccggcccccc   660
tctcntgaan ttttaaaaaa n                                               681

<210> 624
<211> 661
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(661)
<223> n = A,T,C or G

<400> 624
attggtctta ctgtaccacc gggtggaaat cgatggccgc ggcgtctaaa tatccgattt      60
ttttttttttt tcctcttctg actgtccatg gacaaatgaa actaacttaa tctaactaaa    120
aaacacaact atattttgaa gattttctat ctgcactcaa ggacactttc cacncggttg     180
ttgttacctt ttggtcttgt ctctgaacat gaaattnatc tcaagggatt ngatttctgg     240
acctcctatt cctgctatgg gtttgatatt tcttgggctc caggccact gttgcattgg      300
gntgacagnt acctcctagc ccatancctc ctatcttggg aaacaaacct aacaactacg     360
tgtaccttcc atagatctct gattgagtct cagtatncgc ttgctcatgg gcgattcact     420
tgaatccgtn attggtgcca acaatcctga ctcatgggnn aatggatcct atcacgttcc     480
cctgattngc aaccccgta tacatanatc taatcgcata gaatctagcn tnggntatgc      540
gcggctacgc tatcagggnt tgntaactat ngcatggcta cgaancctga tcatgatcna     600
gggtcatgga ctcttatcag ggggggttggg ccgngcttct ttttcnnacc ttggtaaaac    660
c                                                                     661

<210> 625
<211> 181
<212> DNA
<213> Homo sapien

<400> 625
gcaacaatca gatcatgtta aagtaaatct ccattgccct ggatcacttc aggatttaat      60
tgtccaagga gagcagggt ctcctgtgaa aaaaaggtgg ggaaatgttt gagagtaaaa      120
aatacaaaat tcaaccggtc gaaatacac cactccattc agtgctctac ccccataagc      180
```

222

```
c                                                                   181

<210> 626
<211> 181
<212> DNA
<213> Homo sapien

<400> 626
gcaacaatca gatcatgtta aagtaaatct ccattgccct ggatcacttc aggatttaat      60
tgtccaagga gagcagggtt ctcctgtgaa aaaaaggtgg ggaaatgttt gagagtaaaa     120
aatacaaaat tcaaccggtc gaaaatacac cactccattc agtgctctac ccccataagc     180
c                                                                   181

<210> 627
<211> 813
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(813)
<223> n = A,T,C or G

<400> 627
accaagctgg agctcgcgcg cctgcaggtc gacactagtg gatccaaagt gaacgtgaag      60
gtgagcagag gagaacttgc gatggcaaag ttaaaaacaa gaggagatga tggtcttggt     120
gtggcacagg atgttaaaaa aattctcctg tccttaagga gttactgcta tttgagtaat     180
gtgccacttc cctacatagc cttctatgca gaaatgctat atttccactt cacaacccag     240
aacgtgcatt ttattttaca tttagaggag gaacaaacaa ccagaaggca aaaactggtg     300
cattattttt tgcaattctc ttggaaagag ttcgttttta acttctgctc agacagcaca     360
caactactgg gaatatattt taatttcaaa tctgatgtgt gacatctggt aactcattta     420
ttgctaatga agttttcaca ggaagcagca gtcaccagta gctcatctta tttttcagtt     480
ggcaaagtgt tgtttacctt ttattggcct gcatcggtgt ctcttatcac aggatatttta    540
attagaaaac gcaagtagcc taacatagaa nagaaatgga gtggtagata atagtagata     600
gaatggctaa atatttttat tacagtgatg taatatcact gnaatttatg gttaaaaatt     660
atgtaatact caaaaggaat tctcagactg cgcgaaacagc tggncaacag ctntcacagg     720
gctttnanct cctnttgagc tttcccccctg ntggacttta gtcttccttt tacncccgna    780
gttnccattn nttaccaatt gtnccgggaa ana                                  813

<210> 628
<211> 646
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(646)
<223> n = A,T,C or G

<400> 628
tttgggnggn ggtgtctcnt ttgggtggac tttttgggtc gtagggcccc aaggccgtta      60
atcccgtaat aacggaagac gaagaagagt cagaagagtg cttctataag gatcgggacg     120
agactacctt agaggaataa aggaaaaaag cagaggagga agagtggtag aaggagtcag     180
aagaaacccca cacgtcgttc tgaacctgga gccttatcaa aaaggtctag ataaacgata     240
gcgatctcga tatcgagctc aagaggtagg tttagagact tctcgtcctc gagagcgaaa     300
tggaagatct cgacgacgat aagaagttaa agtgtagagg gtgcttgagg agcgcgtgga     360
aggattctgc ggagggaccc atcgacgtag agacttgaag gcctactaag gtccacaaga     420
agcccggctc tttctccgaa tggtcggagc gtacagtatg cgacgtcgat cggcagacaa     480
```

223

```
gctggcggta gactcgaagt gttcgggcga atcgacttat aatagtcgcg cgctagtaac    540
gtaggaacac gaagagtagt cgaaagaaaa cgtttagtga gggaaaagat tagggaaaaa    600
ggagaggctt aataactaag acacttggag cctaggccaa cgcgaa                   646
```

<210> 629
<211> 617
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(617)
<223> n = A,T,C or G

<400> 629
```
gccccccnccc ccctcctngg gcttatnggg acagacccac gtagtactct aaatcttctc     60
ctacgccgga caacggaccc tataccaatt cgaatcttgg acactccgac cgccggattc    120
tcttcccctt tcggcttccc ctttctgtcg gtacccctcc ctagtcgtct cctacacctt    180
cgtaccgtcg atatatagtc gccgcggact agcctattta ggtgtcctag actcgttatt    240
gatccactca ttagtctagt actatgcgtc acgtatctta gttgcctaag agggagatta    300
aatcctccac aagttccgac gaattcctgg actctcgtac tagcaaactt tcttatgagg    360
cttccttgta tatcttctgg atgtttctcg tgtcccggtc ctccgctact actagagctc    420
cttgccctat ctctagaagt agaggactct cgggttcgtt ctccaaatct agcgctagag    480
ctatcgctac ccgctcgatt cccccagcgg aatcttgaaa cctgaggtag tacacaaacc    540
ctccncatct tccctcggtt gctccttctt ctcatccccc cttcccgcct tctcgggaan    600
gaatctactt tancttc                                                  617
```

<210> 630
<211> 644
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(644)
<223> n = A,T,C or G

<400> 630
```
cnntcggcnt gggttttntt ctgagnnncc cccccccccc cccccccaaa cttacaccca     60
ccaaacactt tccgcccccct acctaggaga cattagaagg gtttaggctt cggcgtatag    120
taaagtcctc tacctcggaa gtagagaatt cggtatttaa attcagggtt agaggctcgc    180
tcgttagatt tatagtttag gtttagaatc ggaaaccttc gatcttcctt agaagggtaa    240
taagtgaggc cctaaatccg tctaaccaag gcgttaaggt ccgtacctaa acctagtctt    300
atcttctatc aggcgcacca atataggtag gttctacttt cgtataggcc ttaaggaata    360
gttcggtagt tatcgaaggc actcctctct aggctaggct tttctcagtc ttagtactcc    420
gggaccgtcg tcgcanaaat atcgatggac ggtaggtatc tccgcgttac gcgtcgggct    480
agggatatag agcgaattat cggcgagagg cggtcgctan gaatcggtat caatatgntg    540
ttctttaccc tacggatatc ggcagaaaac ataaaacctt ctnaccangg ataagggatt    600
atcggacccc taaaataaca gtaacattta gantactagt accc                    644
```

<210> 631
<211> 526
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(526)
```

<210> n = A,T,C or G

<400> 631
```
ccntcggctt gggttttttt ctgagccccc cccccccccc cccccccccc ccccccggc   60
cccatagccc caccggnccc acccaaattt taacaaaata aatntaccta tcgntcacct   120
atcccncgta tcgngtaggt cggtaccggt accggngatc ncnacgattn ttcgggtcgt   180
cnccccttaan acggncccgt agccnccgga anaaatacta cgagngactc taatntagca   240
anacccgccg tcnattanta gcatccttag tcttccaatg ncgnggattn ngaatccttn   300
naagttatcg ggtagaacgg gtcccggtcc cccgccctct ttncaattaa cgccgggtac   360
aaantcggtt tctaaattcc ncacgaattt ngncggcaac attcncgggn ccttattanc   420
cntttccaac cccgatacnc nagctcgatc gggctttanc gaatccgggg tcnccccga   480
ngantccggg tcctttgagt ngctctagga cggttacgac ggagga   526
```

<210> 632
<211> 647
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(647)
<223> n = A,T,C or G

<400> 632
```
tttgggnggc gggngctcat ttgggtggac tttttgggtc gtaggaacct ggtatgaggg   60
gtgtttgag tttcttcttc gtcgtctctg ggaggttcgg tttcgattga gattcgggtt   120
cgtctttatc ttacgaggca ccctgatatt gttgcgcttt ggtttggttg tggagagttt   180
tgtcctactc tagcgggtca tgcggatgat atgtagcctg cgtggcctga tagtgatgtt   240
gtgagcttga gaggggagtt gtgggtgttg cgggcggagt aggaggggtt ggagcaccgg   300
gattgggaga tatagaatca taagtgttag gtataggtcg attgagcgag ttcgtggaat   360
tcgtgtggtc atcataatta gagtgaggat gggctctata tttcttagag gacgcacggt   420
cgtgattcgg ggtttgatgg gtgttcttct tgtgggcacg attagcttgt tcatgatggt   480
aaggaccata ctgtttcgaa tgaggattcg tgtcttcgga ttgttgtgga tattgtggnc   540
tanactattt agtgtaagcc ggaggtggtt tgccgtggtg gagtatccga nnttcattcg   600
ganggtatgc gtgcggagcg gtccttgtag acattccgga aaaatgg   647
```

<210> 633
<211> 630
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(630)
<223> n = A,T,C or G

<400> 633
```
tccttcggct tgggtttttt tctgaccccc cccccccccc ccccctcgga aggcctctag   60
gctcccaccc gtctctctaa tcctcaggaa ccgatccacc caaccaactt actaatgtcc   120
tacagtaaac acccgagaat ataaacccac acctaggcct ccaatcctac cagggaagca   180
agaagccgta gtctagcgta ttacgaaccc gagatagaga cggagatact tagtttttatt   240
ctctcggaat aggaaagacg actggggagg gaatataggc tagcgcgggg atagggcta   300
tggcggatat ggggcgggt cgctctctta ttcttctata ccacgtcaat aggaatgtag   360
atatacctag atgttcccgt agaaagagac gttagaggtc tccgaagcta taaaggagag   420
gcgcgaagaa acttcgtact ctagctttat ataggtagtc gctctagtcc cataagcgac   480
gagagatcta ctagatttcg gtatcgccgt cgtatgtatt cgaaatagtc ttcttcccct   540
tttcgatctc ctctctatac tacatggnga ttatagtcnt aagatagtca ggatattagg   600
atattagtta tatgacgttc gacgggacgg   630
```

225

<210> 634
<211> 647
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(647)
<223> n = A,T,C or G

<400> 634
```
ccntcggctt gggttttttt ctgacccccc cccccccccc cctccactaa gancttaacc   60
caaccctata gtttactcgt ataggggaat cgaggagaaa taggaacgaa gagcgggtga   120
taaagagaaa gtactttcct ttatatgtta agagcttagc gtaatgactt tcgttatatg   180
gctagttgat tttatccggc gttatagggc ttagttctgg ttatctcggg tctaattccc   240
ttagtatgct cgggagttta acgaggtcac gggatagcgc gtaccctttc taaggttctt   300
ggaaagctat tcgttatta tcgcgattct cgaggtcgaa aggatcaagg atcttccctt   360
ttactaccct agtcgggtta gcggtcggtc aaaactagtg tagtacctttt acctcctcga   420
aagttatagt cgaaacaacg tattagtcga aattatagcg gatagatcga gacggttctt   480
tctcgggttc tcagccggta atccctctat ttgggggtct tctccctctt cccctttgtc   540
ttccgcctta gcttccaagg ttcctcggaa gcgaggggtt ctacttaagt cgntagcgtt   600
ccttataaac cncctacagg cagacccccct tgtaaacggc tcggggt   647
```

<210> 635
<211> 645
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(645)
<223> n = A,T,C or G

<400> 635
```
ccttcggctt gggttttttt ctgagccccc cccccccccc cccgaaactc gccttaccct   60
agatacccaa agaatagttc cactcaactt cgtctaagta aaactctaga acttccaaac   120
ataaaagact tcgcgcggtt agctacacag cctacgggaa tctcacgaat cccgattcaa   180
gtcccactct cgaccacacc ccggtatcgt cgttttccca taccaatgtc gaaaaataaa   240
ataaaatcca gtcaagcccc acggtaagcg ggggtagggc taggcgaaga ggcaggaacc   300
gttcgaggcc gggggctttc aaaatacaaa acaactactt aaagtttacc ccttctaaag   360
tcggggcaa cggttaaagc acgcctctaa agtactactc gtttcgagaa ggggtagtca   420
tctcccgcat agagactctc gcgtatatca actcgcatcg cttctagcat tccgacggtc   480
gcccgcggct acatatcttg cggattagct ccgagggact ataggggttaa ttagtctagt   540
aaattctctt agaggatagt cggggtcgta gttaggcagt acgaggggac atggnctgcg   600
tcgtgctcta ccttgacagc atactcttat aaacatcttt ttcct   645
```

<210> 636
<211> 643
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(643)
<223> n = A,T,C or G

<400> 636

226

```
ccttcggctt ggg ttttttt ctgacccccc cccccccccc cctagcggaa aacaatcccc      60
accgagattt tattaatcgt aaaactcgcc ttcggtacca agtcttcctc cttcccgtaa     120
cctggctccc tcctagnggc tttacgaacg tccctcctct tcttacggct cggaagtggt     180
tacggttaaa tccggaggng gggctaacga atccaaggct aactcctctt anagtttgtt     240
gtccncncgt ttagtaagga tccgtggagg gcgagtattt gnccccggc ctttattnta     300
tagttcccta gtacgataaa gntaccggct atcctattac agcggataaa agttatttan     360
agggccgacg tcnccgctag acaggctaca gctagnggag gtaccgcctc cgactantcc     420
gttgnttccg acaaggnagt ttcggttaac tccacaaact cctccgccga ctctanggtg     480
gggacggcag ttcccncgtt tagtgtgcgt tatagagaag ggcatttgag ttggacgtta     540
cnttttaaca taggttattc cgtttaggtt cttgcgggcc cgtgggggta gtncnccggc     600
gcgttnntat cggcgatttt ccgcagtttc cgtttccggn tnt                       643
```

```
<210> 637
<211> 631
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(631)
<223> n = A,T,C or G
```

```
<400> 637
gggttntctc atttgggtgg actttttggg tcgtaggaac cggtatgnag gagtaggagt      60
cgctgggaag actagaagtt agctacggac gattagtgtg attccactct taataacgag     120
taatcgttta cgtcgggttg gtgtttcggg gttttggaga gtaagcgtag ttgtggagtt     180
tcgcatatag gtccccttac ttcggcgatc tcgtcttctg tcggttaggt tattattgtt     240
catccttcgc attagtagta gggttggtcg gataaatcga tagctattct ttagaattcg     300
tagtcggaga attcgtgtac gaagtccttt aagttcttta agttcgcgag taagacgtgt     360
acggttattt tgtcgtcgac gtaggtgtcg _tttacgggag tttcgtttta ggggtttacg     420-
tagaacgtta ttaagcacgg taatacgata gaggattacg cgacgtattc gtcttagaac     480
gtcgatttt cgaaggcgca tttgttatcg aaggggagtc cttggagaat cgagatattc     540
caagaatatt acgagagatta cagatcggaa ggctcccgag atcggacgta ttaccggtct     600
cgcccgaaac gagtaggtat cntccggata a                                     631
```

```
<210> 638
<211> 606
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(606)
<223> n = A,T,C or G
```

```
<400> 638
cccccccccc ctcaaccatc nattccccac ctcaacgcga attacggttt cgaaagtcga      60
caataagtcc ggtcgagtag agggaatcag gggctggtan aaaggaccac gggcggaaaa     120
taccggtctc cttccgggga gcgacgtcgg ggaaagggaa gagagcggtc tagttcgtag     180
gcaaacaggt cagaaaagtt aaggttaaag gtcggagggg agaggatagc tagtacgctt     240
agttcggggc tcgggcgcag ggccactttc ctctttcgcg ttcctttact ctgcttacga     300
gttcaggctc cggagttccg cgccggaggt cgtcgcgacg ctaggaatgg ggactcgctc     360
agtccccggt tatccttcgg gattctatgt tttcgccgat agacggagac cgggtagtag     420
ggttccgtcg taccgccact cgtcgccttg atccggcccg ctccgcttaa gggcgatgaa     480
agattaggta ttagggctct acgggacgag gcataggggc ggagaagggg ggaggggtcg     540
ggggtcgaag ggantaagaa atcgcantcg cgcggggtcg gtaggannccg aaattttct     600
cnncgt                                                                 606
```

227

```
<210> 639
<211> 592
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(592)
<223> n = A,T,C or G

<400> 639
tccntcggct tgggtttttt tctgagcccc cccccccccc ccccgggaa cgagaaaaca        60
atcccaccct accgcgggga gtgggttgna cgcttagttc tagaatcctc ggaatcgtcc       120
tccggcgttg gtagttccgg cgattccgag tatgccgaag tgtatcgctc cgtctagagg       180
ttggtatctg tttatcgcga tgacgctatt gactcggatg ctttcgaagt aggggatag       240
gcgcatagat acgcctccgc ggtgtcctct gaagtggccg catccgtgga cgcagcgtag       300
acagctctgg tggacgataa cggcttctcg tactcctact ccggctatta tgttagagag       360
gacttgtttc tgaacggata taccattagc gaaggggtac cctccgctaa cgcaggcgtt       420
tctaacagtt cttccgggcg ctccgaattt agattgacgc ctccgcagca ttgtgggatc       480
ctcttccgtt agccctcttt ataggatttc tcctccgccc cgaaagangg ctggtcgtcc       540
ccggcangta tgtctagctc gaacgctttg ttactccttt gttttcgaaa na              592

<210> 640
<211> 637
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(637)
<223> n = A,T,C or G

<400> 640
ctttgtggcg gtggnigtct catttgggtg gacttttttgg gtcgtaggct tatccgggtn       60
gggctcccga agtagcttag gatcgccggc tagttccggt cccgcccgtc gaaagcgcgg       120
ttcggcgggc ggccccgcgt tcgttcgcgg gctttaccct catagagtgc caggtctcgg       180
ttcttacggg ttcgtcggcg atagattta cggcgagagg tcggtatctt cgccgcttta       240
cgttcggtcg gcatctacgc ctagttcaca ggtagtttat gcgccggagc gcgtgacgga       300
gaggttatac gggacgcgga agaaccgcct ccaaatgact agtacaggct cgttcgggcg       360
tagatctcct cgctcggtcg gcggttctta cttctagggc cgctctacgg tttaaggcgg       420
tcgttagatc ttagaaacta tactcaagtt tcagtcggaa gaaaggaagt agagagaagg       480
gtaaacgatt acctccggtt ctagcccttt ttactcgcat aacgggagaa cggggtccgg       540
ctctcagata cgcctcgcga gacgtcgcga ttcaacttta acctccgcta gggcatccgt       600
atacggttaa cgcggtaaaa gcgacctcgg aaacctc                               637

<210> 641
<211> 649
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(649)
<223> n = A,T,C or G

<400> 641
ctntgtggcg gtggttgtct cagtttgggt ggatttttgg gtcgtaggna acctggtatg        60
aggtctagtt tcttcaacga ttcttggttc agttacgcga ccctatcctt atcttacaat       120
```

228

```
gtcttctaca tcaggttcat caattaatat atcaattaca cattaacgac ggtgtgacgc    180
aatatgagaa agtatacatt aaggttatta tatattattc gcttaaaaag gttcctgaca    240
tgggacaact tcacccacca ttctagaagc ccccctcct gtaggacccc ctcgagttcc      300
ccattatctt agttcagttt tcattttta accaggaggg tatcggtttt taataggtac      360
tattttgtca aacttttcag aagctttatc ttcaaatata cttgcaccat ctgtactagg    420
agcactaact attcgagtct attacagctc aacagaaaat aattgaaatt aaacaaccta    480
agtatcgtcc accataaccc catcgggctc tcaccccatt tcttcataag ttctagagca    540
tcctgagctc tttcctatta cccttgatgg tactcatggt ctaataccc ccgcagttat      600
aggtccttat ggatcctatg ctaccaccgg tctaatccct tctatcacn                649
```

```
<210> 642
<211> 645
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(645)
<223> n = A,T,C or G

<400> 642
tccttcggct tgggttttt ttcgtcgcgg gttactatta tcgattgtta cttgtaaagg      60
cgatactccc accgctcacg atattagacc tgctcctcta gaagcgaacg gcgataggtc    120
tactcggccg gcgaagacgg cgaacgggta ggaggagcca tatgcaaccc taacggagat    180
tataagtact gggaaaaata ctagtattaa ggtagcgggt taagataggt ggagagacac    240
tattcacgag cataagcact tagaaggtct tctcgaggag aggtaggcta cggactacgt    300
tccttcttcc tctagcctcg agagggagta tagatgattc gcaaaagaga atccctccta    360
tacgctggca taactagacg acgcgtcgtc gggaaatctc gccaacccta ttgcgacctc    420
caaaaggaag attgtcgttt catagaacgc taatactccg ggtcttcccg aatcatagcc    480
gcatatcggt aagaagacgg taaaatcgcg cgattctaac aagattctgt agacttaagg    540
ctaagcacta gaagcgatct cgattccgga tcttaagatc atactaatag ttcggtcaca    600
ccagacgacg attagccact agaagcccta ctccgtngaa accgg                     645
```

```
<210> 643
<211> 586
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(586)
<223> n = A,T,C or G

<400> 643
ctttgtggcg gcggtgtctc atttgggtgg attttggt cgtaggaacc tggtatgcag       60
ggtccgcccg gaattaaaag cgggatcccc aaaacgnngn ttcgcaagaa gagaagaatc    120
atagcgatag anctttcata gtacaaaggt aactaagagg aaaataatgc agattcagaa    180
ctagttgcca aattagaact cgattaggcc aaggatccga gcctggcgct atcacttcgg    240
gacttaagct acggtagagc agtcggtcct gaagcatagc tcccgtagga cgtaggaaac  .  300
tagtccggca cggaggacat actctcgagt ctcggaacgt ctatttagaa tataaacgca    360
ttaacctcag aaggcgccga cgcggttact ctctagggaa ctatttcatt ccttccggag    420
ctccctatt tttccaacac atataccggc aaaggaaat cttntgtcct cggtctaaag      480
agagggaaaa aaaacgatat ctaggttcg gtttatccat ttaaaaanat ngacgcgact     540
actcccttc aaagggagtt tccccctagg nagagttcaa cngaag                     586
```

```
<210> 644
<211> 646
<212> DNA
```

229

```
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(646)
<223> n = A,T,C or G

<400> 644
ctttgtggcg gtggttgtct catttgggtg gcatttttgg gtcgtaggaa cctggtatng      60
agggctattt gacttgtttc tcaaatccca tggtatggtg ggtggcgtgc ggggtggcgg     120
tcggttcggc gggggtgggg gtcgtcctcc aaaggagttg ctagagggct tttagtggtt     180
ttagggcggg aaggggttag agcggagaga cgtcgtcgtg gaagcttctg gcggagcgcg     240
agaaggtagt tagcgccggt tcggaagatt ctcagaattc gagaagaggt agtggggcgc     300
ggagagagag tttctaagtc taaacgtaga ggtcgtccta gtcgggccgg gagtagcttt     360
taagctagag gtcgaggtcc tcgtttaggc tccgggctct tcgggcagta tcctctttct     420
cgaggaacgg agcgaccgac gtcgtagccg·gacccgtcta tccgtacgtt tagagatacg     480
ctcacctcca cgggcgtata tgcccgtata cgtataaacg cgtaatatac tcgcgcgtaa     540
aacacgtata cactatatac acgcatcgta·cggaccgtat agcgttatac gcgcgcgtat     600
attaatttac acttatatac gcgttaacac gatatatcac acnccg                   646

<210> 645
<211> 654
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(654)
<223> n = A,T,C or G

<400> 645
nccntcggct tgggtttttt tctgacccccc cccccccccc ccccggtcg acaacgtgcc      60
caccgttgcc atcccagcat agctggttcg ttctgtttta ttcttagtag tttagttcgc     120
ctatagtccc tcgtctatcg tctatcattt aaggaggcgg ggctcgctct ttagggcggg     180
tatcttaggt attcttctgg tttcggctgc cgtctcggag tctggtcctt ttgctttcct     240
ttcttggtcg aacttcgtgt ttgatcgcgt tgtttctttg gggtcgtcat acctaaggcg     300
cacttcgcca acaaacaagt ttgtgtagtc gtttctatta gggttcgctg gccggcgctc     360
ttactggttg gcgatttttta acgcgtttgg ttttaatttg cttcctcccc tagggctcgc     420
tcggtcttct ctctgttcgc tgctctcgtc cggcctttgg tgcggggata gctccggcta     480
ttancgtgcc gtgtccgtgt ggnttttgtc caatgtgaag gcctaggggt gcgggcttct     540
ttggccatgg nttcccctct tgtganccttt aggggtaacg antcgtaatt naaggtcggg     600
ggttggnata cgttntangg gangcctgng tccgntattc cttgttttgg cctn           654

<210> 646
<211> 645
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature ·
<222> (1)...(645)
<223> n = A,T,C or G

<400> 646
tccttcggct tgggtttttt tctgagcccc cccccccccc ccccacgcc aagtacacag       60
acccaccaaa aacaacgtca acacaacttc gggtatacgg accttaagag agaccccgta     120
gtagaccctta ccacagccat ccaatagtca aacaacaagg gcgcacccaa tccatccata     180
gagctatcaa acaacggagg ggaaaggaaa gagcagggtc aacttagcag agatcgaagt     240
```

230

```
cggcactaat tcctttcaag tactcgctcg gcttgtagtt cggggtaaag tccgctctca      300
aagggccaac gaggttttaa agcgacccccc gtatcgagtc ttcttcgtat tcattaaggc      360
gttaaaggta cgagacctag aagagagtag aattagccca ccaaatcgcc taaaccggca      420
aaaacgacca aaagtcaaag acccttacaa atatcacctt aaaacgccaa ccccaaaaac      480
gcgatcagta acgcacgtac ctttcccacg cttttctttc tttcactctc caaaacaaac      540
ccgaatattt agcgcaaaaa atatccgagg gagaattaga agctattacc cgaaaaaaaa      600
ncgganangg antaaatngt ggggaatana cgtttggttt ttctg                     645
```

<210> 647
<211> 753
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(753)
<223> n = A,T,C or G

<400> 647
```
accttacctg gtaccgggcc cccctcgag tttttttttt tccaaataca actcagattg        60
tatacgaaaa gctgataata cattgacttt tgctgtttaa atcccttgag cctttgataa      120
tgattttttt tgtgttaaca attgtagtat ataaaatcgg attcaccatc cttctgatgc      180
catattgatt agtttgattt tatggtgatg ggatcattgt gtgttaactg tattaagaag      240
aaatggattt gattgacttt gcatccattt ttatctgtgt tactttcatg ttttatttaa      300
aagcatttct ggaccagaat aagttaagtg gtataatttg cttttttacac gtttatataa     360
ttgaagttag caatgtggca aaatctctaa tggaaataaa atgcttcaga atgatgacat      420
aaatctgagc tatttcttgc ctggagaaca agtgttattc ataataattt aatagcttct      480
gaggtgtttt gttcatgtga tgaaggctta tccaccttgt atcaattcat gggctctgct      540
ttgtttaatg tagtcaggtt gttaatacna gacttaagag tcatcctact gtgataagtg      600
gtgagtgaag attacatgtc ttangaaaat tatactggga atatctctga cattaatggg      660
tttaaatgtt ttaaggctag gggatgatgc aatgganaan atncttccaa angtttctgg      720
ttgtttatat ttgnggaagn catnaagana ccg                                  753
```

<210> 648
<211> 383
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(383)
<223> n = A,T,C or G

<400> 648
```
gatatcccgg ggaaatgcgg aggcctttng gcttacgtgt ttaccgcgta gggcaaagcc        60
ttgncaaatt cccggccagc ggagcggcga gggtggggac tcacgggaag ttaaacagcc      120
tcgtcggcgt cctcgaggct ccaaaaccag gctctaggcg gggacgactg cagccgttat      180
ggaggccacc gcggctacgg ccgcggctga ggcctcccca ggtggagcgg tggcctggag      240
gggaatcttg atcctgggcc agccacctgt caagaggagg cggagcgtca tgcctctgga      300
agactggatg aatattctcc aggagcctga cgaaggcgaa gaagtctttg cagaggaaat      360
tgaatgctgt ctgatgctac aat                                             383
```

<210> 649
<211> 349
<212> DNA
<213> Homo sapien

<220>

231

```
<221> misc_feature
<222> (1)...(349)
<223> n = A,T,C or G

<400> 649
cgattgtnta cnagtcttag agtaagctta agntcgntac cgagctcgga tccactagtc      60
cagtgtggtg ggaattccat tgtgttgggt cactagtaaa tggatttagc tagacanagg     120
anatttaccc tattccattt agcacagtga gganaggcta nacagctagg atgcaataaa     180
aaaaatttta atgagaaatg tgtgtggtag attaattcta ttaatctcaa gttatagatt     240
aaaaaattta agtaccncat aaatgccatt tgcctttgct aangntacat ttttatgaan     300
aangaccntg catacnnaat ganatactgg actttnggna cttgangga               349

<210> 650
<211> 306
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(306)
<223> n = A,T,C or G

<400> 650
cattgtgttg ggagcatcct tccatcagct cccatgagaa attctctgtt gggtttaagc      60
aatccccaaa tatatcatat tgacatgaat atatcatctc ctcaatgtcc agcattagca     120
gacaagatga gtgctgaaga tgatataact cctacctctt atgtaggcta gaggtaaagt     180
ctggctctgc tgactgtggg gacataccga aaaggaatgt gggttaatat cagangacct     240
ccctgcagat ccganantca gggnctggac tttctgggan aggaagcnna aagttatntc     300
tgaacc                                                             306

<210> 651
<211> 769
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(769)
<223> n = A,T,C or G

<400> 651
cattgtgttg ggcagggtca tttctaaggc atgggctgga agcttttatt taaaacttta      60
catgtcttag aagcactctg gttgttgcta ggcagacaat tttacatctc ttgctatacc     120
agttgcatga agttcatcat gcatattggc tgtggaaaac cttaacagca tcatgtcata     180
aggtttcagt aaggtttaaa tgaaatcatg tattaagcac ttagtatagt gcaccttaaa     240
tgttagcttc aaaacaatga caacctaact aatgttgaaa gaagcttgtg tttgtaaatt     300
atgtcttatt gaaagatgtc atcaaatcct gttatttcta atcccttaaa gtctctcaat     360
gtatttcttt ttgccatatc caatgacagg accttagttt aagccagtgg ttctctcaac     420
ttctaatcca gagatacctg ggtgtcccca agaccttttc agagcatcct tgatgtcaaa     480
accattttca taataatatt aaaatattat ttgctcattg tactcttatt ctctcccaaa     540
tattcagcga gttttccaga agctatataa catgtggtaa catcttatca ctctgacgat     600
taatagaata tgngnttttg gattcttgng tttaaaattt tctcactttg gggttctaat     660
atggnnacga ttaatagata tggnctccat gaccagangg ctttaaagca ntcaataatt     720
tttaagagac taagnactat cctttaaaga tngngaactc catcttaat               769

<210> 652
<211> 267
<212> DNA
```

232

<210> Homo sapien

<220>
<221> misc_feature
<222> (1)...(267)
<223> n = A,T,C or G

<400> 652
nnangcccтt taaccattgn ggcctccacg cnntggcggc cgctctacaa ctagnggatc   60
cgcnactcta gnanaangat tggctcttnt gggntgggcc ggncgggctg gggcgttaag   120
cggggctggg cgcgcgccgn ggttgnacna ggcgccgccg cccncacacn cccggagcac   180
cctcnttgcn gccntncccc gctcacccg cgcgcgccgn tccgcttttt ccncacccan   240
agcnctnttt atctntgtct cctccgg   267

<210> 653
<211> 501
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(501)
<223> n = A,T,C or G

<400> 653
cccnttnacc cattgctgga ctccaccgcg gtggcggccg ctctanaact agtgggatcc   60
ttncnatgag atgngcgang gaggacnnat ttgctatnct ggatggggct gantcntnta   120
gctnctctag cancagatgg gttatcgagg aagatgactc caangggcta nantcctatg   180
cncatcctaa aanncanctg ctgtnttcag agtacgcgac acatcatcnc tnatgcattg   240
ntgancaaga cgggcangtg cttatcctca .gcgangatgc ccttaaccan gagctcgaat   300
ggacntatca ccntanaggt acanntnccg caccacacac cngcttgcnn cctgacgctg   360
gactggatcn cttaggccac caatncccg tttnccacat ncctgggacn ctanananac   420
tcganggggg gcccggtanc caattcgccc taatactgag ccttgntacg nacgctnact   480
nggngtccta ttanaacgtt g   501

<210> 654
<211> 710
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(710)
<223> n = A,T,C or G

<400> 654
gcgnctttan cncatgctgg gctccacgcg gtggcggccg ctctacacta gtggatccca   60
acactgagtc caccacagna aaactcanca ccaggcagac cccacaactg cagaatccag   120
gctgcaattc acagactaat cntctagacc cacctcagta ccagatggta ccacacagct   180
caaggnttta ggtttgcgtg gtanactcaa tctctatctt tcaccactgc cagcctgact   240
tcagagatcc tgngctctgg acagtcctca gtggcaggca actctcagga gcctcaggnt   300
tttggcacat cccagnacca gccagctgcc acaggccctg accttntanc aacactgccc   360
atgtattcca gacttctanc ataccacagt gccatgctga ttgcatctat agangctcag   420
gtgcncctca aanctgtgcc tgctgcagna ngccccacgt ctctggcatg ccccaatgcc   480
atgngtggna acanttgact tctgggcatg ntggaattcc ctaccactga ncctgaccat   540
aggngggganc ccattttttt cgagggggg gcccggcccc caattccncc ntatagngag   600
ncgtanttac gcgcnnctta ctnggccngt ngtttaacaa cgtcnntgan ctggggaaaa   660
cccctggnng cnacccaaat taaacngcnt tgcannacat cccccttтcg   710

233

```
<210> 655
<211> 202
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(202)
<223> n = A,T,C or G

<400> 655
cccctttncc ctttcanccc ccccgttttg gcngccgccn acacctactn catccaccca        60
cantcgacca cccgagcttt tttccgatcc cancatcnat gcngattttn tctntgcntg       120
ctgngcctgc acctttgnta ggtcaagcct ggcccatctt cgacaacttc ctcatcacca       180
acgatgaggc atactctgac ga                                                202


<210> 656
<211> 308
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(308)
<223> n = A,T,C or G

<400> 656
gctgntgaaa gaccacaccg aaaaactctn ctttccgact tccacatgat gatcngcatg        60
tggtggtgag agacttatca tgacgacatc gcttccnacc atcgcanccn ctgcccaagc       120
ccattcatgg aggcctgggn anttctgtga ntgacntnga cnctanacnc tnccactgtn       180
tgctatccag acttgnttng aatatnttat tggcnaaana canttncgga atgctgtgnt       240
tgnncattga angatctgat cactatgaga gggtgaggac nncctgctng ctggcantnt       300
ntaacccn                                                                308


<210> 657
<211> 696
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(696)
<223> n = A,T,C or G

<400> 657
accntttcca caatnctgnn ctccccgcgg tggcggccgc gtcgaccagc aacctcagct        60
gtgggtcttg ttacagtaat gagttactgt aaggaaagtg tgacatttcg agcaatttga       120
tttgtttaaa aactagagca gtttcagggt tttccttgta aatctgtctt atgtgtcttc       180
aatgttcttt cttgaggagt agagaaagga attgttagga atgatgcata aaccatggct       240
tattttatct cgctgccacc cataatcaga gcagattctt gggactatga ccctcatgga       300
gacatgacaa ttgtgtgtgt ggtgggtggg agaaaagagc tgggaatttt tagggtctag       360
agggtccaat caggactatt ttatggagct ctgctcacca actttaagtg agcaccaggg       420
gtgngaaagc gaatcttggg ntcaaaanaa caatggnaag gggtaagttg gtatnctgaa       480
ctggccactt cggactctta tttaactggg tattctcant taaggaggcn ngggtggtct       540
tggcttgtna aggaaagcct gtgcaatgga atgactttaa aacccccat taaaaaaaaa       600
angntataaa tcttgggtct taanaangaa gcctgggttc tnttanccca ttttnccccc       660
gggaaggnaa atnttcttag gnaanggaag ggaagg                                 696
```

234

```
<210> 658
<211> 698
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(698)
<223> n = A,T,C or G

<400> 658
ctggactccc cgcggtggcg gccgctctag aactagtgga tccgtgttgg ctcaattctc        60
aaggctgttg ctgtgcggcc tgttccccac acgtgctgct cagctcaggc aagcaccgag       120
cttgtgttgt ttcatgctca gcgtggaggc ccctcctcca ggtcgctgct ctgtggggtt       180
cccatacact caggctccta ggaggagtcc atttagaaag ccagggtttt tctcagagtc       240
ttagttcctt gtgctgtcat ccatttcaca cgacttgggc cctgctcggg gcaacacagc       300
aagagaaaag acagggaaaa taagagaggg accttgcaca cacacgctct ggaccacaga       360
gccctgtgcc cagctcctct gtcaatacag gtggaatctc gtgcaggatc gcagggatct       420
gtgatgccac caaagagcag gccgggacag ggttaggaga gaaaggagag ggaagtgggg       480
gtttctccta cgcactctta tttgcagagg gaaaggcggg tttgtattgg ggttgtcggt       540
ctttgcaccc acngcacagt tgtgagacac ccccatcctn agatcaaagc cccacataca       600
gcttggggaa aaacaaaacn aaacaaaaca aaaacagtaa acctccatgc canttgttgg       660
gnaagtttttn aatttncttc cccnacccan cttgcttc                              698
```

```
<210> 659
<211> 750
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(750)
<223> n = A,T,C or G

<400> 659
ncaanctggn ctccaccgcg gtggcggccg ctctagacta gtggatcctc ctcatgggcc        60
tggatatctc tgaacatatg atgaacattg cttatgaaaa attatttgta ngaaaattgt       120
gaggcctaag aatgntattt tctttttagtg atggtctttg tttgcttctg taaggnactt      180
gtgggcactc gtaagcttgg atctctttaa tctaatacca gntttgagat tttcttggcc       240
ccatagatga attaaaactg gcgtacttct tgtttacaag anggataagt ctcctagggt       300
aagtcttttg gggtcccaag tcaaaaagat gagggattta ccagttctct aaccttggta       360
gccccagact ccaaactttg ccttctagtc ccaagaggct atcaaaaagc aaaggccatc       420
ttccaccttc ttttccanaa cagcacacat tccagacagt acttgaaagc aggaacctcc       480
ttatccctta aaaacctctt ggaancatct tccctctctt gcttctacta tgcttggccc       540
acctancatt cncnttttc tggaaaccgg aaaaanctn tgacttnngt tggctacatt         600
cagcttggcc ccctacaatn tggtttccat ctgccctaan gaaattttaa agggcacttt       660
ttttntggcc cctgacttc nntttttagg gctttccccc angctttgcc cctttggtta        720
aaggggttat tttccttccc cttttggaag                                        750
```

```
<210> 660
<211> 849
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(849)
```

235

```
<223> n = A,T,C or G

<400> 660
tcggatccac tagtccagtg tggtggaatt cgcggcccgc gtcgacgggc agtagtggta        60
tgcntntcta aatgttataa ttatttcaga attactctgc cagaaagtta tgatcataca       120
tagaagagtt tgtagctaac tttgaaagta gtggaaagtg gttttcatgt attgtttggg       180
ttaatttaat tttgattata tttggttttt agttcaggta attttttttgt tgaaaacttc      240
aaatgacaat ttcttcatgg ttactaaaga tcactcatgt ggagtagttt cagatttttt       300
tctgaataca tgtattactt ttagagatgt aaagatgtga aattactaag agagaaaccc       360
atgtgatttg tttagtggat caaaagtcgg tagctccttt gatcctaagt gccactgata       420
gttaaataga tactgaagct atgggcaggc tggattgata agaaaaaagg agacagagaa       480
atgggaaatt gggaaagaac tgtgcaaata ggaaaaggag agagcaacag aacagaatta       540
gtaccacagt gccgaagtgc cacctcaggt acttccatct cccatctcct gaagaattca       600
gtaacagttt gcaaatggtc aacacaatca tttagtgatc ctggttgata ttttcaatac       660
tttctgggga tttcttggct ggnttcaaaa gatgatgctg atagtttta tgcccctgaa       720
ggtattctga agnttancat aatttattgg tcagtaaaat atttgaataa aagnggganga       780
aggaaaatct ggcntcttat tttgggatnt cngcnggggg aangaggata taattnaccc       840
cggccttgg                                                              849

<210> 661
<211> 653
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(653)
<223> n = A,T,C or G

<400> 661
aacttaagct tggtaccgag ctcggatccc tagtccagtg tggtggaatt cgcggccgcg        60
tcgacctcca ttcgtttctt gtcctttttt ttcatttttt ctcatgttct attcacttta       120
ggtttctaag ataaatatta taaataatt tttacttata aattattcac tgataccctg       180
tctttaacat gtgaaatgaa ttcaaaagga atcttaatga gaaataaat actcatgatg       240
tttaatagat ttgatttcga aataataagc cctctgaagt cctaagttaa aaataaagca       300
acttgtttga taatttttca tcaagaatgt atctgagtct ctgagtaatt attagtagga       360
atattccatt atcacaatta cacagtataa gctatttagt ctaactttac caaaaaaggg       420
agctacttca acactgtgtg agacttttaa tgggtttgca ttgggtatgc actattagca       480
agataaccta ttttacagca gtgtttntta acctttccca tttatttgaa aggcagctaa       540
gatatagtag ttaatntaan gggctgatgc atttatatta catgtagana atgggagata       600
cnaaagggag nggggggana tnttttgnat tcnnaagctt cnttgncaat taa             653

<210> 662
<211> 646
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(646)
<223> n = A,T,C or G

<400> 662
aaacttaagc ttggtacccg agctcggatc cctagtccag tgtggtggaa ttcgcggccg        60
cgtcgaccca gggacaggca gccagngctg gggtcaccag ggtcccctct tgggccctcc       120
aanagcaaca gtactggcaa cagctgggat ttgctgagca cagactctgc agcaggctcg       180
gttgagctct ctgtgcctgt tccttcatac catcctcacg cccatccatg agatgggtcc       240
agctgttttc agatgagaaa atggcacagg aagctggtaa gtgacagtca gaaatgaatg       300
```

236

```
ctggcagctt antccttgga cccaccgcag tgcaggacct tgctcaacag ggatcaccct        360
tgtccgccac ctgttcatga ggccacccag ggtttgtgtg gtcatttgtc tcctttcatc        420
tgcttgcctt caaccagctg ggtcattagg gctggggaac ccagacccca cacagtcctt        480
ctcccagang ccagacacan nctncgccac agnaaggact tcagtccccg aancaaatgt        540
ncctgggcgt anaaactgna gggnccccaa tccctggtgg ggtactgctt tgcactggng        600
gaattcaccc ctcattgnna acctttccct nttnncaccc ctaaac                       646
```

<210> 663
<211> 650
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(650)
<223> n = A,T,C or G

<400> 663
```
aacttaagct tggtacccga gctcggatcc ctagtccagt gtggtggaat tcgcggccgc         60
gtcgacgtcg acgcggcgng ccgtttcgac gcagttgata catattatta tatactacat        120
nggttttcta gaattaaaaa attaatgtgt agtgccagcc ctagatgtaa gttacatata        180
tcaactctat ccaattttgt cagccataaa acttaccttt ttcacatact tctaactcta        240
acaatgtgag aaatgtagat cattgcaatt atacccacaa ggcagatggc tacatgcaga        300
atggatagca gaatctagct acttacgcta gccacatggt agacgttttt tcctttgttt        360
ttgcaaaatt gcaatataag ttgcatatcg ttagagtgaa aagatgtaaa gaacccatag        420
aagccagtga tgaaggacat ttatattttc accttacaa angaccttaa aattgcctat         480
gtggagcaga aactggagga gggcnaancc atcngtaaaa aaaattttgn tnctatttgg        540
atttgggcac cattattacc tccccaggtn ccttttgnt ttaacctttc ttttaaaaaa         600
ataaattcnt aatttttggg caaaaaaaaa caaggttttt attᵗaaattt                   650
```

<210> 664
<211> 678
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(678)
<223> n = A,T,C or G

<400> 664
```
taaaaatcta gactacacta ggaaattatt ttantatcag aagaatatca ggggtgtagt         60
actcatcana gctaaatgag agcgctttaa aaatgttagt ttgtcttccg ccatttctac        120
agaaagctgc aatttcaggt tttcaaccta ataggtgata tttaagaaaa aaaaaaagca        180
atcgcaaata gccccactgc ttttacaaat catttttct cttctaggta tagcctgtca         240
ggtggcctaa tgtaattttt gacatctcta ggaattttaa tagaaccaga aatgggtgcc        300
agagatatgc ctgcactaat cttaagtggg gatttatgta tttctcaagc aagtgattaa        360
agcaaaacta ggcacgattg aaatcaanat cttttaggca agaaagtcat gatgagtttt        420
anaattattt taggactctg tggctttctc ttcatagaaa tagaaaaaaa aaattgtata        480
aaaaccacaa aaggtcctga atagcccaaa gcaacactga acaaaangaa caaagcagga        540
agcaacacac taccggaatt caattatact accaggtgt antaaccaaa acagcattct         600
attgggcata aaatagacca aagaccagtg ggaaacagaa taaagaancc caaaataaat        660
cctatattta cngcccnc                                                      678
```

<210> 665
<211> 694
<212> DNA
<213> Homo sapien

```
<220>
<221> misc_feature
<222> (1)...(694)
<223> n = A,T,C or G

<400> 665
cttttcaaat catttttnct cttctaggta tancctgtca ggtggcctaa tgtaattttt      60
gacatctcta ngaattttaa tagaaccaga aatgggtgcc agagatatgc ctgcactaat     120
cttaagtggg gatttatgta tttctcaagc aagtgattaa agcaaaacta ggcacgattg     180
aaatcaagat cttttaggca anaaagtcat gatgagtttt agaattattt taggactctg     240
tggctttctc ttcatagaaa tagaaaaaaa aattgtataa aaccacaaaa ggtcctgaat     300
agccaaagca acactganca aaaagaacan agcagggaag caacacacta ccngaattca     360
aattatacta ccagggtgta gtaaccaaaa cagcattcta ttggcataaa atagacacca     420
agaccaatgg ancagaataa agaaccccac aaataaatcc atatatntac cgccanctga     480
ttatcaataa cnaacaccaa gaacatatnt taagggacnt nctattcaat aantagtgct     540
ggnaaaaact gggaaatcca tatgcagaaa naatgaaact agacccctat ccctcaccat     600
acgcaaannt caacttcgga atgggattac aaaacttaag acattccaac ccaagaaact     660
atnaaancta ctattaagaa aacagatcnc nccc                                 694

<210> 666
<211> 705
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(705)
<223> n = A,T,C or G

<400> 666
tttaaaaatt tagatacact angaaaatta ttttagtatc agaagaatat caggggggtgt     60
agtactcatc agagcgctaaat gagagcgctt taaaaatgtt agtttgtctt ccgccatttc     120
tacagaaagc tgcaatttca ggttttcaac ctaataggtg atatttaaga aaaaaaaaaa     180
gcaatcgcaa atagccccac tgcttttaca aatcattttt tctcttctag gtatagcctg     240
tcaggtggcc taatgtaatt tttgacatct ctaggaattt taatagaacc agaaatgggt     300
gccagagata tgcctgcact aatcttaagt ggggatttat gtatttctca agcaagtgat     360
taaagcaaaa ctaggcacga ttgaaatcaa gatctttttag gcaagaaagt catgatgagt     420
tttanaatta ttttaggact ctgtggcttt ctcttcatag aaatagaaaa aaaaattgta     480
taaaaccaca aaaggtcctg aatagcccaa gcaacactga acaaaaagaa caaagcagga     540
agcaacacac taccagaatt caaattatac taccaaggtg tagtaaccaa aacagcattc     600
tattgggcnt aaaatagacc naagaccaat ggaacagaat aaagaacccca aaataaatcc     660
atattttac agccagctna ttatcaataa aaacnccaag aacnt                      705

<210> 667
<211> 817
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(817)
<223> n = A,T,C or G

<400> 667
nnangacttt tgtggtntta tacaattntt ttttctattt ctatgaagag aaagccacag      60
agtcctaaaa taattctaaa actcatcatg actttcttgc ctaaaagatc ttgatttcaa     120
tcgtgcctag ttttgcttta atcacttgct tgagaaatac ataaatcccc acttaagatt     180
```

238

```
agtgcaggca tatctctggc acccatttct ggttctatta aaattcctag agatgtcaaa     240
aattacatta ggccacctga caggctatac ctagaagaga aaaaatgatt tgtaaaagca     300
gtggggctat ttgcgattgc tttttttttt tcttaaatat cacctattag gttgaaaacc     360
tgaaattgca gctttctgta gaaatggcgg aagacaaact aacatttta aagcgctctc      420
atttagctct gatgagtact acacccctga tattcttctg atactaaaat aattttccta     480
gtgtagtcta aactttttta aaaagacatg taatccgcgg agtttgtaac tcaaaacgag     540
tgcatctagg aggtatcgca agccgtttct ggattaaatt cccagctagc ttgcttgctt     600
agcaggggcg ggnaaanaag acatctgcag cctaggaag aaaaccttc gcattgttct       660
tacgtgttta cgttatttta tttcctanaa caaggcngaa ttgggactcg aatggttcag     720
ttggggtggg ggatcccctg gtncataaaa ngtcanaaag anggtacagg cggaacncca     780
agggtcgtcc tgcatttana ctcggaattt tggtgcc                             817
```

<210> 668
<211> 826
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(826)
<223> n = A,T,C or G

<400> 668
```
cgggggnnt tacgtctctc tggacgcttt tattgtacca gggcgatccc agcccaactg      60
taccattcga gtccctactc ctgccttgct ctagggaaat aaaataacgt aaacacgtaa     120
gaacaatgcg aaagcgtttt cttccctagg ctgcagattg tcttcttcac cgcccctgct     180
tagctagcta gctagctggg aatttaatcc agaaacggct tgcgatacct cctagatgca     240
ctcgtttga gttacaaact ccgcggatta catgtctttt taaaaaagtt tagactacac     300
tagggaaaat tatttagta tcagaagaat atcagggggt gtagtactca tcagagctna     360
atgagagcgc tttaaaaatg ttagtttgtc ttccgccatt tctacagaaa gctgcaattt     420-
caggttttca ncctaatagg tgatatntaa gaaaaaaaaa acaatcgcan atagcccact     480
gcttttacaa atcattttc tcttctaggt atagcctgtc aggtggccta atgtatttt      540
gacatctcta ggaattttaa tagaccagaa atgggtgcca gagatatgcc tgcactaatc     600
ttaagtgggg atttatgtat ttctcaanca agtgattaaa gcaaaactag gcacgaatga     660
aatcaagatc tttaggccag aaatcatgaa nanttttana attatttan gaatctgtgg      720
cttctcttct taaaatngaa aaaaaaattg tttaaaccca naaggtctga atacccaagc     780
nccctgaacn anagaacaan gccggagcac ccctcccaa atcccc                     826
```

<210> 669
<211> 547
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(547)
<223> n = A,T,C or G

<400> 669
```
cattgtgttg gggaaaaaat gatttgtata agcagtgggg ctatttgcga ttgctttttt     60
ttttcttaa atatcaccta ttaggttgaa aacctgaaat tgcagctttc tgtagaaatg     120
gcggaagaca aactaacatt tttaaagcgc tctcatttag ctctgatgag tactacaccc     180
ctnatattct tctgatacta aataatttt cctagtgtag tctaaacttt tttaaaaaga     240
catgtaatcc gcggagttag taactcaaaa cgagtgcatc tnggaagtat cgcagccgtt     300
nctggatnaa attcccagct tgctngcttg ctnagccggg gggcggtnaa aaaacatct      360
gcagcccngg ggnaaaaacc ttcgcattgt tcttacgtgt ttacgttatt ttatttccct     420
nnagcaaggc ngggganttgg ggactcgaaa tggtacagtt gggctgggga tcgcccttgt     480
tacataaaag ncgtccagaa gagggacggt tacaggcngg ganctccaaa ggtcagtccc     540
```

239

```
tgccatt                                                           547

<210> 670
<211> 232
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(232)
<223> n = A,T,C or G

<400> 670
cgaactattt agactaccta ggaaaattat tttagtatca gaagaatatc agggtgtag       60
tactcatcag agctaaatga gagcgcttta aaaatgttag tttgtcttcc gccatttcta      120
cagaaagctg caatttcagg ttttcaacct aataggtgat atttaanaaa aaaaaaaagc      180
aatcgcaaat agccccactg cttttacaaa tcattttttc cccaacacaa tg              232

<210> 671
<211> 214
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(214)
<223> n = A,T,C or G

<400> 671
ctcccctccc ntccttcgct actncncatt ttcnnaaatt tntttcgcnt atgnggaaaa      60
acacccacat tnttcanctc gcacagaaca ngnnggggtg tgtaaaatga agggcttccn      120
cnctttctct tattnaanaa cactnaaana gggangggct aaaacccgcg ngatntctac      180
nctatcgcgg gcgcttttgg ngttggctag aaga                                 214

<210> 672
<211> 328
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(328)
<223> n = A,T,C or G

<400> 672
ngancagcgg ngtttaaacg ggcctctaga ctcgaggaga cncctgttgg atggtggatc      60
acanntcgnt actactatac aggacagagt atcgggganct cttggntgtt ggngcctgcc     120
aaccactgct nctgttaact gcgtatctga agggactcgg actggcttca gaagaactac      180
cggctcgaat gnaccatgga tgattcncnc tagttgaaaa aaaactcagg cacatgtatt      240
gccactgatg actagcgcca gactnctctc ggctctntaa cgagcccaca tgncngtgtg      300
ncnccgtgc tgnctccaga agaggttc                                         ·328

<210> 673
<211> 223
<212> DNA
<213> Homo sapien

<220>
```

240

```
<221> misc_feature
<222> (1)...(223)
<223> n = A,T,C or G

<400> 673
gggggcaaag ctggctagcg tttaaactta agcttggtac cgagctcgga tcccnnagac          60
attgtgcatg aaaatgcaaa ttgagtgtgg tctatantgc catcntcacc tnctgncngc         120
tcaaaacaac ngctttctgc tgcaatgggt agggctcctn acncacggtc gcnnacggag         180
gccnncttat cctcntcggt nnggatccct ngaagcatnt tct                          223

<210> 674
<211> 256
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(256)
<223> n = A,T,C or G

<400> 674
gngggggtcnt ngatgagcgc gcgtaatacn atcactntcn ggcgngntgg gtaccgggcc         60
cccctcaa gcggccgccc tttttttntt tttttcatn acatgataan ntctttnttc           120
taaacagacc acaccactan agttcctttn ctttngtacg gaattgagtt aaagtagagn         180
atacaatgca gggcttcnnc tctatttcac attccaggnt ggttcngnat ggatcggccc         240
tgcctctccg atgggt                                                        256

<210> 675
<211> 439
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(439)
<223> n = A,T,C or G

<400> 675
nnactagtcc agtgtggtgg aattccattg tgttgggctt gtatgggttt ttttgtctag          60
ttntttggga aatgttngtg ttactatntt ttggatatna tatatgatat gtatggccct        120
tctatgggct cctcanacng aactcaacca ttttccacaa aaccnattcc tcctttccct        180
tcatgactga gtggtgttgg tactatccng gaaactggga cattgtcctt cacatctntc        240
ccttanctgc ctngtccnat tgatgtcttt gagctntgan atgtctttgt taactntctc        300
ctncntctgt actgccggca naattaagca ccatntgtca caaaaagtat tgcgttacct        360
tcacgnatct gttngttncc atncttgctg cttctccngn ggaaaatagg ctnttctggc        420
aaccgaacng aanaaatac                                                     439

<210> 676
<211> 587
<212> DNA
<213> Homo sapien .

<220>
<221> misc_feature
<222> (1)...(587)
<223> n = A,T,C or G

<400> 676
```

241

```
nggnggcctn attaagcgcg cgtaatacna ctcactntgg ggcgaattgg gtaccgggnc        60
cccctcaagt tnatntgccn aacctctctt ttggaataac aaaaggttta acacatatgt       120
cctcataggg acgcgctttc acacnttcct gacngcttca tanacntcat tnctatttct       180
cctcagnaca agttnaggcn gaaggtgagg canacnttat aatttccatt tcacaaatnc       240
ggaaagtgag gctcaaaggg nttaaaaaat aacctgatac aantcataga gccggtntct       300
ggaanaagca ggagcaaagt ccaggcatcc tgatccaagc tnggtccact gccttccact       360
ctggagaggc ttcatctccg acaaaggaag ggacntgagt ggctgganaa tctcatggga       420
taaagacctc agnatttcat gctcctggaa atcccatggg ttgaacaaca ggtntttggc       480
ccgtggttct ntccctttgn ccatctttta accttgggvt aaatgatggc ntctntnagc       540
ntttttttttn aaagagatng aaattgaatg attattngct cattggg                    587
```

`<210> 677`
`<211> 444`
`<212> DNA`
`<213> Homo sapien`

`<220>`
`<221> misc_feature`
`<222> (1)...(444)`
`<223> n = A,T,C or G`

`<400> 677`
```
gtggggcatn attaagcgcg cgtaatacga ctcactatag gggcgaantg ggtaccgggc        60
cccctcgaa gcggccgccc ttttttttt ttttactgt ccaaactntc tatngatnta         120
gttgaactgt ncaacgattt catgaaattc tatacacana gccttcaggt ccagagagta       180
aaacaaattt aaatttnttc accanattgn agcagncana agcatccnat natatccgac       240
tacaatgaat natatgctna nggtanctna tttacccact ntggggtctt tanggtctgt       300
cacaaactat tttcgtaaac atcnntttaa anttnggtga atggacctaa tnccagataa       360
ntctatttna tntadcctag catncctgtg gctnacttn cgggctgtgt tggcntactt        420
ttaggagaaa attggtataa atnn                                              444
```

`<210> 678`
`<211> 670`
`<212> DNA`
`<213> Homo sapien`

`<220>`
`<221> misc_feature`
`<222> (1)...(670)`
`<223> n = A,T,C or G`

`<400> 678`
```
actagtccag tgtggtggaa ttccattgtg ttgggagcag tttaaaaaaa aaaaagacna        60
aatatacnac tcttgatnaa acataaaggt acagtggtct atgaggaana gaaaaggtac       120
ctnaggatgc aaaantacct accacatggg aaccgttngt ccacactcat tccnnanaaa       180
accgagtcct ctcanttnca cacgtgtacg tttcagttgg gaagtgcttg ccattactcc       240
naagcctaga accttcacgt cctgaaggtt ctggaaggtt tttcagattg cttaaganac       300
gcngcccttc catattcntc tccactaccc ngggaacgg aacaaatgga gctgcgacng        360
ggaagcgtcc cttcccntcc gaacgctttc tttcaaacct gcctgccttc cnggcgaatg       420
gaccggaagg tttnctgct tcctttcanc ccnaattact tcctgngttg aaaattggcc        480
tgttggtttg caaatgcngg aatttgttta ctttcntcat gtcctgtgtt gnncnaaccg       540
gctcncttgt tgcctccctt tngaaaggtt ttcatcaggc cccgcccttt ctcttntaan       600
ngtcctaatc cggncnggac cactcgggga aaatttttc ttttcgaaaa gccgccccnt       660
ccgtccggct                                                              670
```

`<210> 679`
`<211> 449`
`<212> DNA`

242

<220>
<221> misc_feature
<222> (1)...(449)
<223> n = A,T,C or G

<400> 679
actagtccag tgtggtggaa ttccattgtg ttgggagtag gtctactaca ncctacttcc   60
cctatcatan aagancttan caacnttcat gatcccccc tcntanncct tttcctcanc   120
tgcntcctag tcctgtttgt cctnttccta acantcntaa ganagatnac taatnctact   180
atctctnacc tccggaanct acaaanacgtc tggaactatt cngaccccat gcanccncat   240
nctccatcgt cctcccagcc cctnccnttc ctttacntta ctnaacgaag gtcgacgatc   300
cctcccntac ctcccnnncc attgggnccc aangganctg gacctcacga ntacaccnac   360
tacggggnga ctaagnctgn aactccttac atatntcccc gttaccccn gaacncagcg   420
aacngcnaca ccttggacnt caagaanta   449

<210> 680
<211> 670
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(670)
<223> n = A,T,C or G

<400> 680
tttcngtgtg gtggaattcg cggccgcgtc gacgagaaga ngǵaggagga naaggagaag   60
gagaagaagg agaanaagga ggagaaggag aagaaggaga agaaatcatc atcatcatca   120
tccactgtct ngcaactatt taagtttgcn antcccttga aaacaggtac ttttgtttca   180
atgtttggga ccactnctga cnatgannag aanaccaata aatgcttgat naatgaaaaa   240
nccacttttt acctgttaga accctgaggc taagagaant gatgtgactc gacttagtta   300
ccacaaacta tgatcctagc atnaattggg gcatctcaac acctcaactc cctgtgcaag   360
aacagatttt caatgtctac tgatgatttt aaatggatta nttcctctct ttacttctta   420
agggcatgaa gntttatgaa acaaaactat ncagttccag acgcttaacc cacatagtgt   480
taatagtcac cttcaacaca cnactaaacc cccaaaaan gnttttttacg gngtttcgac   540
agttttcttt tcttttttgac ttgnttaaca cccnngacaa ctttgtnctn tttccntgaa   600
tcacanctttt cnaanancca atggtncggt tttttctcnt tcngggccct tccttnttn   660
aaaaccanat   670

<210> 681
<211> 494
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(494)
<223> n = A,T,C or G

<400> 681
tcatggtgtc cacagtctga tgtgagcgca ttaaatttaa ggatctccgc ccttctcctt   60
aaaactcagg acttggcaat gancctagga agcgcccctc ccctccccan ccanatccaa   120
gccccggacc gctgcgnctc cagctgcgcc tagtgaaacc gccgaattcg aattcacact   180
cggngggccg gcgaaggtgt gcgcgcccgc gggagcgccg gggcnagccc gagggactgc   240
aagccaanaa nggaggcatg ggtggcgggg ggcgccgtct gatccaggaa ggagcggagg   300
cgccgatcac acactcttna gacgccctgc ccgcgcctgg ccagcgcgca gnctgcagga   360

243

```
cgcgcggagc aggaactcgc tggagtttgc caagccccan gnctctggaa agtntgtagc      420
tccctttcgg ancgnctctt ctggcccttt gggacgggtg tgtcattggg cgggggtctg      480
tataaggggg ggac                                                        494
```

```
<210> 682
<211> 263
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(263)
<223> n = A,T,C or G

<400> 682
tgatcattca agcgntgngc gnataacgat tgctnagccc aacctttcat agggtcgttc       60
ctttgggaat nggatgtcta ttgaatggca gggatagggg cactcggcat tcgcctctgg      120
tacagttttg catatatatc ctcatcgcga gcgagcgtag gggancgtta agtttgggga      180
aatgccnccg catgnccctn ccggagctta aaccccccaac aatncccatt ttnaaaaaag      240
ntttnttant taaaaaaaaa aac                                              263
```

```
<210> 683
<211> 255
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(255)
<223> n = A,T,C or G

<400> 683
cttgcccggc atgcacagac ntntttacgg acacnctact ccaagngagc ctgnanctgt       60
ctacggtcaa nctctaaggt tngncantgc cacanatggc atagtcccga gggcggtnan      120
tctggantgc tctctgcact tgaacntaaa gcgcntttca aganaggnct aatngcctgc      180
ctcttgacaa cnaacaancc cacaccnacc tangaccctn tangcaagga ctggattctg      240
naaatgcaat acaca                                                      255
```

```
<210> 684
<211> 922
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(922)
<223> n = A,T,C or G

<400> 684
accccttcatt tcatgtgctt ctattttcct acatctttta catgactaag ggattaatga      60
aatcacctct tcataatcat gaccataatt tcatccaaca agtactcaag tttggtgtta      120
gcactttatt aatgcttacg aattctctct ctctccctct ttctcttttc cttagtcctt      180
gcacaataag gatttttgaa tgtataatat catcttaggt aagctttcat atggtttttgg      240
catatgaagc ttatgactgt cataagccat accaagcctg tggagtatgg catgattttc      300
attacataat ccaatgaaaa tagacttatt ttaaatccct aactttgtag ttttaatttg      360
tatttcacta tcttgaaatt aacagctagt acttatccat cacagcagtc tcctactgac      420
atgaagcaag ttgttgaatg cagtaganca tgaatgaaag catttaatgt tanacaaaaa      480
tgggtgatac ccaagcattc tgaattattt gcatcaagga atgggacatg tacattagtg      540
```

244

```
gcatcatttc taccaatatg tgacttgaat tgttttttta aaaaaaggan aatganttttc    600
tcaatttgct ttaaaaaatt ttnaaaaagt tcaatggcat gctgctttgt ctggacttaa    660
tttattaaca attnttaanc cttccttaag gacanaattt tggtgttcag gatcnccctg    720
aagggtctta tttttnatan nattccaaac ccaaaaggtg gtttaaaatg ggngggttcc    780
ccccncnaaa atttggaccg gctttttat atttaaaaaa nttnccnttt gngtttgaaa    840
nctnaatacc aattaagggg gaattttacc tnccagtggg aaaaaaaaac nctngccntt    900
naaaaaattc ccnggagnca at                                              922
```

```
<210> 685
<211> 531
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(531)
<223> n = A,T,C or G
```

```
<400> 685
tgaggctctg taaaactgtt cctctgctag gcatacttca tattctctat attaaactca     60
tctttaattg gcatggaaga ttcattgttc caaatctcag atgaagatcc tatattggat    120
gcaattaagc ctggcagcgc cctcaaaaga cagtcttgtc actgctagcc acagccagga    180
cacagtaaca gttccttcta gtgacccnag accataanaa atananatct aaagaattct    240
gactccaaag gcattagccc attcctggta ttgccaatta tgatagaaaa aattgccaag    300
ctcctgggac atggaaatac actcagtaca tttgagaact ggagaactan tttccaaaat    360
agtatgaaga catganggtg attgtagata tntgagtttg gagaanttga gggaaatcng    420
attacacatg tttactacaa gagatgttna taagtaaaga aggcctgata tacaatctaa    480
cagacnantg agatanatct taantcacaa ctgacntccc ttttggggcg g             531
```

```
<210> 686
<211> 336
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(336)
<223> n = A,T,C or G
```

```
<400> 686
ggngncctna tgagcgcgcg taatacgatc atatagggcg aattgggtac cgggcccccc     60
tcaagaacac tacaagctat gtcctcttct canagagccc tgaanttttta acatattgaa    120
agctctnatc ttgccaaana actccactta acttcaaaac acaccctcca cacacatcat    180
gatcaactna gatcttactg aaccagaatc ctnaatggca tacttcagga acaggggtcc    240
anagaagcag ttctcaaant gcagctnaaa aagaaactga aaacccaatt catgcaanac    300
ctagggctta tttgagagca ttttccagtg cagatt                              336
```

```
<210> 687
<211> 271
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(271)
<223> n = A,T,C or G
```

```
<400> 687
```

245

```
aatctgcact ggaaaatgct ctaaaataag ccctaggtct tgcatgaatt gggttttcag          60
tttctttta agctgcactt tgagaactgc ttctctggac ccctgttcct gaagtatgcc          120
atttaggatt ctggttcagt aagatctcag ttaatcatga tgtgtgtgga gggtgtgttt          180
tgaagttnag tggagttctt tggcaagatc agagctttca atatgttnaa acttcagggc          240
tctctgagaa gaggacatag cttgtagtgt t                                          271
```

<210> 688
<211> 740
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(740)
<223> n = A,T,C or G

<400> 688
```
tgatgaagcg cgcgtnntac nactcactat ngggcgaan tatgggtacc gggnccccct          60
cgaagcggcc gccctttttt tnttttttg tgagagttta aataaaatat ttgagtttaa          120
tttaaagttt gagtttaatt aaaatatatg gcatatccca agttgggctt tgcanaaaga          180
acacttctca ggaactgtta gttggtgtac caggaactca gaagggtcct gttattaaat          240
atatttggaa aatgcatgga ttctctgaan atcnctctgc atgtgagcaa cacttacatc          300
ncaaaccaaa attggcattg catacatnaa ccaatatttc ccaaacattt ctggttatgg          360
cccacccct ttgtgtanta cttattgctg ttttttggaa ccctggggaa attacttaaa          420
atattcagct ggaaattaca ggcgttactt ttaagggganc aagaattaca gtgactccca          480
aaattgcaag tgttgattac tatttaagaa cccaagaatt tgaaagaaat tttgaaaagt          540
gaaaacngga aatnttaaat gacttctcaa atttttgaaaa ctcnggnaaa catctccact          600
ttggtncct tcctttaaaa attggctaaa aattnttnt tatnccccacc ccattggaan          660
tncccccccc ctggaacaat tggattcccc tatttcctaa aaaacggccn cccccccgg          720
ggngaacncc nacnttttgn                                                      740
```

<210> 689
<211> 635
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(635)
<223> n = A,T,C or G

<400> 689
```
actagtccag tgtggtggaa ttccattgtg ttgggattac atatactttt agcaattttt          60
aaagaagtgt acaaagttga gatgtttcct gagctctcat atatctgana atgtcatttt          120
acatctccgt cttcacctct caaaacttct ttcaattctt tggctcttaa tagtaatcaa          180
cacttgcact ctggagtcac tgtaattctt gctcctttac agctacncct gttatttcca          240
gctgaatatt tttagttatt tcccagggtt ccaaaaaaca gcaataagta ctacacaaag          300
ggggtgggcc ataaccagaa atgtttggga aatactggct catgtatgca atgccaaatc          360
tggtttgcna ttgtantgtt gctcacatgc agagtgaatc ttcaaanaat ccatgcattt          420
tccaaatata tttaataaca gggaaccttc tganttcctg gntacaccaa ctaacagttc          480
ctgaaaaatg ttctttctgc aaaacccaac ttggggatat gccatatatt ttaattaaac          540
tcaaacttta aattaaactn caattatttt attttaaact cctcaaaaaa aaaaaaaaaa          600
agggggggcc cttccaangg ggggnccggt tcccc                                     635
```

<210> 690
<211> 3923
<212> DNA
<213> Homo sapien

246

<400> 690
```
acagaagaaa tagcaagtgc cgagaagctg gcatcagaaa aacagagggg agatttgtgt    60
ggctgcagcc gagggagacc aggaagatct gcatggtggg aaggacctga tgatacagag   120
gaattacaac acatatactt agtgtttcaa tgaacaccaa gataaataag tgaagagcta   180
gtccgctgtg agtctcctca gtgacacagg gctggatcac catcgacggc actttctgag   240
tactcagtgc agcaaagaaa gactacagac atctcaatgg caggggtgag aaataagaaa   300
ggctgctgac tttaccatct gaggccacac atctgctgaa atggagataa ttaacatcac   360
tagaaacagc aagatgacaa tataatgtct aagtagtgac atgttttgc acatttccag   420
ccccttaaa tatccacaca cacaggaagc acaaaaggaa gcacagagat ccctgggaga   480
aatgcccggc cgccatcttg ggtcatcgat gagcctcgcc ctgtgcctgg tcccgcttgt   540
gagggaagga cattagaaaa tgaattgatg tgttccttaa aggatgggca ggaaaacaga   600
tcctgttgtg gatatttatt tgaacgggat tacagatttg aaatgaagtc acaaagtgag   660
cattaccaat gagaggaaaa cagacgagaa aatcttgatg gcttcacaag acatgcaaca   720
aacaaaatgg aatactgtga tgacatgagg cagccaagct ggggaggaga taaccacggg   780
gcagagggtc aggattctgg ccctgctgcc taaactgtgc gttcataacc aaatcatttc   840
atatttctaa ccctcaaaac aaagctgttg taatatctga tctctacggt tccttctggg   900
cccaacattc tccatatatc cagccacact cattttaat atttagttcc cagatctgta   960
ctgtgacctt tctacactgt agaataacat tactcatttt gttcaaagac ccttcgtgtt  1020
gctgcctaat atgtagctga ctgttttcc taaggagtgt tctggcccag gggatctgtg  1080
aacaggctgg gaagcatctc aagatctttc cagggttata cttactagca cacagcatga  1140
tcattacgga gtgaattatc taatcaacat catcctcagt gtctttgccc atactgaaat  1200
tcatttccca cttttgtgcc cattctcaag acctcaaaat gtcattccat taatatcaca  1260
ggattaactt ttttttttaa cctggaagaa ttcaatgtta catgcagcta tgggaattta  1320
attacatatt ttgtttttcca gtgcaaagat gactaagtcc tttatccctc ccctttgttt  1380
gatttttttt ccagtataaa gttaaaatgc ttagccttgt actgaggctg tatacagcac  1440
agcctctccc catccctcca gccttatctg tcatcaccat caacccctcc cataccacct  1500
aaacaaaatc taacttgtaa ttccttgaac atgtcaggac atacattatt ccttctgcct  1560
gagaagctct tccttgtctc ttaaatctag aatgatgtaa agttttgaat aagttgacta  1620
tcttacttca tgcaaagaag ggacacatat gagattcatc atcacatgag acagcaaata  1680
ctaaaagtgt aatttgatta taagagttta gataaatata tgaaatgcaa gagccacaga  1740
gggaatgttt atgggcacg tttgtaagcc tgggatgtga agcaaaggca gggaacctca  1800
tagtatctta tataatatac ttcatttctc tatctctatc acaatatcca acaagctttt  1860
cacagaattc atgcagtgca aatccccaaa ggtaaccttt atccatttca tggtgagtgc  1920
gctttagaat tttggcaaat catactggtc acttatctca actttgagat gtgtttgtcc  1980
ttgtagttaa ttgaaagaaa tagggcactc ttgtgagcca ctttagggtt cactcctggc  2040
aataaagaat ttacaaagag ctactcagga ccagttgtta agagctctgt gtgtgtgtgt  2100
gtgtgtgtgt gagtgtacat gccaaagtgt gcctctctct cttgacccat tatttcagac  2160
ttaaaacaag catgttttca aatggcacta tgagctgcca atgatgtatc accaccatat  2220
ctcattattc tccagtaaat gtgataataa tgtcatctgt taacataaaa aaagtttgac  2280
ttcacaaaag cagctggaaa tggacaacca caatatgcat aaatctaact cctaccatca  2340
gctacacact gcttgacata tattgttaga agcacctcgc atttgtgggt tctcttaagc  2400
aaaatacttg cattaggtct cagctggggc tgtgcatcag gcggtttgag aaatattcaa  2460
ttctcagcag aagccagaat ttgaattccc tcatctttta ggaatcattt accaggtttg  2520
gagaggattc agacagctca ggtgctttca ctaatgtctc tgaacttctg tccctctttg  2580
tgttcatgga tagtccaata aataatgtta tctttgaact gatgctcata ggagagaata  2640
taagaactct gagtgatatc aacattaggg attcaaagaa atattagatt taagctcaca  2700
ctggtcaaaa ggaaccaaga tacaaagaac tctgagctgt catcgtcccc atctctgtga  2760
gccacaacca acagcaggac ccaacgcatg tctgagatcc ttaaatcaag gaaaccagtg  2820
tcatgagttg aattctccta ttatggatgc tagcttctgg ccatctctgg ctctcctctt  2880
gacacatatt agcttctagc ctttgcttcc acgactttta tcttttctcc aacacatcgc  2940
ttaccaatcc tctctctgct ctgttgcttt ggacttcccc acaagaattt caacgactct  3000
caagtctttt cttccatccc caccactaac ctgaatgcct agacccttat ttttattaat  3060
ttccaataga tgctgcctat gggctatatt gctttagatg aacattagat atttaaagct  3120
caagaggttc aaaatccaac tcattatctt ctctttcttt cacctcctg ctcctctccc  3180
tatattactg attgcactga acagcatggt ccccaatgta gccatgcaaa tgagaaaccc  3240
agtggctcct tgtggtacat gcatgcaaga ctgctgaagc cagaaggatg actgattacg  3300
cctcatgggt ggaggggacc actcctgggc cttcgtgatt gtcaggagca agacctgaga  3360
```

247

```
tgctccctgc cttcagtgtc ctctgcatct cccctttcta atgaagatcc atagaatttg      3420
ctacatttga gaattccaat taggaactca catgttttat ctgccctatc aattttttaa      3480
acttgctgaa aattaagttt tttcaaaatc tgtccttgta aattactttt tcttacagtg      3540
tcttggcata ctatatcaac tttgattctt tgttacaact tttcttactc ttttatcacc      3600
aaagtggctt ttattctctt tattattatt attttctttt actactatat tacgttgtta      3660
ttattttgtt ctctatagta tcaatttatt tgatttagtt tcaatttatt tttattgctg      3720
acttttaaaa taagtgattc ggggggtggg agaacagggg agggagagca ttaggacaaa      3780
tacctaatgc atgtgggact taaaacctag atgatgggtt gataggtgca gcaaaccact      3840
atggcacacg tatacctgtg taacaaacct acacattctg cacatgtatc ccagaacgta      3900
aagtaaaatt taaaaaaaag tga                                              3923
```

```
<210> 691
<211> 882
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(882)
<223> n = A,T,C or G

<400> 691
ttactcacta tagggctcga gcggccgctg aattctgctg cagtgagctg tgattatgtc      60
cctgcactcc agcctggatg acagaacacg atcatttctc taaagacaaa caaaaaacat      120
aaaataaaac tagtataagg atagaagccc agggttgatt taagtctgcg gaaatcataa      180
accataggtc agacttctca ttgatgaggt acttgtgggt tagaatacaa ttaggtatat      240
ttggtctaga aaccaggatg gaattagaga ataaaagact gagcaatagc atgttatagt      300
attagaaata ctatagaaat aggaaaagcc ctgattatga ctttggagtt ctgatccaac      360
atctgggatt attttgatat tttaaaggaa aacgatgact tttagctctc aggatgttag      420
tttcctcaac cataaaatga agagcctcga aaagatttcg tttaccagat tatttctgaa      480
gtcaattcca gttctaaaat tccatcactg ngcactaagg caaattgaat tgaataaagt      540
attgggnatg cataaaatac tctattttta aaaangaata gtaattatcc attggnaaca      600
gacgcantca tccagncatc tcctaccctg ncccatgncn tatgtagana tgtanctcta      660
atcccttaac aaaccgattt tgcaaaggag cttanccttg gggtacttgg tcanggcaac      720
tggtctactt tnaagactca tcttcactta ctgggcacca aatncctacc attgcatcaa      780
actggggttc ccatncaagg caaaccctgn gaaatcttta atcccgaaat tggcgcccaa      840
ttttgngggg tttccnaaaa gaatcntccc ccccgagggg cc                        882
```

```
<210> 692
<211> 235
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(235)
<223> n = A,T,C or G

<400> 692
ccgcactngt aangnccgcc agngngctgn aantccgctn agcncggatc cactagtcca      60
ttgatggtaa aagggtagct tactggnatg tccgnctgct ccanganata atacncagga      120
cttctcanag cacttaatat gttaatataa aactncgnga aaaaagatnt tcnatgaanc      180
nttcctctta ggaggtcagg ngagaatagt gttaatgnca ttaagganag aacga          235
```

```
<210> 693
<211> 383
<212> DNA
<213> Homo sapien
```

248

```
<220>
<221> misc_feature
<222> (1)...(383)
<223> n = A,T,C or G

<400> 693
nttatgtaag aaatgtcata tatcttttat tttctttaaa tcaaaataaa tatgactttg          60
agcatcccat cccatgcccc atcctatcag aatggtagga acatcaacac aaataattag         120
taatgcaccg catctacatt cccatgctct ctttacttct tcagcattgc ctaaaggcat         180
aatacacctt taattaatta attcagcctc ctaatgcaca ttaacaaagc ccctgctaga         240
ctctgtccat aatggnaaac ctgnatgatc cttgatatta acantttaag gaatgctcat         300
ggattggttn cagacttaaa aaattgaggg ggctgaanaa aatctaangg anaaatcatg         360
gaagcatttg cacatattac ata                                                 383

<210> 694
<211> 204
<212> DNA
<213> Homo sapien

<400> 694
tctcttggct ggtcagcctg aagggtggta atgactcacc aacgctacta atccttcttc          60
actgtccctt attttttttcc ctcccaggct cataactcga ggttaaactc tcttttatac        120
aagaaccctg tctgatgaag catcatttca gaattttaag tcaacttaca aatgtggtat         180
tattcacatc tgagtacaaa ttta                                                204

<210> 695
<211> 670
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(670)
<223> n = A,T,C or G

<400> 695
gcaccagccc aggtgctgtt tcttcacttg agctccatga ccctccctgt gtggtgggtt          60
gaacggtgac ctccaaaaga tatgtccacc tggaacctca gaataagatc ttatttggaa         120
tagtctttgt agatgtcagt aaggtaaaga tttgagatg agacctcct ggattagggt           180
aggccctagg tccactggca ggtgtgcttc tcagggtctg aaaggggaag acagggccac         240
ccagaggagg agacggaggc agagacaggg ccacccagag gaggagacgg aggcagagac         300
agggccaccc agaggaggag acggaggcag agacaggggc cacccanagg aggagacgga         360
ggcagagaca gggccacccca gaggaggaga cggaggcaga gacagggcca cccaaaggag        420
gagacggagg cagaanacag gccccccccaa agaaganacc ggaggcanaa aacagggcca        480
cccanaggag gagacggagg canaaacagg gccacccaa aggaggagac ggaggcaaaa         540
cagggccacc caaaggagg aagccggaag gaaaaaacag ggccccccca aaggaggaag         600
ncggagggcn aaaaanaggg ccccccccaa agngagaaaa ccnggnaggc nanaaaaccn        660
ggggcccnnc                                                                670

<210> 696
<211> 317
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(317)
```

249

```
<223> n = A,T,C or G

<400> 696
tgacccgttn tttctgcaaa ggagagtggg gaaggagggn tgggaagaca aaagttacat          60
gttagcaggg aagagaacag aattttatcc acccttatct ctttagtgag tgaacaaaca         120
gcccactgtc atcgtggata catttcactt ttttcacatg actaaggagc tctccggagt         180
gaagagtgag taaatatgtt tattacgcat tcatttgcta agaatcatca agaacccaaa         240
gttagagacg tttcgtggtt gaactttctc cctactgtct agtagaatta tatggggatt         300
ctggatctgc tggtgcc                                                        317


<210> 697
<211> 246
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(246)
<223> n = A,T,C or G

<400> 697
ctncagctct aatcgactnc tatnaggnat gatggcncgt gcngcgcgta cgtantgctt          60
ggatcctcnn anagcggacg cctactacta ctaaattcgc ggncgcgttg actttttttg         120
ttttttttcct tnacagagnt nttttgtgc ccttggttct tatgctcana ctcngcaaaa         180
aanatcaaaa gntacnnatg aaaaacntat nccatctnca naaggaggt gnagntatta          240
ctttct                                                                    246


<210> 698
<211> 3674
<212> DNA
<213> Homo sapien

<400> 698
agaaagtttc cttttttttt tttaatggtg aaaagatata cacatattta gaattagcca          60
gctgggctca gtttagatta ttccaatttt gttggcaaca tccagagcat cgtaatcagg         120
agccagtgaa acatattcct tcttctctcc atcaggccaa atcacggtgt tgaccttggc         180
cacatcaatg tcttagaact tcttcacagc ctgtttgatc tggtgcttgt tggctttaac         240
atccacaatg aacacaagtg tgttgttgtc ttctatcttc ttcgtggtga ctcagtggtc         300
agcggaaact tgatgatagc gtagtggtca agcttgtatc tcctgggagc gctcttccaa         360
agatatttgg gctgcctcgg gagttgcagc gtcttgggcc gccggaaggt gggtgacgta         420
cggatcttct ttttttgtgt ggctgtggac acctttcaac actgtcttct tggcctttaa         480
atccttcgct ttggtttcgg ctataggagg ggcaggagct tccttcttca ctttcggcgc         540
catcttgtga aaaggggaaag tttcctttct aataccattt tcacttctcc cgaattttgt         600
ggatcgtttc ttggtatcta ccccagattt caggagtgtt ggctggatct tagggattgt         660
gaagtcttca tttccctgtg gtgagatctg aggcatgatt ttaaacagtg tgagggaagg         720
agatctccag gcactttaat agaatggaga agcaggatgg gatttgagag gaaatctgat         780
tttgaaaaaa ggagaactag agttgagttc gtaattaact agcaccttaa aggtcattca         840
gcatgcccat ctgcacagtg ggtgtaatca ccctacagaa caaaaacaaa aaggcaatgg         900
agaggaagct gtaaagcact gtacatgttt aactcattgt tatgtaagct agccgaaggc         960
ttcacagact tgaattcatc tcccaagttc tcttcctgta ctggaaactc tgccttaggt        1020
tgcttaaaac ttgagaaaca gaatattgct tcccctgcct gccttcttga gtacacttgc        1080
ctacacaaag atgcacatcc ttgtttgtgt gtgtgtgtcc atttgctgtg acattcttgt        1140
gaaagtcaaa gtttcccagc tgttgacata cacaagtttg tttggtgcaa cctgtcagat        1200
gcatcccttta gacaggcccct ttgatactct gggaaagaca ttggacttac agtcggaacg        1260
aaaagaaaga aatgtgatat gtatagcgtg cagtgagttg gagttttacc tgtattgttt        1320
taatttcaac aagcctgagg actagccaca aatgtacccca gtttacaaat gaggaaacag        1380
gtgcaaaaag gttgttacct gtcaaaggtc gtatgtggca gagccaagat ttgagcccag        1440
ttatgtctga tgaacttagc ctatgctctt taaacttctg aatgctgacc attgaggata        1500
```

250

```
tctaaactta gatcaattgc attttccctc caagactatt tacttatcaa tacaataata    1560
ccacctttac caatctattg ttttgatacg agactcaaat atgccagata tatgtaaaag    1620
caacctacaa gctctctaat catgctcacc taaaagattc ccgggatcta ataggctcaa    1680
agaaacttct tctagaaata taaaagagaa aattggatta tgcaaaaatt cattattaat    1740
tttttcatc catcctttaa ttcagcaaac atttatctgt tgttgacttt atgcagtatg     1800
gcctttaag gattgggggga caggtgaaga acggggtgcc agaatgcatc ctcctactaa    1860
tgaggtcagt acacatttgc attttaaaat gccctgtcca gctgggcatg gtggatcatg    1920
cctgtaatct caacattgga aggccaaggc aggaggattg cttcagccca ggagttcaag    1980
accagcctgg gcaacataga aagaccccat ctctcaatca atcaatcaat gccctgtctt    2040
tgaaaataaa actctttaag aaaggtttaa tgggcagggt gtggtagctc atgcctataa    2100
tacagcactt tgggaggctg aggcaggagg atcactttag cccagaagtt caagaccagc    2160
ctgggcaaca agtgacacct catctcaatt ttttaataaa atgaatacat acataaggaa    2220
agataaaaag aaaagtttaa tgaaagaata cagtataaaa caaatctctt ggacctaaaa    2280
gtatttttgt tcaagccaaa tattgtgaat cacctctctg tgttgaggat acagaatatc    2340
taagcccagg aaactgagca gaaagttcat gtactaacta atcaacccga ggcaaggcaa    2400
aaatgagact aactaatcaa tccgaggcaa ggggcaaatt agacggaacc tgactctggt    2460
ctattaagcg acaactttcc ctctgttgta tttttctttt attcaatgta aaaggataaa    2520
aactctctaa aactaaaaac aatgtttgtc aggagttaca aaccatgacc aactaattat    2580
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aatcacttta aacattaatg aacttaaaaa tgaatttacg gagattggaa tgtttctttc    2700
ctgttgtatt agttggctca ggctgccata acaaaatacc acagactggg aggcttaagt    2760
aacagaaatt catttctcac agttctgggg gctggaagtc cacgatcaag gtgcaggaaa    2820
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gcactgtggg gtgggggtt gtggctgctc tgctctgagt ggccaagata aagcaacaga    3060
aaaatgtcca aagctgtgca gcaaagacaa gccaccgaac agggatctgc tcatcagtgt    3120
ggggacctcc aagtcggcca ccctggaggc aagcccccam agagcccatg caaggtggca    3180
gcagcagaag aagggaattg tccctgtcct tggcacattc ctcaccgacc tggtgatgct    3240
ggacactgcg atgaatggta atgtggatga_gaatatgatg gactcccaga aaaggagacc    3300
cagctgctca ggtggctgca aatcattaca gccttcatcc tggggaggaa ctgggggcct    3360
ggttctgggt cagagagcag cccagtgagg gtgagagcta cagcctgtcc tgccagctgg    3420
atccccagtc ccggtcaacc agtaatcaag ctgagcaga tcaggcttcc cggagctggt     3480
cttgggaagc cagccctggg gtgagttggc tcctgctgtg gtactgagac aatattgtca    3540
taaattcaat gcgcccttgt atccctttt cttttttatc tgtctacatc tataatcact     3600
atgcatacta gtctttgtta gtgtttctat tcmacttaat agagatatgt tatacttaaa    3660
aaaaaaaaa aaaa                                                        3674
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<210> 699
<211> 2051
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(2051)
<223> n = A,T,C or G

<400> 699
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acttttttttt ttgaagcaag tccctgttct tgttcgtcct gactagtccc atcagggccc    120
tggatcccaa gactcagcat ccaaggtccc ctccaggaat cctggcagct cagcatactt     180
tatcctgttt catctgagag caaaaatgta aaattggatg cacagaaaag tgactcaaag     240
tgcttaatga ctagaagaaa tctaggagca gcaagaagag caggacaaac aggccaggcg     300
gtgtcaggag cccaggtctc cagctggang gaacgtcaac cctgcagtgg gagcaggggc     360
cctttgcaca tcctaggcac agatggtaat gtagacacca caggtaagct gggcttggta     420
cctaccccctc cccggattca gaaagaaacc aaacaaggag ctttgtgtgg aatgaaacct     480
cctttcctcc cagaagcact gctgactgtt tggtggttgc catttgtggc agtgagccct     540
```

251

```
tgtttgttct gaggttgggc tggtttctcc tcttggccct gccctacaga tcataaagga      600
gaacagcaag acgtccccag caaacatcca cagatggcct tggaaataag tcaccttcct      660
caccctgcag gaatgccagt gaacatattg ctgacatctt ggagctcagt acctcatagt      720
gtaacggcgt cagtagatct gcctgtgctg ggacttcctg tactacccat tcctgagggg      780
cgatgcttct gcagggcctg tgacttggtg cacaacttca gacaccatca tcttgcagca      840
gcaccgcacc ctcactagcc agggtgttga tgacttcctc aaggccaagg ccacattcaa      900
ggcttcggac ttcattgatg cgcttgtgct gagcaaggtg gcttctccgg gatcttaatt      960
caggaggtag aatggagctt gagatcaagt gtctgatcaa gcctcagtgt atgggcgctg     1020
ttcatcctct ggtgctgaag cagccaagag acccaagtct gcctggctgc ctcttaggat     1080
atgacagcag agccagtggc ctctactaga tcctgtacaa cctcacaaaa cacccagaca     1140
tcgggagtgc tgccagcctg tgatgcaaga gtcctaatcc tgaagacatt gaatgacctg     1200
tcgttgtgct gtttttacca aaaaggatca tgaggatcag agaggaaaag tcacttgccc     1260
aaagtcacac agctgaacag tggtggagtt caactttgac cgtgggctgt ctggcccca      1320
aggtgtatgc ttgcttctct cccaagagac tcctttctta tcaggctcaa atgaatgaaa     1380
ggaggatgtt aaagacaacg ccattattga cgagatcact cccaagcgga ttggagattg     1440
tcccaatatt tagacctata gcaaggcctt gggagaaatg gtggtgcagc aggagagcag     1500
gaacctaacc attgccatcc taaggccctc cattgtgtgg agcaacgtgg caccagcttt     1560
tcctgggttg ggttgataat ctaaatggat gtagccgact cattattgcg gtatgtatag     1620
ggatgaagaa gtaactgtaa tgtagtggag gaatagtaag aaaattctta gtgctggctt     1680
agcttaattg atccaaaaac ataaatgcta ctttactatc aattgaagca tattatttca     1740
attattctgg ttataatatg gaggcaggat gaaattgttt ttattcttttt agaatttttt    1800
tttatcagga aaacagaggt aaagtgctat caattactat ttaagagttc tattttgaaa     1860
agtgagaatt aaggattttt cttttctttt taaaaaaaac tttttttaaa attaaaaata     1920
aaagaagcaa aagtcttagg aaaatgaagc aagtagccct gccactctat gtacagtaat     1980
aacaatatct gtcccagtta ttatgtacaa tattataaaa aatgtcgcag acagtaaaaa     2040
aaaaaaaaaa a                                                          2051
```

<210> 700
<211> 2841
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(2841)
<223> n = A,T,C or G

<400> 700
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gcagagcaca gcatagctgc tttaccaaat catggccaga ctgcttctgt aagcaggccc       60
ctgatcctgt tccacctcac tggacaggac ctcccaactg gggcatccag ctacccccac      120
cagcatccct tggccaatgg aaatttgaaa tgttcctggg acagagctcc tggagagagg      180
ggcaggccac cacctttgct gtttgggtga ctagccgttc tggcctgcag gctttggaga      240
gcccaagctg acaaggggta gaagaggtgc ctcagcacag cacagccacg ctacgaaaac      300
atggccagac tcttgtttaa gtcagtcccc gaacacattt ctagtcagtg ggtgaagtct      360
ttcaaccagg gtctctggct accttgactg ctgttctctg gccgacagag gtctcaggcc      420
tccctgagtc agagctcccg gggggaggac cagattgcta tctttgctgt ttgggtgacc      480
cagccatttc agccttaggg cttcagagtg tctgaggtag ccaggggctg aagtgaaccc      540
ccagcacagc acagctgctg tataaaaacg tggccagact ttttctttaa gcaagtccct      600
gttcttattc ctcctgacta ggtaagactt ctcaacttgc ctccagccac atcttattgg      660
tgtgttcaga ttggcaacag gtttgtacct cagtggtaca gagctcccag aggaaggggt      720
aggctatcat cttccctgga aaatacgagt caattaggga cttgagggga cccccagcat      780
tccacagcag cccttcagaa aagtggccag actctgtact tgatgggcag atcctcctgg      840
cctgtgtctc tagccagccc accactggag ctatcaagcc agtagcaact cagcagttcc      900
ttggacagag cttccaggag caaatgaaat cctttctgcc actgcctttg cagtgaactg      960
cccttgctat cctcagaaga tatatcacgg gagcaaagac cctaagtgcc atatcaacac     1020
ctccaataag ctgcagttga cccaaagaac aagccaatcc atctcccaca ggttccacac     1080
acactccact actcatcacc agacagggaa ccctggcttg ggcccacagc acagaccctc     1140
catcctgggc cgattacact gagtgattgc taactcacat gtctctggga tggagcaccc     1200
```

252

```
aggagacaag caaagtggtg gagcagcaag tcaggtgatg tggagcccag agggcaggga   1260
gagctatctc tctgggctcc acttgccctt gtgagacact ttgtcccagc actccttagt   1320
ctgcttgcct ctcccagggc cccagcctgg ccacacctgc ttacagggca ctctcagatg   1380
cccataccat agtttctgtg ctagtggacc gtaccatatc agtggagagc tgcagcaagg   1440
tggcccntac ggccacgcac cagcctgcac attacctctc catactgcag cccttttatat  1500
ggaaacttcc tacatcactt tgctgtgtgt gtttacacag gtggattttg ctttacttgc   1560
actgacagca cacaggaggg cagcacacac cccaacccac atcaactgcc attaaagaaa   1620
agaaatttca gcccataatt tcatgtccag caaaattagg catcataagt gaaggagaaa   1680
taagatcctt ttcagacaag caaatgctga gggaattcaa tatcaccaga tctaccttac   1740
aagagctcct gaaggaagca ctaaatatgg aaagaaaaaa ccatcaccag ccactacaaa   1800
aatgcagtga agaacgcagt gaattacgca gtccagtgat gctaaaaacc aaccacatac   1860
gttaagtctg caaaataacc agctgacagc atgacgacag gataaatcca cacataccat   1920
tactaacctt aaatgaaaat gggctaaatg ctcccattga aagacatggg gcaagctgga   1980
taaagaacca agacccactg gagtatgctg tcttcaagaa acccatctca catgcggtgg   2040
catacatagg ctcaaaataa aggaatggag aaaaatattt caagcaaatg gaaaacagaa   2100
aaaagcaggt gttgcactcc tactttctga caaaacagac tatgcgaata aagataaaaa   2160
agagaaggac attacaaagg tggtcctgac ctttgatata tctcattgct tgataccaac   2220
ctgggctgtt ttaattgccc aaanccaata ggataatttg ctgaggttgt ggagcttctc   2280
ccctgcagag agtccctgat ctcccaaaat ttggttgaga tgtaaggttg attttgctgt   2340
acaactcctt ttctgaagtt ttactcattt ccaaaaagga aggcaagttt tcctgcttcc   2400
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tgagtgtaag ttttttccag cttctaagat ggcagagaac gatcaccagc ctgagcctta   2520
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gtaagattac ccaccagctg cttttaattt ctcccttagc attagaacac tcagtaatca   2640
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tattgttgtt gtttcacttt tctcccatct cttcctgact tggtcaaatc caaaggaatg   2760
ttcgaaattg tggggagcaa ggcatctgaa atggctaaaa ctcctgtggc tgcaaaaaat   2820
agaaataaaa aaaaaaaaaa a                                             2841
```

```
<210> 701
<211> 3228
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(3228)
<223> n = A,T,C or G

<400> 701
tccgccccat tgacgcaaat ggcggtaggc gtgtacggtg ggaggtctat ataagcagag    60
ctctcnggct aactagagaa cccactgctt actggcttat cgaaattaat acgactcact   120
atagggagac ccaagctggc tagcgtttaa acttaagctt ggtaccgagc tcggatccac   180
tagtccagtg tggtggaatt ccattgtgtt gggcaggaaa caagcaaagt ggtggagcag   240
caagtcaggt gatgtggagc ccagaggtcg gggatggctg tctctctagg gtccacttgc   300
ccttgtgaga cactttatcc cagcacttta ggaatactga ggtcatacca gccacatctt   360
atatgcaaga ttgcccagca gagatcaggt ccgagagttc ccttttttaa aaaaggagac   420
ttgcttaata aaagaagtct agccacgttt gtgtagagcg gctgtgctgt gctgggggtt   480
cactttgag agagttctcc tctgagacct gatctctgga ggctgggcaa tcttgcactt    540
gagatggggc tggtctgatc tcagcactcc ttagtctgct cgcctctccc atggccccag   600
cctggccaca cctgcttacg gggcactctt agatgcccac accataactt ccatgctagt   660
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tgcacattgc ctctccatac ggcagccctt tatttggaaa cttcctaaat cactttgctg   780
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cacaccccaa cccacatcaa ctgccattaa agaaaagaaa tttcagccca gaatttcatg   900
tccagcaaaa ttaagcatca taagtgaagg agaaataaga tccttttcag acaagcaagt   960
gctgagggaa tttggtatca ccagatctac cttacgagag ctcctgaagg aagcactaaa   1020
tatggaaaga aaagatcatc acctgctact acaaaaacac actgaagtac acagtccaat   1080
```

253

```
gatgctaaaa agcaagcaca tatgtaagtc tgcaaaataa ccagctgaca gcatgacgac    1140
aggataaaat ccacacatac cattactaac cttaaatgta aatgggctaa atgctcccat    1200
tgaaagacac ggggcaagct gggtaaagaa ccaagaccca ctggagtatg ccgtcttcaa    1260
gcaacccatc tcacgtgcag tgccatacat aggctcaaaa taaaggaatg gagaaaaata    1320
tttcaagcaa atggaaaaca gaaaaaaggt gttgcactcc cagtttctga caaaacagac    1380
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ttgctgaggt tgtggagctt ctccccttca cagagtccct gatctccgaa aatttggttg    1560
agatgtaagg ttgattttgc tgtacaactc ctttttgaa gttttactca tttccaacaa     1620
ggaaggcaag ttttcctgct tccattgaca aaggagagca ggcacctcct ttcctgagtt    1680
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gacgtgcatt gggcctgtgg tcccatttgt gttattttc tgggaaattt cttccctttg     1800
gagtgagaaa gcttacccaa tgcctgtacc atcatcgtac cttaaaagaa ctccatttta    1860
agttcaggga ctccttggca gaagagaccg tagccttgta tcagatcata aaggagaaga    1920
gcaagaggtc cccggcaaac atccacagat ggccttggaa ataagtcacc ttgctcaccc    1980
tgcaggaatg ccagtgaact tattgctgac atcttggagc tcagtaccct catagtgtaa    2040
cggcgtcagc agatctgcct gtgctgggac ttcctgtact acccattcct gaggggcgat    2100
gcttctgcag ggcctgtgac ttggtgcaca acttcagaca ccatcatctt gcagcagcac    2160
cgcaccctca ctagccaggg tgttgatgac ttcctcaagg ccaaggccac attcaaggct    2220
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cagcagagcc agtggcctct actagatcct gtacaacctc acaaaacacc cagacatcgg    2460
gagtgctgcc agcctgtgat gcaagagtcc taatcctgaa gacattgaat gacctgtcat    2520
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tcacacagct gaacagtggt ggagttcaac tttgaccgtg ggctgtctga ccccaaggtg    2640
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atgttaaagg taggatctct gaagcctgtg ccagtggaac cgcagctcat ggctggcacc    2760
tgtgttctca ttcttacctc attaagagta aagtttattg agtttattga atttaagtat    2820
ctttagtgag atcatatatt attagtaaga actgggacca aacagatttt ctgactctaa    2880
aagagagatt ttcacagaaa cagatatata cctgtaagta tacagacacg catacacaca    2940
tttctttact gctcataaaa attagtcctt attagaatgt gggatgtata aatgtaagag    3000
aattttcatg ttaaaattga cagatacatt tttaaattgt cctaaaataa atttaattat    3060
ttttntttta gaattttcca ttattaatgt tatttttatg agaaactata taactttatt    3120
gataatacat acaataaccc tttgtttttc aaattgaaaa tacagtgtat tttgcaaata    3180
actaagtcct aattttgtat taaaattta aattttcaaa aaaaaaaa            3228
```

<210> 702
<211> 4894
<212> DNA
<213> Homo sapiens

<400> 702
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ctgcacgcgc tggctccggg tgacagccgc gcgcctcggc caggatctga gtgatgagac 60
gtgtccccac tgaggtgccc cacagcagca ggtgttgagc atgggctgag aagctggacc 120
ggcaccaaag ggctggcaga aatgggcgcc tggctgattc ctaggcagtt ggcggcagca 180
aggaggagag gccgcagctt ctggagcaga gccgagacga agcagttctg gagtgcctga 240
acggccccct gagccctacc cgcctggccc actatggtcc agaggctgtg ggtgagccgc 300
ctgctgcggc accggaaagc ccagctcttg ctggtcaacc tgctaacctt tggcctggag 360
gtgtgtttgg ccgcaggcat cacctatgtg ccgcctctgc tgctggaagt gggggtagag 420
gagaagttca tgaccatggt gctgggtgag tcactacatc ctccttcctt cctgttccag 480
atacatgcca cctggcatgt gggacaggag tacctctgcc ctgggagctg cttggaggga 540
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259

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<210> 706
<211> 123
<212> PRT
<213> Homo sapiens

<400> 706

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Met Gly Ser Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu Val Phe
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Ser Leu Val Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg Ala Val
             20                  25                  30
Tyr Leu Ala Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala Thr Cys
         35                  40                  45
Leu Ser His Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu Thr Gly
     50                  55                  60
Phe Thr Phe Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala Ser Leu
 65                  70                  75                  80
Tyr His Arg Glu Lys Gln Val Leu Ile Gly Gln Trp Val Glu Ser Gly
                 85                  90                  95
Trp Glu Gly Trp Ser Gly Phe Leu Gly Gly Gln Leu Ala Gln Asn Leu
                100                 105                 110
```

260

Val Ser Gly Lys Gln Leu Trp Arg Met Leu Leu
        115   120

<210> 707
<211> 150
<212> PRT
<213> Homo sapiens

<400> 707
Met Val Gln Arg Leu Trp Val Ser Arg Leu Leu Arg His Arg Lys Ala
                  5   10   15
Gln Leu Leu Leu Val Asn Leu Leu Thr Phe Gly Leu Glu Val Cys Leu
            20   25   30
Ala Ala Gly Ile Thr Tyr Val Pro Pro Leu Leu Leu Glu Val Gly Val
        35   40   45
Glu Glu Lys Phe Met Thr Met Val Leu Gly Glu Ser Leu His Pro Pro
    50   55   60
Ser Phe Leu Phe Gln Ile His Ala Thr Trp His Val Gly Gln Glu Tyr
65   70   75   80
Leu Cys Pro Gly Ser Cys Leu Glu Gly Glu Val Val Cys Trp Glu Gly
                85   90   95
Ile Ala Gly Gln Glu Gly Asp Pro Gly Leu Arg Gly His Thr Lys Arg
            100   105   110
Lys Lys Arg Ile Pro Arg Thr Tyr Pro Ser His Leu Trp Ile Pro Gly
        115   120   125
Pro Ala Gln Ser Leu Ala His Arg Arg His Trp Arg Asn Ala Pro Asn
    130   135   140
Leu Trp Leu Ala Leu Leu
145   150

<210> 708
<211> 371
<212> PRT
<213> Homo sapiens

<400> 708
Met Leu Phe Pro Ser Phe Ser Arg Ser Leu Val Pro Leu Pro Leu Ala
                  5   10   15
Leu Tyr Leu Ser Gln Pro Leu Thr His Thr Thr Ser Leu Leu Ala Gly
            20   25   30
Ile Gly Pro Val Leu Gly Leu Val Cys Val Pro Leu Leu Gly Ser Ala
        35   40   45
Ser Asp His Trp Arg Gly Arg Tyr Gly Arg Arg Arg Pro Phe Ile Trp
    50   55   60
Ala Leu Ser Leu Gly Ile Leu Leu Ser Leu Phe Leu Ile Pro Arg Ala
65   70   75   80
Gly Trp Leu Ala Gly Leu Leu Cys Pro Asp Pro Arg Pro Leu Glu Leu
                85   90   95
Ala Leu Leu Ile Leu Gly Val Gly Leu Leu Asp Phe Cys Gly Gln Val
            100   105   110
Cys Phe Thr Pro Leu Glu Ala Leu Leu Ser Asp Leu Phe Arg Asp Pro
        115   120   125
Asp His Cys Arg Gln Ala Tyr Ser Val Tyr Ala Phe Met Ile Ser Leu
    130   135   140
Gly Gly Cys Leu Gly Tyr Leu Leu Pro Ala Ile Asp Trp Asp Thr Ser
145   150   155   160
Ala Leu Ala Pro Tyr Leu Gly Thr Gln Glu Glu Cys Leu Phe Gly Leu
            165   170   175

```
Leu Thr Leu Ile Phe Leu Thr Cys Val Ala Ala Thr Leu Leu Val Ala
        180                     185                 190
Glu Glu Ala Ala Leu Gly Pro Thr Glu Pro Ala Glu Gly Leu Ser Ala
        195                     200                 205
Pro Ser Leu Ser Pro His Cys Cys Pro Cys Arg Ala Arg Leu Ala Phe
    210                     215                 220
Arg Asn Leu Gly Ala Leu Leu Pro Arg Leu His Gln Leu Cys Cys Arg
225                     230                 235                 240
Met Pro Arg Thr Leu Arg Arg Leu Phe Val Ala Glu Leu Cys Ser Trp
            245                     250                 255
Met Ala Leu Met Thr Phe Thr Leu Phe Tyr Thr Asp Phe Val Gly Glu
        260                     265                 270
Gly Leu Tyr Gln Gly Val Pro Arg Ala Glu Pro Gly Thr Glu Ala Arg
        275                     280                 285
Arg His Tyr Asp Glu Gly Lys Ala Leu Ala Ala Ser Arg Gly Trp Cys
    290                     295                 300
Gly Ser Arg Pro Pro Glu Thr Thr Leu Gly Ala Val Ser Gly Leu Val
305                     310                 315                 320
Pro Leu His Pro Gly Pro Asp Phe Ser Val Arg Lys Val Gly Met Asp
            325                     330                 335
Pro Ile Cys Ile His Gly Phe Ser Trp Val Trp Asn Ile Ser Ala Cys
            340                     345                 350
Gly Phe Arg Lys Ala Ser Gly Cys Ser Arg Ser Leu Ile Arg Val Val
        355                     360                 365
Ala Pro Val
    370
```

<210> 709
<211> 141
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(141)
<223> n=A,T,C or G

<400> 709
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tacggcgtgg tgcggagggc ggtaccccac aaataacacn nacacccat  cctatctgtg 60
tccacanata aantgactca ttcctctcct cgcatanccc actntcccct ngcgataccg 120
taacnaancc cttcccccctt t                                          141
```

<210> 710
<211> 196
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(196)
<223> n=A,T,C or G

<400> 710
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cnatccttcn cntacacccca tgangtccat gtcgcacgtc cacctcccct caaaacttgg 60
gtccncatcc acccgtcact ctcccntaa ncnataaccc cttttngcga atagacccca 120
ccttancaat nggttttttcn ttttttgtcc ctnggnccgn gcgattcaan aaattgaagg 180
cccanaaaaa cccct                                                  196
```

262

```
<210> 711
<211> 177
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(177)
<223> n=A,T,C or G

<400> 711
ntacntcnct ccnaatgaaa ttcgaanctc ggttacccgg gggnattccg attaggngcg  60
tantctcgga tgtgcagtca caagtctttt gctaatnctt ataattntcn ctacccttc  120
ttcnacaata ctgctatcct anttnttctn tcncctctct cccannttac taaccac     177


<210> 712
<211> 185
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(185)
<223> n=A,T,C or G

<400> 712
aaacgnacca nngccaacga tangtgttgg ngttggttgc ggttgttcct cttatntgca  60
ctggttgtcc gtgtcgcacg ganggccacg tccctctgnc ntgagtanca catagcatcc  120
acgtttagtc gactntnccg ggcggccgct ctacccntnt atngattctt attaaaantc  180
ggatc                                                              185


<210> 713
<211> 172
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(172)
<223> n=A,T,C or G

<400> 713
nntggtcgcc tgngcgtnta ctctaaagga tntactatnc atatggantc naanacgact  60
cactacacgg cnctctncgg agccnnggtc agtgcctnct nggagacctt ctctggggca  120
ggangagcac tnggtatgtt cacgtatcnc ttcntaaana tacnnccctc cg          172


<210> 714
<211> 112
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(714)
<223> n=A,T,C or G

<400> 714
nttgcgtgcc tggacgtnta ctctgcanga tctactactc atgngaattc taantacgga  60
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263

ctcactatnc ggcancgcag gcgcagcagg gaangggtca cctcccagtc tc   112

<210> 715
<211> 326
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(326)
<223> n=A,T,C or G

<400> 715
tactctanag gatctncgng tcatntggat tctatntcga ctcactctag ggctcnagcn 60
gtcngccggg caagttattc ggatcgtcgg gntccgagct tcgcaattaa ntgtgccatc 120
gttctncaac gttcctgact nggaancccc ngcngttcng atccncnggt acctagctcc 180
anntcccccg tnctccttct ggngtntcat naangaggac cnccctcgat cncccttcct 240
taatctgcnc acnctgaacg nccaatggac atngtgcgtt taatntanna ggcccgnttc 300
gngtgccctt cccgtnannt cagctc   326

<210> 716
<211> 122
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(122)
<223> n=A,T,C or G

<400> 716
nntgcgtcgc ctgngcgtnt actctagatg atctgantag tcatatggat tctaatacga 60
ctcannatag ggctctagcg nggatncnga ttcgtcntcc ngattcantg acnccggtan 120
ca   122

<210> 717
<211> 203
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(203)
<223> n=A,T,C or G

<400> 717
cntgcatgcc tgcaggtcga ctctagagga tctactagtc atatggatcg agcggccgcc 60
cgggcaggtg tnaatgataa anatgcatca tactanccta cagaanggag agataatgtt 120
ngntggacca ngttggtttt cttgcgtgtg tgtggcagta gtaagttatt agttttttana 180
atcantaccg ccctccgcac cac   203

<210> 718
<211> 168
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature

264

```
<222> (1)...(168)
<223> n=A,T,C or G

<400> 718
ggcagganga tcncttgagc cccngaggtc gaggctacag tgagccanga gtgcactact 60
gtnncgccct ccgcatncac gngtggtccg atccccgggt accganctng anttcactgg 120
anttcttttt aancgtnttg antggtacna ccctcgantc cctggctg              168

<210> 719
<211> 210
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(210)
<223> n=A,T,C or G

<400> 719
cancgtcgnc ataacacgta ttttntgatn aagattctna ctgacccatn aantctacnt 60
ctcaagctct tncanngtcc agtnaangga atgtgtatnn gtngggatnc cacanaaaaa 120
aganatntcg gncgcttcat tantcatcct tcttacccan ntctctngat ncncagtntg 180
ancntgaacg cacactacng gatntctcca                                  210

<210> 720
<211> 131
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(131)
<223> n=A,T,C or G

<400> 720
tccatcctaa tacgactcac tatagggctg ccaacctgcc atccactact gaggaagacc 60
cgnanactta ggggctcact gcgagccacc ggccacaggt cgtatagggc aaagcacgng 120
gaagcacccc t                                                      131

<210> 721
<211> 121
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(121)
<223> n=A,T,C or G

<400> 721
tccatcctaa tacgactcac tatagggccg ntgantnctg gcgaaaggct tacaattaag 60
naggaaaaan ganccaacaa ctaaaaaaaa nncggncgtg ncagcttnga tgactngtcc 120
a                                                                 121

<210> 722
<211> 246
<212> DNA
<213> Homo sapiens
```

265

```
<220>
<221> misc_feature
<222> (1)...(246)
<223> n=A,T,C or G

<400> 722
anctggagtc gcgcgctgca gtcacattgt ggatccanaa aatcggcaca agctctcntg 60
gnttcntcga tatgaanaac actaatccca tgtngtntgn gtctccgtga ttcatccctc 120
gcacnggtcc ccntccnaac cnttgcatag gtgttatgtt gtantctccc cagtgcacaa 180
agattnacac tctctcantg tctganatat gcacgagttc attgtcctgt cnccgtnaac 240
atcaag                                                          246

<210> 723
<211> 160
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(160)
<223> n=A,T,C or G

<400> 723
cctccggaaa atccaantag agtaantncn ctctaatccg gggnaattgg nggggtnnat 60
acgtcctcct cccccagnt aggattnana aaaggnctcc cagancaaaa nctccaaagt 120
gnatcnanta gccgtncccg anatncaacg cccctacgtc                    160

<210> 724
<211> 156
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(156)
<223> n=A,T,C or G

<400> 724
tnanccnata tacaccaaat tctgattcta aantcccacc caagggaaaa aagttgagaa 60
gagcctttcc acttttctac taataaaaaa atgcaccagc ccctaccann agtgnggaaa 120
acctccttag gcccttgnnt ggaacaancg aaaatc                        156

<210> 725
<211> 347
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(347)
<223> n=A,T,C or G

<400> 725
aganggttnt atncatgctg tactcgcgcg cctgcagtcg acactagtgg atccaaagaa 60
ttcggcacga gagacggtgc gcgatggacc gagggcccca gccggngagg cgccgccgcc 120
gagcccgcgg ncagacgccc catcagtagc gtccgcaccg ggnagccgcg gntctcgccc 180
gagccgtggg cgcgcccgag gggcgggctc gcctcccgcc gtccctcgca gctctgccgg 240
```

266

```
gcccgagccc gcgccgtcgc cgccgccgnc ttgccgctcg gnccgcgcgg nccggnaaac 300
gcggtcgagg tctggatgng gcanngcccg cncctntcgc tgagcct              347
```

```
<210> 726
<211> 162
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> misc_feature
<222> (1)...(162)
<223> n=A,T,C or G
```

```
<400> 726
ttgggtgggt tgggtggggg naaatttncc catttgggtg ggtttggggg ggnaaatact 60
tcccgccttt tnggtnccca aaganacnaa gggggagtcc cttnatagag gnagngcgat 120
ncntcncaac nacntngact ttgnccatgg ggagnaaggt gg                  162
```

```
<210> 727
<211> 120
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> misc_feature
<222> (1)...(120)
<223> n=A,T,C or G
```

```
<400> 727
gtgtgggtgg ggaattccat tgtggttggg ggnaaatctc cgcttgtcca aagnacaggg 60
ggggtcnctt anagngnagg gggttcctcc ccaccacttg ncttgnccat tgngagnaag 120
```

```
<210> 728
<211> 130
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> misc_feature
<222> (1)...(130)
<223> n=A,T,C or G
```

```
<400> 728
gacccactgc agcgttnaac ttagcttgga ccgagctcgg atccctagtc cgtgtggtgg 60
aattccatgt gtcgagagag gggcaaatac nctccaanac ancnccctca tgctcnacac 120
atattcgcat                                                     130
```

```
<210> 729
<211> 182
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> misc_feature
<222> (1)...(182)
<223> n=A,T,C or G
```

```
<400> 729
```

```
cngactgctn gcgtttaaac ttaagcnagg taccgaacgg ggatnnacga ctantgatcg 60
gctggctgct tccagtcgat tanatttgtg aaaaagctga accncngccn gttaaggggg 120
annatgcaaa anatncatcc nnctgccccn taaactgntc tntccnaggg aaaaaangga 180
ag                                                                182
```

<210> 730
<211> 678
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(678)
<223> n=A,T,C or G

<400> 730
```
cactcncact ccggacctag gcncttcacc actgctctct tcctcctcct cctcctcntc 60
ctcggggctg ggggaccttc cccagtgacc atctcacttt ggctgaancc cactcggggc 120
agcctgagtt tggggctctt ggccttctca ccctcctcgg ccccctcctt ggcccgcacc 180
aggccaaacc ggggcagccg taccttgagc ttgtgtccgg cctctccctc cccctctgcc 240
acctggtact cggcatggtt gcccccggga tggcgagagc tccacgtcgg gcagtgagaa 300
gcagaaagta cgctcggccc ctgggggctg ctcctcagca ccctcgcccc ccaccctagc 360
tctggccccc agtgtgggca acttcagcct cagcccaccc tcgcctgtgg ccgcctcgcc 420
cgcctgtgcc tctcggctta gccccacgtc caactcaagc tggggcactg tcacggtggg 480
catcttaaag acaccctcac ccaccagcag ctcaccacct gcaacctggg ctccaggcaa 540
aaaaagggtc acctggggca nctgaaccct gtacctgctg tgccctctgc tgaanggaat 600
gttatctgaa cctgctgccc tgggggtact gccttcccaa aaccgggtca antccacctg 660
ttggaaggna aatncccc                                                678
```

<210> 731
<211> 135
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(135)
<223> n=A,T,C or G

<400> 731
```
gagatccgac gtcaccccct tccggcggcc caagacgctg caactcccga ggcngcccaa 60
atatctttgg aagagcgctc ccagcccaac acaatggaat tccaccacac tggnntagtg 120
gatccgagct aagcc                                                  135
```

<210> 732
<211> 660
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(660)
<223> n=A,T,C or G

<400> 732
```
gcttggtacc gagctnggat ccctagtaac ggccgccagt gtgctggaat tcggctttct 60
tcaatcagnt nacgagctgc atggtctgct aacattgtca taattgctgg catagattac 120
tgaaaataaa gaaaaaaaat tgaagctgcc tatcaagttt tggtattatc aaaaacttcc 180
```

268

```
tacaagttat tttacttcaa ccatgttatt acaaatattt taatgaatac tttagagact 240
ttaattacaa aaaactgaga tagtaaaagc aagtaataaa agctgaaatt acttagctat 300
ttgataatta cataaattat tatggtccat tcaacttttc tagtgtttag tttatacacc 360
aggaagactt tcctattcta ctaacattta taaagtatgc taacctatta tttaaacgca 420
tccactatta ggattttatg gcctaaaacg tgatacagtt cagtatcttg atgtcaaaac 480
tttttaagca agtagggatt aagttcaagt gaatgtgatt ttctttcttc ccagtagggt 540
cttctgaata actcagnaaa gctcacttcc attatcttac tttataaaaa aatgctataa 600
gacagaatgg gccgacgtgg nggctccacc tgtatccacc tttggaggcg agnggcgaat 660
```

<210> 733
<211> 836
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(836)
<223> n=A,T,C or G

<400> 733
```
aattaatgac ttttttttccg ccctgccaag ctagtttgtc taaatataat gtaaagaaat 60
tagctactca ttttctggtc cacgaaggtt cctaaaatgg gaagaagtgg agatctgacc 120
ttgttagttc taaatacact aaactgggag tgccatggat ggctttcagg atgtcctgaa 180
tcctctataa ttgtatacaa aatcgtgagt tttttaaaaac tgggttagag ctattggttc 240
ctcagagtct caggcatctt agaccccccaa aaaggttaag gactactgac ttaaccaatt 300
aggtttgagt ggcattggct ttgaagaaaa gcagaggaaa gatatatttt ataattctgg 360
gcaacaaaaa agtggatgtg tgccagcatc ttagagtaga atcctcttaa aaggatagca 420
ctgcatatga actagtaggt tttaaccagt gcatatttag gcgaagtagc tcatttttct 480
gttagaattc tttttttattt gggaatgggc aagctttttac agcttttacc ttgccaatga 540
atacctggaa tttaaaaaat cttgttaggc .atattgccca taaagttttt tttcctagat 600
catatattca gtaaatatgt ttgtagcttt atttcaatcc cccaattcat tgagggttga 660
aacaatttga atggtttgag tgtagaagct aagttatttc tgtagaggct aagggcattt 720
ataccaanat atgttagact tgnggntcct gttaaccatg ctgtanacaa taggaattac 780
tgtatatcca cattttaatt ttaacatctt ctgctttgnt gntggtttga gangga     836
```

<210> 734
<211> 694
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(694)
<223> n=A,T,C or G

<400> 734
```
nagtnctatt tncactaaac tgngagtgcc ttggatggct ttcaggatgt cctgaatcct 60
ctataattgt atacaaaatc gtgagttttt aaaaactggg ttagagctat tggttcctca 120
gagtctcagg catcttagac ccccaaaaag gttaaggact actgacttaa ccaattaggt 180
ttgagtggca ttggctttga agaaaagcag aggaaagata tatttttataa ttctgggcaa 240
caaaaaagtg gatgtgtgcc agcatcttag agtagaatcc tcttaaaagg atagcactgc 300
atatgaacta gtaggtttta accagtgcat atttaggcga agtagctcat ttttctgtta 360
gaattctttt ttatttggga atgggcaagc ttttacagct tttaccttgc caatgaatac 420
ctggaattta aaaatcttg ttaggcatat tgcccataaa gtttttttc ctagatcata 480
tattcagtaa atatgtttgt agctttattt caatccccca attcattgag ggttgaaaca 540
atttgaatgg tttgagtgta gaagctaagt tatttctgta gaggctaagg gcatttatac 600
caagatatgt tagacttgtg gttcctgtta accattgctg tagacaatag gaattactgt 660
atatccacat tttaattttt aacatcattc tgtc                                694
```

269

```
<210> 735
<211> 126
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(126)
<223> n=A,T,C or G

<400> 735
ncnttgaaac nggttgacca gacttcaggc ctgtgcgctc aatcgtggag aatctcgtgc     60
cgaattcggc acgagtctct ctctctctct ctctctctct ctctctctct ntctctctct    120
ctctct                                                               126

<210> 736
<211> 165
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(165)
<223> n=A,T,C or G

<400> 736
cagaagcctt taaaccggtt ngaccagact tcaggcctgt gcgctcaatc gtggagaatc     60
tcgtgccgaa ttcggcacga gtctctctct ctctctctct ctctctctct ctctctctct    120
ctctctctct ctctctctct ctctctctct ctctctctct ctctc                   165

<210> 737
<211> 125
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(125)
<223> n=A,T,C or G


<400> 737
ggnagcccct ttaaccgttt gtccagactt caggcctgtg cgctcaatcg tggagaatct     60
cgtgccgaat tcggcacgag tctctctctc tctctctctc tctctctctc tctctntctc    120
tctct                                                                125

<210> 738
<211> 137
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(137)
<223> n=A,T,C or G

<400> 738
```

270

```
ggagncnctt gancaggatg accgacttca ggcctgtgcg ctcaatcgtg gagaatctcg 60
tgccgaattc ggcacgagtc tctctctctc tctctctctc tctctctctc tctctctctc 120
tctctctctc tctctct                                                137
```

<210> 739
<211> 970
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(970)
<223> n=A,T,C or G

<400> 739
```
aggcctattt aggtgacact atagaacaag tttgtacaaa aaagcaggct ggtaccggtc 60
cggaattcgc ggccgcgtcg acggcccttn gtgccactag ntctttcatt cttccccccc 120
atcaatcagt gaactttta gcctactcaa agctttgctc caatgcatag gatttatgat 180
tgtgggggatt tccagataat ataaatattc aacatgaata ttttaaatta aggcatgaga 240
catttttcct aactgagcat agccatgaac ctctcacgtc tgttcctctg tgtcagtttg 300
tancactgaa tacagcagcc ctcctaaaag tccaggcagt gcacaggtct tgacatgatg 360
aagtgacgtg ttgctatggt gattttgcag ctggccaaat agtcactggt tgattttacc 420
cagcaggaga tttttgcaaa aatttcctgg gtgagagtga aatcaaactc ctattttgnt 480
tctcctctgc aagctgnagt taagatggat taatgagtac ttttagatta attaactctg 540
aagagaaaat gggagaaaag tgaggaaggt tgttggcaga agtcattgct ggaatccttc 600
tgaagggagt actgacttca cttgcaaaga cnagagacta naagacaatg aagttaaact 660
tggcctgtct ctcatatgat agatgctgag agtcaggntc agggaaattt aattctgtca 720
tacgcatatn ggattatgtg gtcatggatt tgttggcact aaccngcctn taatcagnat 780
aagaaaagtg ttttggtaga naaagaaaat tatggcccag aaaaacctgg aanacttgga 840
aaaaatgntn gggggccttg ggtggtggtc tnaaaanacc ccctggggat ntttaaacca 900
aaantgaaga agggaaaaat ntttcccccnt ntttttnttt tttgccccct tgggattggn 960
ttttntttcc                                                        970
```

<210> 740
<211> 739
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(739)
<223> n=A,T,C or G

<400> 740
```
gntgtcnaaa aagcaggctg gtaccggtcc ggaattcgcg ccgcgtcga cggcccttgg 60
tgccactagt tctttcattc ttccccncca tcaatcgcg aactttttag cctactcaaa 120
gctttgctcc aatgcatagg atttatgatt gtggggattt ccagataata taaatattca 180
acatgaatat tttaaattaa ggcatgagac attttttccta actgagcata gccatgaacc 240
tctcacgtct gttcctctgt gncagtttgt agcactgaat acagcagccc tcctaaaagt 300
ccaggcagtg cacaggtctt gacatgatga agtgacgtgt tgctatggtg attttgcagc 360
tggccaaata gtcactggtt gattttaccc agcaggagat ttttgcaaaa atttcctggg 420
tgagagtgaa atcaaactcc tattttgttt ctcctctgca agctgnagtt aanatggatt 480
aatgagtact tttagattaa ttaactctga agagaaaatg ggagaaaagn gaggaaggtt 540
gttggcagaa gtcattgctg gaatccttct gaagggagta ctgacttcac ttgcaaagac 600
aagagactan aagacaatga agttaaactt ggcctgtctn tcatatgata gatgcttgag 660
agttacaggnt cagggaaatt ttaattctgn catacgcata ttggattatg tgggtcatgg 720
ctttgtttgg cncctaacc                                              739
```

271

```
<210> 741
<211> 1171
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(1171)
<223> n=A,T,C or G

<400> 741
gccttgnggt gacactatag aacatgtttg tacaaaaaag caggctggta ccggtccgga 60
attcgcggcc gcgtcgacgg cccttnntgc cactagttct ttcattcttc cccccatca 120
atcagtgaac tttttagcct actcaaagct ttgctccaat gcataggatt tatgattgtg 180
gggatttcca gataatataa atattcaaca tgaatatttt aaattaaggc atgagacatt 240
tttcctaact gagcatagcc atgaacctct cacgtctgtt cctctgtgtc agtttgtagc 300
actgaataca gcagccctcc taaaagtcca ggcagtgcac aggtcttgac atgatgaagt 360
gacgtgttgc tatggtgatt ttgcagctgg ccaaatagtc actggttgat tttacccagc 420
aggagatttt tgcaaaaatt tcctgggtga gagtgaaatc aaactcctat tttgtttctc 480
ctctgcaagc tgtagttaag aagggattaa tggagtactt tttaagaatt aaattaacct 540
cttgaaagaa gaaaadatgg gggaagaaaa aaagtggaag ggaaaagggn ttggttttgg 600
gccnaaaaaa aagttccaan tttnggcntt ggggaaaaat tccccntttt ccttggnaaa 660
agggggggnaa ggttaancct tgggaacctt tttccnncct tttnggccca aaagggggaac 720
ccanggggaa agaacctta ggnaaaggaa acccatttgg gaangggttt naaaaccntt 780
ngggcccccg ggccctcctc caanaaggga aaaaaaaagg cctggaaaan gtaccagggt 840
ttcangggna aaanttaaaa ttcttggcca atancnccat aattgggaat tatggggggg 900
ccatgggctt ttggtttggg cncttaaccc cgcnttttaa attcaaanna aaaaaaagng 960
gtttggaaaa nnaaanaaaa aaaattnaan ggncccnaaa aaaaaccctg gaaaacctt 1020
ggaaaaaaat tngnngggggg gccntttggt tgggggggtt tnaaaaaacc ccctnggggg 1080
ttttttaagc ccaaaagggg gggaggggna aaanggtncc cttntttttt ttttnngccc 1140
cccttgggga atggnttant tcangggggcc c                           1171

<210> 742
<211> 739
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(739)
<223> n=A,T,C or G

<400> 742
gntgtcnaaa aagcaggctg gtaccggtcc ggaattcgcg gccgcgtcga cggcccttgg 60
tgccactagt tctttcattc ttcccccncca tcaatcagtg aactttttag cctactcaaa 120
gctttgctcc aatgcatagg atttatgatt gtggggattt ccagataata taaatattca 180
acatgaatat tttaaattaa ggcatgagac attttttccta actgagcata gccatgaacc 240
tctcacgtct gttcctctgt gncagtttgt agcactgaat acagcagccc tcctaaaagt 300
ccaggcagtg cacaggtctt gacatgatga agtgacgtgt tgctatggtg attttgcagc 360
tggccaaata gtcactggtt gattttaccc agcaggagat ttttgcaaaa atttcctggg 420
tgagagtgaa atcaaactcc tattttgttt ctcctctgca agctgnagtt aanatggatt 480
aatgagtact tttagattaa ttaactctga agagaaaatg ggagaaaagn gaggaaggtt 540
gttggcagaa gtcattgctg gaatccttct gaagggagta ctgacttcac ttgcaaagac 600
aagagactan aagacaatga agttaaactt ggcctgtctn tcatatgata gatgcttgag 660
agtacaggnt cagggaaatt ttaattctgn catacgcata ttggattatg tgggtcatgg 720
ctttgtttgg cncctaacc                                          739
```

272

```
<210> 743
<211> 610
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(610)
<223> n=A,T,C or G

<400> 743
ctgtccttat ttctttagca aaaatttccc aagagaagaa ttgctgggat aatgcacatt 60
taaatttttg atagacattc ccaaatatta tacctgtttt tgagaccttt aattcctgtt 120
gtcaaattgc cctatatatg gagtaataaa cacgatttaa agaaatgagg actaaaaaaa 180
gattatatat aacccaacat aaaggcaacc tcttaggcgt tgacagaaac tgacaacttt 240
ttatctgtgg gtgcgatcca ttataagtaa cctgagcacc ttattttttc tttttaaact 300
ctaggtagga tacccgaggt ccacaaattt ttcataagaa atatttttc tctgccctat 360
gagattttaa aaaatattat actgcttcaa ttgcatcaaa agaaatggac cctaatatct 420
atgatgaagg atttggagtt agaagacctg agtttcaatt ttggcatggc tgtttgtcta 480
gctctgngat cttggacagg tcaattgact tggcttaatc ttctcatcca tttagnggag 540
acagcaccac tattcacagg actattgncn gaattaccag acaatagcat aggngaaaat 600
ataangcctt                                                       610

<210> 744
<211> 127
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(127)
<223> n=A,T,C or G

<400> 744
ttnacctccc tggaccgggc ccccttccc cgggcggntc ccccgggctg caggaattct 60
gcacgaggga gagagagttn gagagagaga gagagagaga gagagagaga gagananaga 120
gagagag                                                          127

<210> 745
<211> 458
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(458)
<223> n=A,T,C or G

<400> 745
gatatcccgg gattcgcggc cgcgtcgacg tggcctctag tttgtcctgg tccaaagcag 60
ggaagctggg ctacgtcctg cccaggtcag ccttaggtta agggctgcct ggggggaggga 120
acttcctggg ccttcgggtc tctgtgcact ggggtggctc ctgtggccca gaatgccctg 180
gagaagggtc ctactggaag cgaaggtgca gggcagcagg gcctgaggcg caggagctgg 240
tggaggctcc cagcacaggt cgccgcccca gtcacatcac tgctgatggt ggggggactt 300
ggggagtttc ccccgagaat gggaggtctc acagtccccg tgctgcaatg ctgtcggtgc 360
actgngncng caatgtgctc atggncactt gctttttctc tgtggccccg gccgatttat 420
ccagcanngc accctcttc tnctctccgg anaaagcc                         458
```

273

```
<210> 746
<211> 893
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(893)
<223> n=A,T,C or G

<400> 746
aagcaggctg gtaccggtcc ggaattcgcg gccgcgtcga cgtgggggagt tagctctctg  60
gaccccgtca tagagtaagt catcgataga gcatttgctt gatgggggact tccagaaggc 120
canngaaagt cctgccgact tcctgggggaa gcccatccgc acgtgggggtg agggtcccca 180
natggaagca gctgtgtatg caggggaggg gcagaggctg ctgccaatgg gcatgtccct 240
tacctgaaag ggccacctct ccaggtgaca tgtcctgggg gagccggggc cgtctgctcc 300
ggccagaggc gctcagctca ggccacacca ggcagggcac ctcccaacct ggacaggtgg 360
ggaccaaggt ggccttggac aaaactctct gtgtttgcca agcacccaat cggacacaga 420
gagtcaacca caccccagtc acatggtgtc cacacngcag gggtcaagga ggcccggccc 480
ctcccccctca gacgtccctg ggcctctggg agtcagcaag gacgaggacg gcattgccct 540
tcgagacagg aagggggagtga cctcctcccg gcggcatcca ggctcngctt ctccggagag 600
gagaggggggc tacttgctgg ataaancggc cggggccaca gagaaaaagc aaggtgacca 660
tgagcacctt gcaaacacag tgcacccacc agcatttnag caccngggac tgtgaagacc 720
tcccatttct tcggggggaa acncgcccaa ngttccccc accntcacta gtgnattgtg 780
acctgggggggn cgggccgacc cctgtngctt gggnnagccc tccncccagg tttctnnggc 840
ngcccnttaa nggncccctng nttggcccct tggccncctt tncgcttttc cca       893
```

```
<210> 747
<211> 738
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(738)
<223> n=A,T,C or G

<400> 747
gatatcccgg gaattcgcgg ccgcgtcnac gaagcacaga cctgngccct gctctcatgg  60
ggcagactgc catttgtcat tnattactga aggaaagggga tcctcagttt gcttgtggac 120
atttcaaatt tgaggtgaga gttggataag taagaataaa gctgctcttc aaagagatga 180
atatagaaaa agaaacaaga tacagncttg gcagtaaggc tgggaggaag gggaaaaggt 240
aataaagaat gaaagagtga gaaatgtgag caggagctga acacagaaaa gttcagngac 300
agaagcanaa ggagggaaga aggggaggagg gtccctttca cagaggctca cgaggatgct 360
ttatgngtgc catgcagtcc atgttcagga tgtctgcttc ttanctctct acttttctaa 420
tanaaatttg gatacttact gatcctacat atgtaacagg gagagaaggt gaatttcaaa 480
gcantaaatt gaaaaattgt tcacaatttc attttttaaa aaaagggagc taacagaaga 540
agaggttaat gtggtaatta taggatgnct cttgcgacac atgaatgnat ctggtatcat 600
ctgagtggga ggggagctgt cttcctgacc caaaaggatc ctttcgttan ccngnactta 660
ngtcccaaaa cctcaccacc ttggagaaat natttccttt tggggggtntc attaaancct 720
tttggncccc gcaaaagc                                                 738
```

```
<210> 748
<211> 647
<212> DNA
<213> Homo sapiens

<220>
```

274.

```
<221> misc_feature
<222> (1)...(647)
<223> n=A,T,C or G

<400> 748
ctntgtggcg gtggctgtct catttgggtg gactttttgg gtcgtaggaa cctggtatng 60
aggtcgagag taagacgggc tattagtagt cgcatcggag ttatttgtga aaacctggtt 120
agggcctctg tctccgctgc gctcgcctaa attggtatgg ctcgacttgg aaacacggtt 180
ctaacacgcg ttgttagcgc ccttgctagc atgtgaagga cactggccct accaagaaag 240
attcgagtcg ctccttccgg tatcgttcac ggaggcgata tttactcttc ttactacggt 300
tacttcgaga ttgtctgtga agtttaagac tactaaaaag agtattaagc ctatcggaa 360
ttagctagat cgacacgcta aaaccaaggg caatcggcgg aaatatagag gcaccaataa 420
tagggcctac agaaggcccg agggttagac tcacgtttaa taccggccac gggagaaata 480
aaaagataaa gtatacatcg tttagcggtc ctcggaagcc ttcggcttta atgccaagga 540
gtcggaagca tcgtcggcga gtaataaact ccatcgcgcc gagactatct acgacgccct 600
ccttaanatc cgtaaattac tcccggaaag agtatttagg cggctct             647
```

```
<210> 749
<211> 642
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(642)
<223> n=A,T,C or G

<400> 749
ctntgtggcg gtggntgtct catttgggtg gactttttgg gtcgtaggaa cctggtatgc 60
aggtccgcgg agcgtgggct ctcgtcgtgg atgttggggg ttggtgtggt gccggttgtt 120
tttggttctg ttgagcgtag tgtgtttgaa ggttagcgtt cgtgtcttgc ttgtggtttg 180
gtgtttaggg cgggtgggga ggttgttgtg tagctgttgt atgtcatatt gttggtgttg 240
ctgccctgtg ctgtttgtcc ttggttattg tggttgttac cccgcctgtg tggaagtgtt 300
gtggcagggc gggaatttaa gtgggagagt tgtgggaccc gtggttgttg ttacgttgct 360
gcttttgtcg tgggcggtgg cggcgcgtct gataattaga attggatacg gagtgtataa 420
tacttctagt aaatggggac ctagtgcttg acttcccgga atagggatct atgcgaagtc 480
cttaggatag tcttttgataa gtttaacgcc cacgacccta aaattataca cgattagacg 540
cataacgact cctccaggaa agataaagaa tctcacatat agaacgggac cccatacacg 600
tcggatagga aacaagagaa ctaattttng ttaaaaagac tt                 642
```

```
<210> 750
<211> 639
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(639)
<223> n=A,T,C or G

<400> 750
tttgtggcgg tggtgtctca tttgggtgga tttttgggtc gtaggtaacc tggtatngag 60
gtatagatgc cgattggtcc cgacgagcgt cacgataaat tcggtagttt cgcccttttt 120
agaaggcgct agtactcgga acttcacttc atctcggtag tttactttgg cgtatatagc 180
cttctccctc gaagactagc cgtcacattc gttccctagg aatcgtttct gcccctaaga 240
atccgagagc gagatcccga aactagagga accttagaag agtcgtattt ccacaaggac 300
cccacagtca ttccgggaaa atccctagga ccatacggtt aggattcccc cggaacccgg 360
agcaaagctc atgatttccc acaccgcgag agcgcctata accctatccc atttcttcgg 420
```

275

```
gttatcgagg atattacgat caagccgaga gaaccgctag aaccgctttc ttcgctttct 480
cacggaacct ataagtagaa agagaaactc aggtcttaag ggggcgcttc ggctaacgaa 540
acttctactt acgaagagag tatctagaca ttaagtcata aaaatccact acgcacctcg 600
tgtacgatat catcgggagc ggttcataga cggtgtccg                        639
```

```
<210> 751
<211> 637
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(637)
<223> n=A,T,C or G

<400> 751
cttttgtggc ggnggtgtct catttgggtg gattttggg tcgtaggnaa cctggtatng 60
aggcagctct gagcccccc ccccccccc cccccnccc ccccccccta ggnggttggg 120
aanacggtgg atacctaaat cgagtgngtt cattaaaagt agttgattac nccctaaaat 180
aanaanaggg cttcgtcggg anaaatcggt aagganaagt ctttntggca tcataanaat 240
actggctcgg gtcctaanat ntttaaggng gtcnccgagg gtnttcatac cgataanaaa 300
cgttttccta tcggcaacgg gcttacctga gggnggactt ctcncggngc ggngattnan. 360
acgaanacgt agaggattnc cgntacttnt tganatcacn cgtatcatac ttgtaagcat 420
aattntcctg aaaagtgtta taanaatacg cncgcatatt cgcttttcg tcctagggat 480
gcttaaatgg cgatactgct atagcgggtg agcgttggtt ctcgagnaan aaagcgtgtc 540
ctaatgcgtc taaggnttta aggncgttgg tttaaaaata nccttagaaa cctcgaggcg 600
gatactggtt tnttttttaac gaaacaaagc accccnn                         637
```

```
<210> 752
<211> 644
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(644)
<223> n=A,T,C or G

<400> 752
tntgtggcgg tggtgctcat ttgggtggat ttttgggtcg taggaacctg gtatgaggtc 60
ttgcgagttg ttggtgtgtc ctgtcgttcg gtggttccct tttgagttga gtttgtcctt 120
tgaggttgtt agctgctgtt cgtttgtgtt cgtgtagtgc tttgggttga qaqgqttatg 180
gtggtggtta cggtgtattg tcgcccgtgg tcgcgggggtt ggggtggtcg tcggttttgt 240
ggttcatagt agtcttctgc gttcggtggt gcgggtttgg gtgagtagtt tcgttcttgg 300
atgtcccatt gacccgccat aatctaagta agggttagta gaaacctctc cccgatagac 360
acaaccgtcg tccactaaag acctcgcctc tgatttttaa aaggacccga aaaacatccc 420
ttcaacggaa aaaacggaaa aaaagtcagc gaattcaaag aagccacggg agagaaaaaa 480
gaactaaagt tagtccgtca ttatatgtct cctcggagga ggaagcggcg gtggcggaaa 540
atgaggcggt aagaaagacg acctctatcg gcggcttang ccctaaaagg gcgatacctt 600
acgggatgat aaggacccta ggacgcctcc ttctcggatc gtcc                 644
```

```
<210> 753
<211> 635
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
```

276

```
<222> (1)...(635)
<223> n=A,T,C or G

<400> 753
ctttgtggcg gtggtgctca tttgggtgga ttttttgggtc gtaggaacct ggtatgaggg 60
aatcagctcg acccccccccc ccccccccct ccgaagcaga gcccaaccca aagtccaccg 120
actacccgag taaactctcg gagggtagaa taagaaggag taggtcctag ccaatagaag 180
tagttccgag ccgttaggac agcggacgga acattnaaga aagagcctat attagggagg 240
aagtaacgtt cctctttcgg agctctttaa ggggtagtcc cagaacaagg gaagaggacc 300
cgtcggctat tgcccgtcga tacgggctct cacggngagc ctaggttcga ggatagggcc 360
gctcgtaaaa ttatacggtt tccgagaaac gcttccgtag accgggtcct aaatcgtccg 420
gagtattngg agagggatcc ttcggaccct agggacagag agaggagaac ggaggttaca 480
ggaggagaac gtntcctcnc tagttttctt tangtcgaaa aatttcttac cgatagggtt 540
cctagggtcg gngaatttac ggttcgaaaa acggtagtnc ctaanggntg ntattngggg 600
tagtatcggg tcgtttacaa ntcgtccgtc ttntg                        635

<210> 754
<211> 721
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(721)
<223> n=A,T,C or G

<400> 754
accggattng ttnctgagcg cgtgactgct aataaaaaag atggantgcc atctttttttt 60
ttnccttgct ttatatatcc agcagcaaaa caaaattgtt ctgcngggct ataaaatttg 120
gcttgtgagt cntgtacaca actcaggagt gtgacacagc taccagcttt cctcctaact 180
ctcaagggaa gaaaattcaa gttctgtcta ggctcactct gtaaagtggg aaacttgctg 240
gttttgtagg cttttttttcc ccttcttttcc ctctctcagc ttctccctgc ttctcagaan 300
atggagttgt gatgcctgca acttaccaaa tttatctatg aatcagattc cagtgggaga 360
cccctaaagc agagggagaa taaggagttc tccccatgat ggaaaatatc caaagacaag 420
gtttcatgga gcaaagaatt ctggctagat ttggtttgta agtggatccc tccccactgc 480
gtgtacactt tatctgtctc tttgcttctt ccccaccctc tttcccagct ctctctctgt 540
ctctctcttg ntcccctgac cctttttttct tcccantgca tactttttttn tttccctttt 600
ttaatcttct atantcttaa ncctaccaan gggccctcnt gannaatttn tcacccctga 660
atagggggatt ctntangccc tgagaatttc nttatcanaa aaatatttt ttaaagcatt 720
a                                                             721

<210> 755
<211> 721
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(721)
<223> n=A,T,C or G

<400> 755
accggattng ttnctgagcg cgtgactgct aataaaaaag atggantgcc atctttttttt 60
ttnccttgct ttatatatcc agcagcaaaa caaaattgtt ctgcngggct ataaaatttg 120
gcttgtgagt cntgtacaca actcaggagt gtgacacagc taccagcttt cctcctaact 180
ctcaagggaa gaaaattcaa gttctgtcta ggctcactct gtaaagtggg aaacttgctg 240
gttttgtagg cttttttttcc ccttcttttcc ctctctcagc ttctccctgc ttctcagaan 300
atggagttgt gatgcctgca acttaccaaa tttatctatg aatcagattc cagtgggaga 360
```

277

```
cccctaaagc agagggagaa taaggagttc tccccatgat ggaaaatatc caaagacaag 420
gtttcatgga gcaaagaatt ctggctagat ttggtttgta agtggatccc tccccactgc 480
gtgtacactt tatctgtctc tttgcttctt ccccaccctc tttcccagct ctctctctgt 540
ctctctcttg ntcccctgac ccttttttct tcccantgca tactttttta tttccctttt 600
ttaatcttct atantcttaa ncctaccaan gggccctcnt gannaatttn tcaccccctga 660
ataggggatt ctntangccc tgagaatttc nttatcanaa aaatattttt ttaaagcatt 720
a                                                              721
```

<210> 756
<211> 873
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(873)
<223> n=A,T,C or G

<400> 756
```
ggaagaatac agtaagtttg caaattaaaa tttctctatt tttctgttat ttattcattt 60
ggaaactgtc agcctgtctc tttcactttg ggcaagtgaa agcaaagacg tccagtccta 120
tcagcaatta ggctgaaagt caacgccaag ctggcgggca agggctggtc tgagtagagg 180
ttccctaggc aggcaagaga gagactccca ctcgatactc ccagctcggc aactgcctga 240
atgccaatga gcactcatta taacccgccc tatttttatag gatttaattt tacacttcag 300
gcttaatcag tctgaaagtt aaactgacag tgttaagtta cggaatcaat gacatttagg 360
ctttatgact ttgtagctga atatctatgg gctatatttc cattctaaca gtgatatcct 420
gttccagaat ctcattcttt ggtgatggca ctttctagtg gagcagtcat ggtaacagtc 480
cacacccatt accatgtggg tgctttacag catactgacg gaaggactga ggagccaccg 540
gagcaggagt tcctctcagg gaggacgctg acacttccac agctgcctan gtatgggcac 600
ctgatgccaa cgaanaaccc aaagcgctct cccttccaga tggaagctgc cccacactgg 660
gctgacagca tctggagctg ctctggctca aatcccggaa tcgcacanct cctancgggg 720
gcgtttanag atcctcnggg ccagctaccg accacttttg acaagggnct taggagcgat 780
aactagnctg gcgcgttaca cncggatgga acgtcttgga cttgagacct cttgggggan 840
atggcncccc caaataantt gggaaaaantn ggg                          873
```

<210> 757
<211> 782
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(782)
<223> n=A,T,C or G

<400> 757
```
ggcccctcga gggatactct agagcggccg ccgactagtg agctcgtcga cgatatcccg 60
ggatttgaga ccaggagaca gctccagatg ctgtcagccc agtgctgggg gcaggcttcc 120
atctgtgaag tggagaggcg ctttgggctt cttcgttggc atcaggtgcc catacctagg 180
gcagctgtgg aagtgtcagc gtcctccctg agaggaactc ctgctccggt ggctcctcag 240
tccttccgtc agtatgctgt aaagcaccca catggtaatg ggtgnggact ggtaccatga 300
ctgntccctt aaaaggtggc cttcccnaag aaaggagaat tcttggacna gggatttcac 360
ttgnttagaa atgggaaaaa ttacccatta gaattttcgn ttccaaggcn tnaagnccta 420
aaaggccttt gattcccgaa ccttaaccct gggcagttaa cctttcaaac gggataaacc 480
ctganggggga aaatnaaatc ctttaaaaaa ggggggggttt naaggagggc tctttggctt 540
tcaggcantt gccaacctgg gaaattcana ggggaagtnt ttttttttgc ctgcctaggg 600
aacctttact taaacnaacc cttgncccc catttggggt tgactttcan cctaattgct 660
gaaaggaccg ggccgntttt gntttccttt gncccaaagg naaanaaacg ggtgccantt 720
```

278

```
cccangggat tanttcccga aaatttggnn aatttttntt tgnaactttt tgggtttttt 780
cc                                                              782
```

```
<210> 758
<211> 647
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(647)
<223> n=A,T,C or G

<400> 758
ntttgtggcg gtggtgtctc atttgggtgg actttttggg tcgtaggaac ctggtatnga 60
gggaagagcg ccgtcggtcc gagtacagta tggagtagta tagtcttcgc gccttctcgg 120
gcggcggggc tattctctcc aaaggcagag gtccctagtc gacctcgctc ccctaggtta 180
ggaacagccg tcgaatattt taggttcgtc gaggctttct tccgagctct acgcctaagt 240
agctccgcga gcaaagtatc ggtcattttc ccctatccat cactccccta agtacgcctc 300
attattccgg aaggcaagag gccagcattc ctccttagag tagagggtag gtacctccgt 360
cgcgtgccgc gaaagggcag agcttcgtgt cttccctccg cagcagctta acggtctacg 420
taggcgttct cgatcttttc acgggaatcg gggtccggga gggcggcgga aaacgtcgac 480
gtctcggtca ccgtcaccgc cccgaacaac tagcggcttt ccgctttcaa ctgaggaacc 540
ccgcacccct cattagcgct tacgaaatcg gggangtgat tgcgccaatt cgttagcctt 600
cgataattat tctctattag cggtcctatc tcgcgctttc gatttat            647
```

```
<210> 759
<211> 657
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(657)
<223> n=A,T,C or G

<400> 759
ctttgtggcg gtggtgtctc atttgggtgg actttttggg tcgtaggaac ctggtatnga 60
gggctctata gaaagcctct tgtctttaga tacgggcttt ctggtccttc gttctggaag 120
tgtagtagta ggtactgcgg gaaggcgaag agtcctttca aggacgattt acttaagttg 180
gcttattcta tagttccttc gggacataag gtcggtacga tctatactgc gtgggaagct 240
gataggttgg gacttaaggc gaataagaag gaggcggcgg aggtcgcgat taccgcagag 300
atattattta cggcggccgc gggtaccgcg ggtcatgcgg aaattttctg aggttcttgg 360
attcctaaga tcgctcccgt cgagtatact agcgacgaac gtaagagtgc cctcacaaga 420
accggtacaa actcaagaag aagttcccat taagcatcgt aagaaacggt aggacgagga 480
cggtaagaag taatcggaga aaggatccta gtngttacga agaagcatcg ttnagctact 540
ttgcgctacc gtttatattt agacgtgttc cgtccttctc cgtgtttana aaaaaggttt 600
attccgacgg gagacttagg cgaatggagg gttccgcggt tganaatcgg ancgggg   657
```

```
<210> 760
<211> 644
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(644)
<223> n=A,T,C or G
```

```
<400> 760
ctttgtggcg gtggtgtctc atttgggtgg acttttttggg tcgtaggaac ctggtatgna 60
ggaaaagaag taagcctcga agcctatctc cgaccgtatt tatttcgcag aagacggaac 120
tacggacgtc gttaacccccg agtagccccc gtaagaaagg actaaagcga atggaaaagt 180
cgggaattcc ggcggagggg cggcgattac tgaaaggagt aagagtaaga ctattgcgat 240
acttgaggcg ttccctctta aaaggcaccc gaaacactct attaaaaaac acccgaagaa 300
gaacaactca tgcgatcggc cgtgtgcagc cgtcaatagt aaagagagcc atgaaccatg 360
ccatccttag accaattagg atgaagaaga ggaggaagat gaggaccaaa ccctacccac 420
tcggaaaacc ccgcacgagc ctccgaacaa aatccgggaa ttaaaacggc ggcccacttc 480
cgcactctcg tagcgcggac cgaatagaaa accggaaact acagctaaag ggtcctttcc 540
ggcctgttat ctacccaccc gcaatccgat cctccccccc cctcgtccaa aaaccctaac 600
ctctgcggca acattagagc agaaggagag ggcgatccct tgan              644
```

```
<210> 761
<211> 647
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(647)
<223> n=A,T,C or G
```

```
<400> 761
ctttgtggcg gtggtgtctc atttgggtgg acttttttggg tcgtaggaac ctggtatnga 60
ggcgggtact ctctgggata atcggtataa gtgttgtaaa attgggggta agagaaagtt 120
tcattataag aagtggaagc acgagccggg gtgtttagtc gttaatatta agaccggttt 180
ttgttgtact tatatagctt gcgcgtgggg aggcaataag aaacattgcg tttcgaggcc 240
ggatgcgggg aaccctcttc ggggtctaga gcgccgcatc tgcaaaataa ggactactga 300
cgccgctcat aacgtactca acaatgagtc ggcctgcatt aagatttcgg cgaagaaccg 360
tactgcgtct actgatagta tattgcattg atagcggcat gagctttatc acgtgtcgtt 420
ttcgggttgt aagaagggag ttaagtcgat cttcgaggaa gaagagaccc caaataaaaa 480
atgactcaaa aaaacctaga agaaacacga cgaaaggaaa aagaacgtta aaactagtag 540
ctcttcggan gagtagcctt agtagggtaa gtcctccgtg cgtactgtcc taaggtttgg 600
atagcgcggt tgaatagacg gtcacgcgtc agaaggtaaa aanccgg          647
```

```
<210> 762
<211> 628
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(628)
<223> n=A,T,C or G
```

```
<400> 762
cattgtgttg gggtcactga gcccactttt ttccagattt tttgtaaaat tgtttcgcat 60
tgtgttccct ttattcgctt gtattaatat ttgcgtagtg gattaaacaa atacttggtg 120
ttgactgtca gtcttagagg actgactaga agtagttttc atttgggggct caggaaatac 180
ctactttata tttctagcta attaggaaag tcattttttca gttaggttgg tgttttggtt 240
caggcactcg ctagctagat gacctaacat gctacttaat ttctgagtgt ttgtgtccat 300
ccctgtagga ttgttgcggg gttaaatgaa attgtgtata tttgtaaagc atttacctca 360
gtgcccagac tgtgacagag tagattatta ggcttgctct tatttctgtg attaaattta 420
gtgtcagatt agcaacctat agctacttct aaagctgctg ctgctttctt tgtttagggt 480
taggaagaaa catgctggac agtttgccaa atgagagtta catgatgtgg cttgtgggaa 540
cattctaact tggaacttgc ccatttccag gactttgngg ttcanagatt tttggggata 600
```

280

```
gatgtaaggg ttaaaaaaaa cngaaaac                                        628

<210> 763
<211> 147
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(147)
<223> n=A,T,C or G

<400> 763
cattgtgttg gggcagagat aaataattcc tctgaaaagt gttttattgg aatttcaaat 60
gaaaagctaa ctggataact tacagcatgt ttctgccaat aatctcttan aacaggcctc 120
tttttttttat gcacaccacc ttcnggc                                       147

<210> 764
<211> 146
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(146)
<223> n=A,T,C or G

<400> 764
cattgtgttg ggtatgtttt ttgaaggcag gtggacagga tttgctgatg ggtaaatggc 60
agagttaggg ggactgttag aacagagaaa.ganatcatgg ggttgggttt gagtctgatg 120
nnnaactggt gccgnntgct cagtat                                         146

<210> 765
<211> 129
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(129)
<223> n=A,T,C or G

<400> 765
tncncgattc gntnctagcg tntacactna tgtcttggta ccgagctcgg atccactagt 60
ccagtgtggg nggaattcca ttgtgttggg gcaggaggng ctttgngtac ngtgcggctg 120
nagaggcgg                                                            129

<210> 766
<211> 175
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(175)
<223> n=A,T,C or G

<400> 766
```

```
cattgtgttg ggcctagtcc gaatactttt agtaacttca gacagatctc ctcatctctt 60
tctggggctt ggnttttctc ctttgtanaa tgatgccttt ctgtggtttt gtcatttcta 120
acattctgtg ngtgatgagg tgtatattcg anganctcta tcnccanagt actct    175
```

<210> 767
<211> 602
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(602)
<223> n=A,T,C or G

<400> 767
```
nnntttaaaa nctgtnctcc ccgcggtggc ggccgctcta gaactagtgg atcctttcca 60
cctggtttgt tttcagtgtt taatcctatt agtatcagca ggatataggt caggatatca 120
ggtgcagaac ctgtggaatc agccaatttg gcttgctcat ttactttaat aaggtcccat 180
aatgagtgag agtacaaagt tcaagccctg ttgagggtct gcattaaact ctcagaagta 240
tttagagtgt gccaggagcc gcgaaggtct ggttcgggtg gtggcgggaa ctgtattaga 300
gtgctaggca cggcgcgaca aagtctgtcc aacccaaaac ggtgctgagg cgttgggtgt 360
gagctccagt actcagaaaa gcatctcagc aggtactcaa cagatcctca ggggcttggg 420
ggcccagcac tggcagtgag ggcatgaaag acataaaagg gcactacctg tgggtatttt 480
ctgttctcca aggaggaagt agcaaaaatt aggacgctgg aatatcctat gttgtagcaa 540
tcccagaaca actgatgctc aacaaatacc acacaaaca aattttttaa aatttaatct 600
ta                                                              602
```

<210> 768
<211> 671
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(671)
<223> n=A,T,C or G

<400> 768
```
tccaccgcgg tggcggccgc tctagactag tggatccact agtccagtgt gggtgggaat 60
tcgcggcncg cgtcgacaaa aatactgcta aagtaatatt tttatagatg actatttgcc 120
ttggggccag gaaaagcagc tggagttatt cacttagtac cattttaca tactaacttt 180
gcctttcca tgcttgcttg atgcggcttg cagcactgaa gaacagtttc aattgctagc 240
caaccagaga gcatgatcaa accaaacaag ttccctgttt caggaaaaac aggttttagg 300
taactgaagg gttaccagtt actgattcca caatcttctc tgtaaaanat ttctgcctat 360
tatgcagact gggcggctt aaanntggta aaactatnaa atacccatac aatatttaa 420
nggggccccn ttatnaagct tttcaggcct tcccctttcc atagcattgg tgggatacaa 480
gaaaccttta aacagcaacn agctatcnag gcccaaaagg aaagtaattn tgatttttta 540
nagattccgn aacgaaaaa tggctgggtt caaatacnac cttcttttta aaatggnttc 600
cttattaaac ntttttttttt tttaattttta ccccatggtc ntgatnttng ngcttccgcc 660
canaaaatng n                                                    671
```

<210> 769
<211> 877
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature

282

```
<222> (1)...(877)
<223> n=A,T,C or G

<400> 769
aaagctggag ctccccgcgg tggcggccgc tctagaacta gtggatccac tagtccanng 60
nggggggaatt cgcggccgcg tcgacctcta taccttttgnt catgcagctt cctctgactg 120
ggtttgttct tcacttggct aacccctctt ttacttaagc acaccttgaa cattccctcc 180
ttccccattt ccccgcagng cccctaatgg acatacttct gaataacaca ggtggtattc 240
cttccttgtt ggaacctcct ggaggaagag acagatgatt aacaaatcct tccatcaacc 300
cctttgacca tgacatcaac agtgctccaa attatggggt accgtattag cctatgtcta 360
tcttgatcag aatccttacc tcggtgtatt gaaattatct atttcgtgcc tgcctcttta 420
aagtcagggt ttgccttatc tattgtctaa caccatgcag taggtaacat gcagtaggaa 480
acatggcatt aaattatttg ggttcaaatc ccagttatgg tgtgtaaatg cctaccaggc 540
cgtgaggcac ctgctaagca ggttgcacgc atcatttgaa ttcacaccac ccttttgcaa 600
tagaacagat aggcaacaga ggctcatttg ggctaaagga tttgatggag gggaagtgcc 660
aggattccca ccaaggcctc anggcccagg tccanggacc atgtctgttg tgacaactgg 720
agtgcatttc atatcccctn ctctgnnggg naaggtccct cncgnggaga acnnttaaaa 780
caatcatntc tnggggggntt aatgcttctt ncccccagtgt ggtncactgc ngccacgagt 840
cccanccact agtcccangt ctgtcatgaa ccancccc               877

<210> 770
<211> 874
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(874)
<223> n=A,T,C or G

<400> 770
ctggnctccc cgcggtggcg gccgctctag aactagtgga tccactagtc cagtgtggtg 60
gaattcgcgg ccgcgtcgac cttttcaaag gttaacttat ttaattatca cannngcaac 120
ccgatgagta ggtaacagta ttttactgat aggtaatcta aagaaggagg ctaaataaat 180
tgcccaattt cgaacagtga gaggaagaat taggattgaa acacatatag tggcttcaga 240
atctgtaacc ctcacgatgc cactactact tctttcagaa taccctttgc ctatctattc 300
tgttcctatg tcatcaaatt atacttactt taaaaagtat ttgtctttat tattttaaa 360
aaaacacagg gaagtatttc tgatcagggg cagtattggt tctgaaagac aagccagtgt 420
ttttgagggt ttctcccttg ccagtttttc tatgctgggt tattcaagtc ctaagaattg 480
tgtagctatt acagaaccgc tttagcaaat gtgttccatt aatcaaggtg atttataaca 540
aaatttcatc caagtttgga gtgctctgaa aacatagcca aaatgttcgc agggtctacc 600
cctctcgtgt gtcccttttt tttagctatt tcagaagcac actggtgcaa tatttttacga 660
aatgagtttc ttccccttac ctctgcatcc tctaagaaaa aatcattgnt gtttatgaa 720
natgaanatc ctgctatttc atatcttgat tggagctgct taattaaatg accatttttna 780
aatttgtttt gattccnngc aaaaaaagtt tnttnttgga tgtaggggggc tcnnaaagnc 840
caaaacccc caaaattttt nnttgggaac ccna               874

<210> 771
<211> 156
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(156)
<223> n=A,T,C or G

<400> 771
```

```
ttaaaaanct ggnctccccg cggtggcggc cgctctagaa ctagtggatc cactagtcca 60
gtgtggtgga attcgcggcc gcgtcgaccg cgagcggtcg cccttttttt tttttttttn 120
ngtttttttg aanaattcat tgggtattta ttattc                            156
```

```
<210> 772
<211> 586
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(586)
<223> n=A,T,C or G

<400> 772
ncaanctggn ctccaccgcg gtggcggccg ctctagacta gtggatccac tagtccagtg 60
tggtggaatt cgcggccgcg tcgatcacaa agtgctcaca agtccngnat ttattttatc 120
tccagatatg aaacttaccc ccagctatgg tcttctattt gttatttaat ttctaggcca 180
attttttcca cttgaatgtc agtattttaa ttcaaagtca ccttgtccaa ataccaagtc 240
atcaacttac cctcaaatta tatcctcatt cagaaaatct acatctatta atggtagcta 300
ttttatccct gccccctgct ttttcttttt atatttaatt aatttgntca tccagcaaat 360
gcttattgag caggtattgt aggctaaaca attctanact ttaaggggac acagnttgca 420
aaacaaaatc ctgccttgna tggatactta tgnnatggng ggatacagac aatcaacata 480
atgangngca tcatatataa tggttagnan aatgataagg gnttttggga aaaaaatgca 540
cccanccaan anggattggg aagtggangg ganggtcang ggangg              586
```

```
<210> 773
<211> 2983
<212> DNA
<213> Homo sapiens

<400> 773
agagatagag tcttccctgg cattgcagga gagaatctga agggatgatg gatgcatcaa 60
aagagctgca agttctccac attgacttct tgaatcagga caacgccgtt tctcaccaca 120
catgggagtt ccaaacgagc agtcctgtgt tccggcgagg acaggtgttt cacctgcggc 180
tggtgctgaa ccagccccta caatcctacc accaactgaa actggaattc agcacagggc 240
cgaatcctag catcgccaaa cacaccctgg tggtgctcga cccgaggacg ccctcagacc 300
actacaactg gcaggcaacc cttcaaaatg agtctggcaa agaggtcaca gtggctgtca 360
ccagttcccc caatgccatc ctgggcaagt accaactaaa cgtgaaaact ggaaaccaca 420
tccttaagtc tgaagaaaac atcctatacc ttctcttcaa cccatggtgt aaagaggaca 480
tggttttcat gcctgatgag gacgagcgca aagagtacat cctcaatgac acgggctgcc 540
attacgtggg ggctgccaga agtatcaaat gcaaaccctg gaactttggt cagtttgaga 600
aaaatgtcct ggactgctgc atttccctgc tgactgagag ctccctcaag cccacagata 660
ggagggaccc cgtgctggtg tgcagggcca tgtgtgctat gatgagcttt gagaaaggcc 720
agggcgtgct cattgggaat tggactgggg actatgaagg tggcacagcc ccatacaagt 780
ggacaggcag tgccccgatc ctgcagcagt actacaacac gaagcaggct gtgtgctttg 840
gccagtgctg ggtgtttgct gggatcctga ctacagtgct gagagcgttg ggcatcccag 900
cacgcagtgt gacaggcttc gattcagctc acgacacaga aaggaacctc acggtggaca 960
cctatgtgaa tgagaatggc aagaaaatca ccagtatgac ccacgactct gtctggaatt 1020
tccatgtgtg gacggatgcc tggatgaagc gaccggatct gcccaagggc tacgacggct 1080
ggcaggctgt ggacgcaacg ccgcaggagc gaagccaggg tgtcttctgc tgtgggccat 1140
caccactgac cgcatccgc aaaggtgaca tctttattgt ctatgacacc agattcgtct 1200
tctcagaagt gaatggtgac aggctcatct ggttggtgaa gatggtgaat gggcaggagg 1260
agttacacgt aatttccaatg gagaccacaa gcatcgggaa aaacatcagc accaaggcag 1320
tgggccaaga caggcggaga gatatcacct atgagtacaa gtatccagaa ggctcctctg 1380
aggagaggca ggtcatggat catgccttcc tccttctcag ttctgagagg gagcacagac 1440
gacctgtaaa agagaacttt cttcacatgt cggtacaatc agatgatgtg ctgctgggaa 1500
```

284

```
actctgttaa tttcaccgtg attcttaaaa ggaagaccgc tgccctacag aatgtcaaca 1560
tcttgggctc ctttgaacta cagttgtaca ctggcaagaa gatggcaaaa ctgtgtgacc 1620
tcaataagac ctcgcagatc caaggtcaag tatcagaagt gactctgacc ttggactcca 1680
agacctacat caacagcctg gctatattag atgatgagcc agttatcaga ggtttcatca 1740
ttgcggaaat tgtggagtct aaggaaatca tggcctctga agtattcacg tctttccagt 1800
accctgagtt ctctatagag ttgcctaaca caggcagaat tggccagcta cttgtctgca 1860
attgtatctt caagaatacc ctggccatcc ctttgactga cgtcaagttc tctttggaaa 1920
gcctgggcat ctcctcacta cagacctctg accatgggac ggtgcagcct ggtgagacca 1980
tccaatccca aataaaatgc accccaataa aaactggacc caagaaattt atcgtcaagt 2040
taagttccaa acaagtgaaa gagattaatg ctcagaagat tgttctcatc accaagtagc 2100
cttgtctgat gctgtggagc cttagttgag atttcagcat ttcctacctt gtgcttagct 2160
ttcagattat ggatgattaa atttgatgac ttatatgagg gcagattcaa gagccagcag 2220
gtcaaaaagg ccaacacaac cataagcagc cagacccaca aggccaggtc ctgtgctatc 2280
acagggtcac ctcttttaca gttagaaaca ccagccgagg ccacagaatc ccatcccttt 2340
cctgagtcat ggcctcaaaa atcagggcca ccattgtctc aattcaaatc catagatttc 2400
gaagccacag agtctctccc tggagcagca gactatgggc agcccagtgc tgccacctgc 2460
tgacgaccct tgagaagctg ccatatcttc aggccatggg ttcaccagcc ctgaaggcac 2520
ctgtcaactg gagtgctctc tcagcactgg gatgggcctg atagaagtgc attctcctcc 2580
tattgcctcc attctcctct ctctatccct gaaatccagg aagtccctct cctggtgctc 2640
caagcagttt gaagcccaat ctgcaaggac atttctcaag ggccatgtgg ttttgcagac 2700
aaccctgtcc tcaggcctga actcaccata gagacccatg tcagcaaacg gtgaccagca 2760
aatcctcttc ccttattcta aagctgcccc ttgggagact ccagggagaa ggcattgctt 2820
cctccctggt gtgaactctt tctttggtat tccatccact atcctggcaa ctcaaggctg 2880
cttctgttaa ctgaagcctg ctccttcttg ttctgccctc cagagatttg ctcaaatgat 2940
caataagctt taaattaaac tctacttcaa gaaaaaaaaa ccg               2983
```

```
<210> 774
<211> 3064
<212> DNA
<213> Homo sapiens
```

```
<400> 774
aattctaaaa atgcttttgc aagcttgcat gcctgcaggt gcagcggccg ccagtgtgat 60
ggatatctgc agaattcggc ttgcgctcag ctggaattcc gcagagatag agtcttccct 120
ggcattgcag gagagaatct gaagggatga tggatgcatc aaaagagctg caagttctcc 180
acattgactt cttgaatcag gacaacgccg tttctcacca cacatgggag ttccaaacga 240
gcagtcctgt gttccggcga ggacaggtgt ttcacctgcg gctggtgctg aaccagcccg 300
tacaatccta ccaccaactg aaactggaat tcagcacagg gccgaatcct agcatcgcca 360
aacacaccct ggtggtgctc gacccgagga cgccctcaga ccactacaac tggcaggcaa 420
cccttcaaaa tgagtctggc aaagaggtca cagtggctgt caccagttcc cccaatgcca 480
tcctgggcaa gtaccaacta aacgtgaaaa ctggaaacca catccttaag tctgaagaaa 540
acatcctata ccttctcttc aacccatggt gtaaagagga catggttttc atgcctgatg 600
aggacgagcg caaagagtac atcctcaatg acacgggctg ccattacgtg ggggctgcca 660
gaagtatcaa atgcaaaccc tggaactttg gtcagtttga gaaaaatgtc ctggactgct 720
gcatttccct gctgactgag agctccctca gcccacagea taggagggac cccgtgctgg 780
tgtgcaggge catgtgtgct atgatgagct ttgagaaagg ccagggcgtg ctcattggga 840
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tcctgcagca gtactacaac acgaagcagg ctgtgtgctt tggccagtgc tgggtgtttg 960
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tggtgaagat ggtgaatggg caggaggagt tacacgtaat ttcaatggag accacaagca 1380
tcgggaaaaa catcagcacc aaggcagtgg gccaagacag gcggagagat atcacctatg 1440
agtacaagta tccagaaggc tcctctgagg agaggcaggt catggatcat gccttcctcc 1500
ttctcagttc tgagagggag cacagacagc ctgtaaaaga gaactttctt cacatgtcgg 1560
```

285

```
·tacaatcaga tgatgtgctg ctgggaaact ctgttaattt caccgtgatt cttaaaagga 1620
agaccgctgc cctacagaat gtcaacatct tgggctcctt tgaactacag ttgtacactg 1680
gcaagaagat ggcaaaactg tgtgacctca ataagacctc gcagatccaa ggtcaagtat 1740
cagaagtgac tctgaccttg gactccaaga cctacatcaa cagcctggct atattagatg 1800
atgagccagt tatcagaggt ttcatcattg cggaaattgt ggagtctaag gaaatcatgg 1860
cctctgaagt attcacgtca aaccagtacc ctgagttctc tatagagttg cctaacacag 1920
gcagaattgg ccagctactt gtctgcaatt gtatcttcaa gaataccctg gccatccctt 1980
tgactgacgt caagttctct ttggaaagcc tgggcatctc ctcactacag acctctgacc 2040
atgggacggt gcagcctggt gagaccatcc aatcccaaat aaaatgcacc ccaataaaaa 2100
ctggacccaa gaaatttatc gtcaagttaa gttccaaaca agtgaaagag attaatgctc 2160
agaagattgt tctcatcacc aagtagcctt gtctgatgct gtggagcctt agttgagatt 2220
tcagcatttc ctaccttgtg cttagctttc agattatgga tgattaaatt tgatgactta 2280
tatgagggca gattcaagag ccagcaggtc aaaaaggcca acacaaccat aagcagccag 2340
acccacaagg ccaggtcctg tgctatcaca gggtcacctc ttttacagtt agaaacacca 2400
gccgaggcca cagaatccca tcccttttcct gagtcatggc ctcaaaaatc agggccacca 2460
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tatggcagc ccagtgctgc cacctgctga cgaccctga gaagctgcca tatcttcagg 2580
ccatgggttc accagccctg aaggcacctg .tcaactggag tgctctctca gcactgggat 2640
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atccaggaag tccctctcct ggtgctccaa gcagtttgaa gcccaatctg caaggacatt 2760
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atccactatc ctggcaactc aaggctgctt ctgttaactg aagcctgctc cttcttgttc 3000
tgccctccag agatttgctc aaatgatcaa taagctttaa attaaaccgg aatccgcgga 3060
attc                                                         3064
```

<210> 775
<211> 684
<212> PRT
<213> Homo sapiens

<400> 775

```
Met Met Asp Ala Ser Lys Glu Leu Gln Val Leu His Ile Asp Phe Leu
                5                   10                  15
Asn Gln Asp Asn Ala Val Ser His His Thr Trp Glu Phe Gln Thr Ser
            20                  25                  30
Ser Pro Val Phe Arg Arg Gly Gln Val Phe His Leu Arg Leu Val Leu
        35                  40                  45
Asn Gln Pro Leu Gln Ser Tyr His Gln Leu Lys Leu Glu Phe Ser Thr
    50                  55                  60
Gly Pro Asn Pro Ser Ile Ala Lys His Thr Leu Val Val Leu Asp Pro
65                  70                  75                  80
Arg Thr Pro Ser Asp His Tyr Asn Trp Gln Ala Thr Leu Gln Asn Glu
                85                  90                  95
Ser Gly Lys Glu Val Thr Val Ala Val Thr Ser Ser Pro Asn Ala Ile
            100                 105                 110
Leu Gly Lys Tyr Gln Leu Asn Val Lys Thr Gly Asn His Ile Leu Lys
        115                 120                 125
Ser Glu Glu Asn Ile Leu Tyr Leu Leu Phe Asn Pro Trp Cys Lys Glu
    130                 135                 140
Asp Met Val Phe Met Pro Asp Glu Asp Glu Arg Lys Glu Tyr Ile Leu
145                 150                 155                 160
Asn Asp Thr Gly Cys His Tyr Val Gly Ala Ala Arg Ser Ile Lys Cys
            165                 170                 175
Lys Pro Trp Asn Phe Gly Gln Phe Glu Lys Asn Val Leu Asp Cys Cys
        180                 185                 190
Ile Ser Leu Leu Thr Glu Ser Ser Leu Lys Pro Thr Asp Arg Arg Asp
```

286

```
            195                    200                    205
Pro Val Leu Val Cys Arg Ala Met Cys Ala Met Met Ser Phe Glu Lys
    210                    215                    220
Gly Gln Gly Val Leu Ile Gly Asn Trp Thr Gly Asp Tyr Glu Gly Gly
225                    230                    235                    240
Thr Ala Pro Tyr Lys Trp Thr Gly Ser Ala Pro Ile Leu Gln Gln Tyr
                245                    250                    255
Tyr Asn Thr Lys Gln Ala Val Cys Phe Gly Gln Cys Trp Val Phe Ala
            260                    265                    270
Gly Ile Leu Thr Thr Val Leu Arg Ala Leu Gly Ile Pro Ala Arg Ser
            275                    280                    285
Val Thr Gly Phe Asp Ser Ala His Asp Thr Glu Arg Asn Leu Thr Val
    290                    295                    300
Asp Thr Tyr Val Asn Glu Asn Gly Lys Lys Ile Thr Ser Met Thr His
305                    310                    315                    320
Asp Ser Val Trp Asn Phe His Val Trp Thr Asp Ala Trp Met Lys Arg
                325                    330                    335
Pro Asp Leu Pro Lys Gly Tyr Asp Gly Trp Gln Ala Val Asp Ala Thr
            340                    345                    350
Pro Gln Glu Arg Ser Gln Gly Val Phe Cys Cys Gly Pro Ser Pro Leu
            355                    360                    365
Thr Ala Ile Arg Lys Gly Asp Ile Phe Ile Val Tyr Asp Thr Arg Phe
    370                    375                    380
Val Phe Ser Glu Val Asn Gly Asp Arg Leu Ile Trp Leu Val Lys Met
385                    390                    395                    400
Val Asn Gly Gln Glu Glu Leu His Val Ile Ser Met Glu Thr Thr Ser
                405                    410                    415
Ile Gly Lys Asn Ile Ser Thr Lys Ala Val Gly Gln Asp Arg Arg Arg
            420                    425                    430
Asp Ile Thr Tyr Glu Tyr Lys Tyr Pro Glu Gly Ser Ser Glu Glu Arg
            435                    440                    445
Gln Val Met Asp His Ala Phe Leu Leu Leu Ser Ser Glu Arg Glu His
    450                    455                    460
Arg Arg Pro Val Lys Glu Asn Phe Leu His Met Ser Val Gln Ser Asp
465                    470                    475                    480
Asp Val Leu Leu Gly Asn Ser Val Asn Phe Thr Val Ile Leu Lys Arg
                485                    490                    495
Lys Thr Ala Ala Leu Gln Asn Val Asn Ile Leu Gly Ser Phe Glu Leu
            500                    505                    510
Gln Leu Tyr Thr Gly Lys Lys Met Ala Lys Leu Cys Asp Leu Asn Lys
            515                    520                    525
Thr Ser Gln Ile Gln Gly Gln Val Ser Glu Val Thr Leu Thr Leu Asp
    530                    535                    540
Ser Lys Thr Tyr Ile Asn Ser Leu Ala Ile Leu Asp Asp Glu Pro Val
545                    550                    555                    560
Ile Arg Gly Phe Ile Ile Ala Glu Ile Val Glu Ser Lys Glu Ile Met
                565                    570                    575
Ala Ser Glu Val Phe Thr Ser Phe Gln Tyr Pro Glu Phe Ser Ile Glu
            580                    585                    590
Leu Pro Asn Thr Gly Arg Ile Gly Gln Leu Leu Val Cys Asn Cys Ile
            595                    600                    605
Phe Lys Asn Thr Leu Ala Ile Pro Leu Thr Asp Val Lys Phe Ser Leu
    610                    615                    620
Glu Ser Leu Gly Ile Ser Ser Leu Gln Thr Ser Asp His Gly Thr Val
625                    630                    635                    640
Gln Pro Gly Glu Thr Ile Gln Ser Gln Ile Lys Cys Thr Pro Ile Lys
                645                    650                    655
Thr Gly Pro Lys Lys Phe Ile Val Lys Leu Ser Ser Lys Gln Val Lys
```

287

```
                    660                665                  670
Glu Ile Asn Ala Gln Lys Ile Val Leu Ile Thr Lys
        675                680


<210> 776
<211> 679
<212> PRT
<213> Homo sapiens


<400> 776
Met Met Asp Ala Ser Lys Glu Leu Gln Val Leu His Ile Asp Phe Leu
                5                    10                    15
Asn Gln Asp Asn Ala Val Ser His His Thr Trp Glu Phe Gln Thr Ser
            20                    25                    30
Ser Pro Val Phe Arg Arg Gly Gln Val Phe His Leu Arg Leu Val Leu
        35                    40                    45
Asn Gln Pro Leu Gln Ser Tyr His Gln Leu Lys Leu Glu Phe Ser Thr
    50                    55                    60
Gly Pro Asn Pro Ser Ile Ala Lys His Thr Leu Val Val Leu Asp Pro
65                    70                    75                    80
Arg Thr Pro Ser Asp His Tyr Asn Trp Gln Ala Thr Leu Gln Asn Glu
                85                    90                    95
Ser Gly Lys Glu Val Thr Val Ala Val Thr Ser Ser Pro Asn Ala Ile
            100                   105                   110
Leu Gly Lys Tyr Gln Leu Asn Val Lys Thr Gly Asn His Ile Leu Lys
        115                   120                   125
Ser Glu Glu Asn Ile Leu Tyr Leu Leu Phe Asn Pro Trp Cys Lys Glu
    130                   135                   140
Asp Met Val Phe Met Pro Asp Glu Asp Glu Arg Lys Glu Tyr Ile Leu
145                   150                   155                   160
Asn Asp Thr Gly Cys His Tyr Val Gly Ala Ala Arg Ser Ile Lys Cys
                165                   170                   175
Lys Pro Trp Asn Phe Gly Gln Phe Glu Lys Asn Val Leu Asp Cys Cys
            180                   185                   190
Ile Ser Leu Leu Thr Glu Ser Ser Leu Lys Pro Thr Asp Arg Arg Asp
        195                   200                   205
Pro Val Leu Val Cys Arg Ala Met Cys Ala Met Met Ser Phe Glu Lys
    210                   215                   220
Gly Gln Gly Val Leu Ile Gly Asn Trp Thr Gly Asp Tyr Glu Gly Gly
225                   230                   235                   240
Thr Ala Pro Tyr Lys Trp Thr Gly Ser Ala Pro Ile Leu Gln Gln Tyr
                245                   250                   255
Tyr Asn Thr Lys Gln Ala Val Cys Phe Gly Gln Cys Trp Val Phe Ala
            260                   265                   270
Gly Ile Leu Thr Thr Val Leu Arg Ala Leu Gly Ile Pro Ala Arg Ser
        275                   280                   285
Val Thr Gly Phe Asp Ser Ala His Asp Thr Glu Arg Asn Leu Thr Val
    290                   295                   300
Asp Thr Tyr Val Asn Glu Asn Gly Glu Lys Ile Thr Ser Met Thr His
305                   310                   315                   320
Asp Ser Val Trp Asn Phe His Val Trp Thr Asp Ala Trp Met Lys Arg
                325                   330                   335
Pro Tyr Asp Gly Trp Gln Ala Val Asp Ala Thr Pro Gln Glu Arg Ser
            340                   345                   350
Gln Gly Val Phe Cys Cys Gly Pro Ser Pro Leu Thr Ala Ile Arg Lys
        355                   360                   365
Gly Asp Ile Phe Ile Val Tyr Asp Thr Arg Phe Val Phe Ser Glu Val
    370                   375                   380
```

288

```
Asn Gly Asp Arg Leu Ile Trp Leu Val Lys Met Val Asn Gly Gln Glu
385           ·           390               395               400
Glu Leu His Val Ile Ser Met Glu Thr Thr Ser Ile Gly Lys Asn Ile
            405                   410                   415
Ser Thr Lys Ala Val Gly Gln Asp Arg Arg Arg Asp Ile Thr Tyr Glu
            420                   425               430
Tyr Lys Tyr Pro Glu Gly Ser Ser Glu Glu Arg Gln Val Met Asp His
        435               440               445
Ala Phe Leu Leu Leu Ser Ser Glu Arg Glu His Arg Gln Pro Val Lys
    450               455               460
Glu Asn Phe Leu His Met Ser Val Gln Ser Asp Asp Val Leu Leu Gly
465               470               475               480
Asn Ser Val Asn Phe Thr Val Ile Leu Lys Arg Lys Thr Ala Ala Leu
            485               490                   495
Gln Asn Val Asn Ile Leu Gly Ser Phe Glu Leu Gln Leu Tyr Thr Gly
        500               505               510
Lys Lys Met Ala Lys Leu Cys Asp Leu Asn Lys Thr Ser Gln Ile Gln
        515               520               525
Gly Gln Val Ser Glu Val Thr Leu Thr Leu Asp Ser Lys Thr Tyr Ile
    530               535               540
Asn Ser Leu Ala Ile Leu Asp Asp Glu Pro Val Ile Arg Gly Phe Ile
545               550               555               560
Ile Ala Glu Ile Val Glu Ser Lys Glu Ile Met Ala Ser Glu Val Phe
            565               570               575
Thr Ser Asn Gln Tyr Pro Glu Phe Ser Ile Glu Leu Pro Asn Thr Gly
            580               585               590
Arg Ile Gly Gln Leu Leu Val Cys Asn Cys Ile Phe Lys Asn Thr Leu
        595               600               605
Ala Ile Pro Leu Thr Asp Val Lys Phe Ser Leu Glu Ser Leu Gly Ile
    610               615               620
Ser Ser Leu Gln Thr Ser Asp His Gly Thr Val Gln Pro Gly Glu Thr
625               630               635               640
Ile Gln Ser Gln Ile Lys Cys Thr Pro Ile Lys Thr Gly Pro Lys Lys
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<210> 777
<211> 5668
<212> DNA
<213> Homo sapiens

<400> 777
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289

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290

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<212> PRT
<213> Homo sapiens

<400> 778
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Thr Lys Asp Ser Lys Ala Thr Glu Asn Val Cys Lys Cys Gly Tyr Ala
      50                  55                  60
Gln Ser Gln His Met Glu Gly Thr Gln Ile Asn Gln Ser Glu Lys Trp
65                  70                  75                  80
Asn Tyr Lys Lys His Thr Lys Glu Phe Pro Thr Asp Ala Phe Gly Asp
                  85                  90                  95
Ile Gln Phe Glu Thr Leu Gly Lys Lys Gly Lys Tyr Ile Arg Leu Ser
              100                 105                 110
Cys Asp Thr Asp Ala Glu Ile Leu Tyr Glu Leu Leu Thr Gln His Trp
          115                 120                 125
His Leu Lys Thr Pro Asn Leu Val Ile Ser Val Thr Gly Gly Ala Lys
      130                 135                 140
Asn Phe Ala Leu Lys Pro Arg Met Arg Lys Ile Phe Ser Arg Leu Ile
145                 150                 155                 160
Tyr Ile Ala Gln Ser Lys Gly Ala Trp Ile Leu Thr Gly Gly Thr His
                  165                 170                 175
Tyr Gly Leu Thr Lys Tyr Ile Gly Glu Val Val Arg Asp Asn Thr Ile
              180                 185                 190
Ser Arg Ser Ser Glu Glu Asn Ile Val Ala Ile Gly Ile Ala Ala Trp
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291

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Leu Tyr Ile Leu Asp Asn Asn His Thr His Leu Leu Leu Val Asp Asn
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Gly Cys His Gly His Pro Thr Val Glu Ala Lys Leu Arg Asn Gln Leu
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Glu Lys His Ile Ser Glu Arg Thr Ile Gln Asp Ser Asn Tyr Gly Gly
        275                 280                 285
Lys Ile Pro Ile Val Cys Phe Ala Gln Gly Gly Gly Lys Glu Thr Leu
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Lys Ala Ile Asn Thr Ser Ile Lys Asn Lys Ile Pro Cys Val Val Val
305                 310                 315                 320
Glu Gly Ser Gly Arg Ile Ala Asp Val Ile Ala Ser Leu Val Glu Val
            325                 330                 335
Glu Asp Ala Pro Thr Ser Ser Ala Val Lys Glu Lys Leu Val Arg Phe
            340                 345                 350
Leu Pro Arg Thr Val Ser Arg Leu Ser Glu Glu Glu Thr Glu Ser Trp
        355                 360                 365
Ile Lys Trp Leu Lys Glu Ile Leu Glu Cys Ser His Leu Leu Thr Val
    370                 375                 380
Ile Lys Met Glu Glu Ala Gly Asp Glu Ile Val Ser Asn Ala Ile Ser
385                 390                 395                 400
Tyr Ala Leu Tyr Lys Ala Phe Ser Thr Ser Glu Gln Asp Lys Asp Asn
            405                 410                 415
Trp Asn Gly Gln Leu Lys Leu Leu Leu Glu Trp Asn Gln Leu Asp Leu
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Ala Asn Asp Glu Ile Phe Thr Asn Asp Arg Arg Trp Glu Ser Ala Asp
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Leu Gln Glu Val Met Phe Thr Ala Leu Ile Lys Asp Arg Pro Lys Phe
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Val Arg Leu Phe Leu Glu Asn Gly Leu Asn Leu Arg Lys Phe Leu Thr
465                 470                 475                 480
His Asp Val Leu Thr Glu Leu Phe Ser Asn His Phe Ser Thr Leu Val
            485                 490                 495
Tyr Arg Asn Leu Gln Ile Ala Lys Asn Ser Tyr Asn Asp Ala Leu Leu
            500                 505                 510
Thr Phe Val Trp Lys Leu Val Ala Asn Phe Arg Arg Gly Phe Arg Lys
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Glu Asp Arg Asn Gly Arg Asp Glu Met Asp Ile Glu Leu His Asp Val
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Ser Pro Ile Thr Arg His Pro Leu Gln Ala Leu Phe Ile Trp Ala Ile
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Gly Cys Thr Leu Ala Ala Leu Gly Ala Ser Lys Leu Leu Lys Thr Leu
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Ala Asn Glu Tyr Glu Thr Arg Ala Val Glu Leu Phe Thr Glu Cys Tyr
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Ser Ser Asp Glu Asp Leu Ala Glu Gln Leu Leu Val Tyr Ser Cys Glu
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Ala Trp Gly Gly Ser Asn Cys Leu Glu Leu Ala Val Glu Ala Thr Asp
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Gln His Phe Thr Ala Gln Pro Gly Val Gln Asn Phe Leu Ser Lys Gln
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292

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Lys Lys Pro Val Asp Lys His Lys Lys Leu Leu Trp Tyr Tyr Val Ala
705                 710                 715                 720
Phe Phe Thr Ser Pro Phe Val Val Phe Ser Trp Asn Val Val Phe Tyr
                725                 730                 735
Ile Ala Phe Leu Leu Leu Phe Ala Tyr Val Leu Leu Met Asp Phe His
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Ser Val Pro His Pro Pro Glu Leu Val Leu Tyr Ser Leu Val Phe Val
        755                 760                 765
Leu Phe Cys Asp Glu Val Arg Gln Trp Tyr Val Asn Gly Val Asn Tyr
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Phe Thr Asp Leu Trp Asn Val Met Asp Thr Leu Gly Leu Phe Tyr Phe
785                 790                 795                 800
Ile Ala Gly Ile Val Phe Arg Leu His Ser Ser Asn Lys Ser Ser Leu
                805                 810                 815
Tyr Ser Gly Arg Val Ile Phe Cys Leu Asp Tyr Ile Ile Phe Thr Leu
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Arg Leu Ile His Ile Phe Thr Val Ser Arg Asn Leu Gly Pro Lys Ile
        835                 840                 845
Ile Met Leu Gln Arg Met Leu Ile Asp Val Phe Phe Phe Leu Phe Leu
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Phe Ala Val Trp Met Val Ala Phe Gly Val Ala Arg Gln Gly Ile Leu
865                 870                 875                 880
Arg Gln Asn Glu Gln Arg Trp Arg Trp Ile Phe Arg Ser Val Ile Tyr
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Glu Pro Tyr Leu Ala Met Phe Gly Gln Val Pro Ser Asp Val Asp Gly
                900                 905                 910
Thr Thr Tyr Asp Phe Ala His Cys Thr Phe Thr Gly Asn Glu Ser Lys
        915                 920                 925
Pro Leu Cys Val Glu Leu Asp Glu His Asn Leu Pro Arg Phe Pro Glu
        930                 935                 940
Trp Ile Thr Ile Pro Leu Val Cys Ile Tyr Met Leu Ser Thr Asn Ile
945                 950                 955                 960
Leu Leu Val Asn Leu Leu Val Ala Met Phe Gly Tyr Thr Val Gly Thr
                965                 970                 975
Val Gln Glu Asn Asn Asp Gln Val Trp Lys Phe Gln Arg Tyr Phe Leu
                980                 985                 990
Val Gln Glu Tyr Cys Ser Arg Leu Asn Ile Pro Phe Pro Phe Ile Val
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Phe Ala Tyr Phe Tyr Met Val Val Lys Lys Cys Phe Lys Cys Cys Cys
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Lys Glu Lys Asn Met Glu Ser Ser Val Cys Cys Phe Lys Asn Glu Asp
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Lys Ile Asn Thr Lys Ala Asn Asp Thr Ser Glu Glu Met Arg His Arg
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Glu Ile Ala Asn Lys Ile Lys
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<211> 3639

<212> DNA
<213> Homo sapiens

<400> 779
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<212> PRT
<213> Homo sapiens

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Val Asn Phe Ile Gln Ala Asn Phe Lys Lys Arg Glu Cys Val Phe Phe
            35   40   45
Thr Lys Asp Ser Lys Ala Thr Glu Asn Val Cys Lys Cys Gly Tyr Ala
      50   55   60
Gln Ser Gln His Met Glu Gly Thr Gln Ile Asn Gln Ser Glu Lys Trp
65   70   75   80
Asn Tyr Lys Lys His Thr Lys Glu Phe Pro Thr Asp Ala Phe Gly Asp
               85   90   95
Ile Gln Phe Glu Thr Leu Gly Lys Lys Gly Lys Tyr Ile Arg Leu Ser
            100   105   110
Cys Asp Thr Asp Ala Glu Ile Leu Tyr Glu Leu Leu Thr Gln His Trp
         115   120   125
His Leu Lys Thr Pro Asn Leu Val Ile Ser Val Thr Gly Gly Ala Lys
      130   135   140
Asn Phe Ala Leu Lys Pro Arg Met Arg Lys Ile Phe Ser Arg Leu Ile
145   150   155   160
Tyr Ile Ala Gln Ser Lys Gly Ala Trp Ile Leu Thr Gly Gly Thr His
               165   170   175
Tyr Gly Leu Met Lys Tyr Ile Gly Glu Val Val Arg Asp Asn Thr Ile
            180   185   190
Ser Arg Ser Ser Glu Glu Asn Ile Val Ala Ile Gly Ile Ala Ala Trp
         195   200   205
Gly Met Val Ser Asn Arg Asp Thr Leu Ile Arg Asn Cys Asp Ala Glu
      210   215   220
Gly Tyr Phe Leu Ala Gln Tyr Leu Met Asp Asp Phe Thr Arg Asp Pro
225   230   235   240
Leu Tyr Ile Leu Asp Asn Asn His Thr His Leu Leu Leu Val Asp Asn
               245   250   255
Gly Cys His Gly His Pro Thr Val Glu Ala Lys Leu Arg Asn Gln Leu
            260   265   270
Glu Lys Tyr Ile Ser Glu Arg Thr Ile Gln Asp Ser Asn Tyr Gly Gly
         275   280   285
Lys Ile Pro Ile Val Cys Phe Ala Gln Gly Gly Gly Lys Glu Thr Leu
      290   295   300
Lys Ala Ile Asn Thr Ser Ile Lys Asn Lys Ile Pro Cys Val Val Val

295

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305                     310                     315                     320
Glu Gly Ser Gly Gln Ile Ala Asp Val Ile Ala Ser Leu Val Glu Val
                325                     330                     335
Glu Asp Ala Leu Thr Ser Ser Ala Val Lys Glu Lys Leu Val Arg Phe
            340                     345                     350
Leu Pro Arg Thr Val Ser Arg Leu Pro Glu Glu Glu Thr Glu Ser Trp
        355                     360                     365
Ile Lys Trp Leu Lys Glu Ile Leu Glu Cys Ser His Leu Leu Thr Val
    370                     375                     380
Ile Lys Met Glu Glu Ala Gly Asp Glu Ile Val Ser Asn Ala Ile Ser
385                     390                     395                     400
Tyr Ala Leu Tyr Lys Ala Phe Ser Thr Ser Glu Gln Asp Lys Asp Asn
                405                     410                     415
Trp Asn Gly Gln Leu Lys Leu Leu Leu Glu Trp Asn Gln Leu Asp Leu
            420                     425                     430
Ala Asn Asp Glu Ile Phe Thr Asn Asp Arg Arg Trp Glu Ser Ala Asp
        435                     440                     445
Leu Gln Glu Val Met Phe Thr Ala Leu Ile Lys Asp Arg Pro Lys Phe
    450                     455                     460
Val Arg Leu Phe Leu Glu Asn Gly Leu Asn Leu Arg Lys Phe Leu Thr
465                     470                     475                     480
His Asp Val Leu Thr Glu Leu Phe Ser Asn His Phe Ser Thr Leu Val
                485                     490                     495
Tyr Arg Asn Leu Gln Ile Ala Lys Asn Ser Tyr Asn Asp Ala Leu Leu
            500                     505                     510
Thr Phe Val Trp Lys Leu Val Ala Asn Phe Arg Arg Gly Phe Arg Lys
        515                     520                     525
Glu Asp Arg Asn Gly Arg Asp Glu Met Asp Ile Glu Leu His Asp Val
    530                     535                     540
Ser Pro Ile Thr Arg His Pro Leu Gln Ala Leu Phe Ile Trp Ala Ile
545                     550                     555                     560
Leu Gln Asn Lys Lys Glu Leu Ser Lys Val Ile Trp Glu Gln Thr Arg
                565                     570                     575
Gly Cys Thr Leu Ala Ala Leu Gly Ala Ser Lys Leu Leu Lys Thr Leu
            580                     585                     590
Ala Lys Val Lys Asn Asp Ile Asn Ala Ala Gly Glu Ser Glu Glu Leu
        595                     600                     605
Ala Asn Glu Tyr Glu Thr Arg Ala Val Glu Leu Phe Thr Glu Cys Tyr
    610                     615                     620
Ser Ser Asp Glu Asp Leu Ala Glu Gln Leu Leu Val Tyr Ser Cys Glu
625                     630                     635                     640
Ala Trp Gly Gly Ser Asn Cys Leu Glu Leu Ala Val Glu Ala Thr Asp
                645                     650                     655
Gln His Phe Ile Ala Gln Pro Gly Val Gln Asn Phe Leu Ser Lys Gln
            660                     665                     670
Trp Tyr Gly Glu Ile Ser Arg Asp Thr Lys Asn Trp Lys Ile Ile Leu
        675                     680                     685
Cys Leu Phe Ile Ile Pro Leu Val Gly Cys Gly Phe Val Ser Phe Arg
    690                     695                     700
Lys Lys Pro Val Asp Lys His Lys Lys Leu Leu Trp Tyr Tyr Val Ala
705                     710                     715                     720
Phe Phe Thr Ser Pro Phe Val Val Phe Ser Trp Asn Val Val Phe Tyr
                725                     730                     735
Ile Ala Phe Leu Leu Leu Phe Ala Tyr Val Leu Leu Met Asp Phe His
            740                     745                     750
Ser Val Pro His Pro Pro Glu Leu Val Leu Tyr Ser Leu Val Phe Val
        755                     760                     765
Leu Phe Cys Asp Glu Val Arg Gln Trp Tyr Val Asn Gly Val Asn Tyr
```

296

```
       770  \              775                 780
Phe Thr Asp Leu Trp Asn Val Met Asp Thr Leu Gly Leu Phe Tyr Phe
785                 790                 795                 800
Ile Ala Gly Ile Val Phe Arg Leu His Ser Ser Asn Lys Ser Ser Leu
                805                 810                 815
Tyr Ser Gly Arg Val Ile Phe Cys Leu Asp Tyr Ile Ile Phe Thr Leu
            820                 825                 830
Arg Leu Ile His Ile Phe Thr Val Ser Arg Asn Leu Gly Pro Lys Ile
            835                 840                 845
Ile Met Leu Gln Arg Met Leu Ile Asp Val Phe Phe Phe Leu Phe Leu
        850                 855                 860
Phe Ala Xaa Trp Met Val Ala Phe Gly Val Ala Arg Gln Gly Ile Leu
865                 870                 875                 880
Arg Gln Asn Glu Gln Arg Trp Arg Trp Ile Phe Arg Ser Val Ile Tyr
            885                 890                 895
Glu Pro Tyr Leu Ala Met Phe Gly Gln Val Pro Ser Asp Val Asp Gly
            900                 905                 910
Thr Thr Tyr Asp Phe Ala His Cys Thr Phe Thr Gly Asn Glu Ser Lys
            915                 920                 925
Pro Leu Cys Val Glu Leu Asp Glu His Asn Leu Pro Arg Phe Pro Glu
        930                 935                 940
Trp Ile Thr Ile Pro Leu Val Cys Ile Tyr Met Leu Ser Thr Asn Ile
945                 950                 955                 960
Leu Leu Val Asn Leu Leu Val Ala Met Phe Gly Tyr Thr Val Gly Thr
                965                 970                 975
Val Gln Glu Asn Asn Asp Gln Val Trp Lys Phe Gln Arg Tyr Phe Leu
            980                 985                 990
Val Gln Glu Tyr Cys Ser Arg Leu Asn Ile Pro Phe Pro Phe Ile Val
            995                 1000                1005
Phe Ala Tyr Phe Tyr Met Val Val Lys Lys Cys Phe Lys Cys Cys Cys
        1010                1015                1020
Lys Glu Lys Asn Met Glu Ser Ser Val Cys Cys Phe Lys Asn Glu Asp
1025                1030                1035                1040
Asn Glu Thr Leu Ala Trp Glu Gly Val Met Lys Glu Asn Tyr Leu Val
                1045                1050                1055
Lys Ile Asn Thr Lys Ala Asn Asp Thr Ser Glu Glu Met Arg His Arg
            1060                1065                1070
Phe Arg Gln Leu Asp Thr Lys Leu Asn Asp Leu Lys Gly Leu Leu Lys
        1075                1080                1085
Glu Ile Ala Asn Lys Ile Lys
        1090                1095 ·
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<210> 781
<211> 15
<212> PRT
<213> Homo sapiens

<400> 781

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Arg Met Pro Thr Val Leu Gln Cys Val Asn Val Ser Val Val Ser
                5                 10                15
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<210> 782
<211> 45
<212> DNA
<213> Homo sapiens

<400> 782

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agaatgccta ccgtgctgca gtgcgtgaac gtgtcggtgg tgtct                45


<210> 783
<211> 45
<212> DNA
<213> Homo sapiens

<400> 783
gagccaggga gccagatggt ggaggccagc ctctccgtac ggcac                45


<210> 784
<211> 45
<212> DNA
<213> Homo sapiens

<400> 784
gaggccgacc aagagccagg gagccagatg gtggaggcca gcctc                45


<210> 785
<211> 45
<212> DNA
<213> Homo sapiens

<400> 785
ggcctgcaca gtcttgaggc cgaccaagag ccagggagcc agatg                45


<210> 786
<211> 45
<212> DNA
<213> Homo sapiens

<400> 786
tacaccatcg ggctgggcct gcacagtctt gaggccgacc aagag                45


<210> 787
<211> 42
<212> DNA
<213> Homo sapiens

<400> 787
ttccagaact cctacaccat cgggctgggc ctgcacagtc tt                   42


<210> 788
<211> 45
<212> DNA
<213> Homo sapiens

<400> 788
ctgtcagccg cacactgttt ccagaactcc tacaccatcg ggctg                45


<210> 789
<211> 45
<212> DNA
<213> Homo sapiens

<400> 789
catccgcagt gggtgctgtc agccgcacac tgtttccaga actcc                45
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298

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<210> 790
<211> 45
<212> DNA
<213> Homo sapiens

<400> 790
tcgggcgtcc tggtgcatcc gcagtgggtg ctgtcagccg cacac              45

<210> 791
<211> 45
<212> DNA
<213> Homo sapiens

<400> 791
aacgaattgt tctgctcggg cgtcctggtg catccgcagt gggtg              45

<210> 792
<211> 45
<212> DNA
<213> Homo sapiens

<400> 792
gcactggtca tggaaaacga attgttctgc tcgggcgtcc tggtg              45

<210> 793
<211> 51
<212> DNA
<213> Homo sapiens

<400> 793
tcgcagccct ggcaggcggc actggtcatg gaaaacgaat tgttctgctc g       51

<210> 794
<211> 45
<212> DNA
<213> Homo sapiens

<400> 794
atcagcattg cttcgcagtg ccctaccgcg gggaactctt gcctc              45

<210> 795
<211> 45
<212> DNA
<213> Homo sapiens

<400> 795
tccgtgtccg agtctgacac catccggagc atcagcattg cttcg              45

<210> 796
<211> 45
<212> DNA
<213> Homo sapiens

<400> 796
atcaagttgg acgaatccgt gtccgagtct gacaccatcc ggagc              45

<210> 797
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299

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<211> 45
<212> DNA
<213> Homo sapiens

<400> 797
aacgacctca tgctcatcaa gttggacgaa tccgtgtccg agtct                    45

<210> 798
<211> 45
<212> DNA
<213> Homo sapiens

<400> 798
agacccttgc tcgctaacga cctcatgctc atcaagttgg acgaa                    45

<210> 799
<211> 15
<212> PRT
<213> Homo sapiens

<400> 799
Glu Pro Gly Ser Gln Met Val Glu Ala Ser Leu Ser Val Arg His
                5                  10                  15


<210> 800
<211> 15
<212> PRT
<213> Homo sapiens

<400> 800
Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val Glu Ala Ser Leu
                5                  10                  15


<210> 801
<211> 15
<212> PRT
<213> Homo sapiens

<400> 801
Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met
                5                  10                  15


<210> 802
<211> 15
<212> PRT
<213> Homo sapiens

<400> 802
Tyr Thr Ile Gly Leu Gly Leu His Ser Leu Glu Ala Asp Gln Glu
                5                  10                  15


<210> 803
<211> 14
<212> PRT
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300

<213> Homo sapiens

<400> 803
Phe Gln Asn Ser Tyr Thr Ile Gly Leu Gly Leu His Ser Leu
                  5   10

<210> 804
<211> 15
<212> PRT
<213> Homo sapiens

<400> 804
Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu
                  5   10   15

<210> 805
<211> 15
<212> PRT
<213> Homo sapiens

<400> 805
His Pro Gln Trp Val Leu Ser Ala Ala His Cys Phe Gln Asn Ser
                  5   10   15

<210> 806
<211> 15
<212> PRT
<213> Homo sapiens

<400> 806
Ser Gly Val Leu Val His Pro Gln Trp Val Leu Ser Ala Ala His
                  5   10   15

<210> 807
<211> 15
<212> PRT
<213> Homo sapiens

<400> 807
Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln Trp Val
                  5   10   15

<210> 808
<211> 15
<212> PRT
<213> Homo sapiens

<400> 808
Ala Leu Val Met Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val
                  5   10   15

<210> 809

301

```
<211> 17
<212> PRT
<213> Homo sapiens

<400> 809
Ser Gln Pro Trp Gln Ala Ala Leu Val Met Glu Asn Glu Leu Phe Cys
                 5                  10                  15

Ser


<210> 810
<211> 15
<212> PRT
<213> Homo sapiens

<400> 810
Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly Asn Ser Cys Leu
                 5                  10                  15


<210> 811
<211> 15
<212> PRT
<213> Homo sapiens

<400> 811
Ser Val Ser Glu Ser Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser
                 5                  10                  15


<210> 812
<211> 15
<212> PRT
<213> Homo sapiens

<400> 812
Ile Lys Leu Asp Glu Ser Val Ser Glu Ser Asp Thr Ile Arg Ser
                 5                  10                  15


<210> 813
<211> 15
<212> PRT
<213> Homo sapiens

<400> 813
Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser
                 5                  10                  15


<210> 814
<211> 15
<212> PRT
<213> Homo sapiens

<400> 814
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302

Arg Pro Leu Leu Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu
                5   10   15

<210> 815
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 815
ggaccagcat atgaggaaca gaaggaatga cactc   35

<210> 816
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 816
ccgctcgagt ccaccccaag cttcacagg   29

<210> 817
<211> 1959
<212> DNA
<213> Homo sapiens

<400> 817
atgaggaaca gaaggaatga cactctggac agcacccgga ccctgtactc cagcgcgtct 60
cggagcacag acttgtctta cagtgaaagc gacttggtga attttattca agcaaatttt 120
aagaaacgag aatgtgtctt ctttaccaaa gattccaagg ccacggagaa tgtgtgcaag 180
tgtggctatg cccagagcca gcacatggaa ggcacccaga tcaaccaaag tgagaaatgg 240
aactacaaga aacacaccaa ggaatttcct accgacgcct ttggggatat tcagtttgag 300
acactgggga agaaagggaa gtatatacgt ctgtcctgcg acacggacgc ggaaatcctt 360
tacgagctgc tgacccagca ctggcacctg aaaacaccca acctggtcat ttctgtgacc 420
gggggcgcca agaacttcgc cctgaagccg cgcatgcgca agatcttcag ccggctcatc 480
tacatcgcgc agtccaaagg tgcttggatt ctcacgggag gcacccatta tggcctgatg 540
aagtacatcg gggaggtggt gagagataac accatcagca ggagttcaga ggagaatatt 600
gtggccattg gcatagcagc ttggggcatg gtctccaacc gggacaccct catcaggaat 660
tgcgatgctg agggctattt tttagcccag taccttatgg atgacttcac aagagatcca 720
ctgtatatcc tggacaacaa ccacacacat ttgctgctcg tggacaatgg ctgtcatgga 780
catcccactg tcgaagcaaa gctccggaat cagctagaga agtatatctc tgagcgcact 840
attcaagatt ccaactatgg tggcaagatc cccattgtgt gttttgccca aggaggtgga 900
aaagagactt tgaaagccat caatacctcc atcaaaaata aaattccttg tgtggtggtg 960
gaaggctcgg gccagatcgc tgatgtgatc gctagcctgg tggaggtgga ggatgccctg 1020
acatcttctg ccgtcaagga gaagctggtg cgcttttttac cccgcacggt gtccggctg 1080
cctgaggagg agactgagag ttggatcaaa tggctcaaag aaattctcga atgttctcac 1140
ctattaacag ttattaaaat ggaagaagct ggggatgaaa ttgtgagcaa tgccatctcc 1200
tacgctctat acaaagcctt cagcaccagt gagcaagaca aggataactg gaatgggcag 1260
ctgaagcttc tgctggagtg gaaccagctg gacttagcca atgatgagat tttcaccaat 1320
gaccgccgat gggagtctgc tgaccttcaa gaagtcatgt ttacggctct cataaaggac 1380
agacccaagt ttgtccgcct ctttctggag aatggcttga acctacggaa gtttctcacc 1440
catgatgtcc tcactgaact cttctccaac cacttcagca cgcttgtgta ccggaatctg 1500

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cagatcgcca agaattccta taatgatgcc ctcctcacgt ttgtctggaa actggttgcg 1560
aacttccgaa gaggcttccg gaaggaagac agaaatggcc gggacgagat ggacatagaa 1620
ctccacgacg tgtctcctat tactcggcac cccctgcaag ctctcttcat ctgggccatt 1680
cttcagaata agaaggaact ctccaaagtc atttgggagc agaccagggg ctgcactctg 1740
gcagccctgg gagccagcaa gcttctgaag actctggcca aagtgaagaa cgacatcaat 1800
gctgctgggg agtccgagga gctggctaat gagtacgaga cccgggctgt tgagctgttc 1860
actgagtgtt acagcagcga tgaagacttg gcagaacagc tgctggtcta ttcctgtgaa 1920
gcttggggtg gactcgagca ccaccaccac caccactga                         1959
```

<210> 818
<211> 652
<212> PRT
<213> Homo sapiens

<400> 818

```
Met Arg Asn Arg Arg Asn Asp Thr Leu Asp Ser Thr Arg Thr Leu Tyr
                5                   10                  15
Ser Ser Ala Ser Arg Ser Thr Asp Leu Ser Tyr Ser Glu Ser Asp Leu
            20                      25                  30
Val Asn Phe Ile Gln Ala Asn Phe Lys Lys Arg Glu Cys Val Phe Phe
        35                      40                  45
Thr Lys Asp Ser Lys Ala Thr Glu Asn Val Cys Lys Cys Gly Tyr Ala
    50                      55                  60
Gln Ser Gln His Met Glu Gly Thr Gln Ile Asn Gln Ser Glu Lys Trp
65                      70                  75                  80
Asn Tyr Lys Lys His Thr Lys Glu Phe Pro Thr Asp Ala Phe Gly Asp
                85                  90                  95
Ile Gln Phe Glu Thr Leu Gly Lys Lys Gly Lys Tyr Ile Arg Leu Ser
            100                 105                 110
Cys Asp Thr Asp Ala Glu Ile Leu Tyr Glu Leu Leu Thr Gln His Trp
        115                 120                 125
His Leu Lys Thr Pro Asn Leu Val Ile Ser Val Thr Gly Gly Ala Lys
    130                 135                 140
Asn Phe Ala Leu Lys Pro Arg Met Arg Lys Ile Phe Ser Arg Leu Ile
145                 150                 155                 160
Tyr Ile Ala Gln Ser Lys Gly Ala Trp Ile Leu Thr Gly Gly Thr His
            165                 170                 175
Tyr Gly Leu Met Lys Tyr Ile Gly Glu Val Val Arg Asp Asn Thr Ile
            180                 185                 190
Ser Arg Ser Ser Glu Glu Asn Ile Val Ala Ile Gly Ile Ala Ala Trp
        195                 200                 205
Gly Met Val Ser Asn Arg Asp Thr Leu Ile Arg Asn Cys Asp Ala Glu
    210                 215                 220
Gly Tyr Phe Leu Ala Gln Tyr Leu Met Asp Asp Phe Thr Arg Asp Pro
225                 230                 235                 240
Leu Tyr Ile Leu Asp Asn Asn His Thr His Leu Leu Leu Val Asp Asn
                245                 250                 255
Gly Cys His Gly His Pro Thr Val Glu Ala Lys Leu Arg Asn Gln Leu
            260                 265                 270
Glu Lys Tyr Ile Ser Glu Arg Thr Ile Gln Asp Ser Asn Tyr Gly Gly
        275                 280                 285
Lys Ile Pro Ile Val Cys Phe Ala Gln Gly Gly Gly Lys Glu Thr Leu
    290                 295                 300
Lys Ala Ile Asn Thr Ser Ile Lys Asn Lys Ile Pro Cys Val Val Val
305                 310                 315                 320
Glu Gly Ser Gly Gln Ile Ala Asp Val Ile Ala Ser Leu Val Glu Val
            325                 330                 335
Glu Asp Ala Leu Thr Ser Ser Ala Val Lys Glu Lys Leu Val Arg Phe
```

304

```
                 340                      345                      350
Leu Pro Arg Thr Val Ser Arg Leu Pro Glu Glu Glu Thr Glu Ser Trp
        355                      360                      365
Ile Lys Trp Leu Lys Glu Ile Leu Glu Cys Ser His Leu Leu Thr Val
        370                      375                      380
Ile Lys Met Glu Glu Ala Gly Asp Glu Ile Val Ser Asn Ala Ile Ser
385                      390                      395                      400
Tyr Ala Leu Tyr Lys Ala Phe Ser Thr Ser Glu Gln Asp Lys Asp Asn
                405                      410                      415
Trp Asn Gly Gln Leu Lys Leu Leu Glu Trp Asn Gln Leu Asp Leu
                420                      425                      430
Ala Asn Asp Glu Ile Phe Thr Asn Asp Arg Arg Trp Glu Ser Ala Asp
        435                      440                      445
Leu Gln Glu Val Met Phe Thr Ala Leu Ile Lys Asp Arg Pro Lys Phe
        450                      455                      460
Val Arg Leu Phe Leu Glu Asn Gly Leu Asn Leu Arg Lys Phe Leu Thr
465                      470                      475                      480
His Asp Val Leu Thr Glu Leu Phe Ser Asn His Phe Ser Thr Leu Val
                485                      490                      495
Tyr Arg Asn Leu Gln Ile Ala Lys Asn Ser Tyr Asn Asp Ala Leu Leu
                500                      505                      510
Thr Phe Val Trp Lys Leu Val Ala Asn Phe Arg Arg Gly Phe Arg Lys
        515                      520                      525
Glu Asp Arg Asn Gly Arg Asp Glu Met Asp Ile Glu Leu His Asp Val
        530                      535                      540
Ser Pro Ile Thr Arg His Pro Leu Gln Ala Leu Phe Ile Trp Ala Ile
545                      550                      555                      560
Leu Gln Asn Lys Lys Glu Leu Ser Lys Val Ile Trp Glu Gln Thr Arg
                565                      570                      575
Gly Cys Thr Leu Ala Ala Leu Gly Ala Ser Lys Leu Leu Lys Thr Leu
                580                      585                      590
Ala Lys Val Lys Asn Asp Ile Asn Ala Ala Gly Glu Ser Glu Glu Leu
        595                      600                      605
Ala Asn Glu Tyr Glu Thr Arg Ala Val Glu Leu Phe Thr Glu Cys Tyr
        610                      615                      620
Ser Ser Asp Glu Asp Leu Ala Glu Gln Leu Leu Val Tyr Ser Cys Glu
625                      630                      635                      640
Ala Trp Gly Gly Leu Glu His His His His His His
                645                      650
```

<210> 819
<211> 132
<212> PRT
<213> Homo sapien

<400> 819
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Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe
1               5               10              15
Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser
        20              25              30
Gly Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly
        35              ᵢ 40             45
Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val
        50              55              60
Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val
65              70              75              80
Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala
```

305

```
                          85                 90                 95
       Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Asn Trp
                     100                 105                 110
       Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu
                 115                 120                 125
       Gly Pro Pro Ala
          130
```

<210> 820
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 820
ggggaattca tgatccggga gaaatttgcc cactgc   36

<210> 821
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 821
gggctcgagt caggagtttg agaccagcct ggc   33

<210> 822
<211> 675
<212> DNA
<213> Homo sapiens

<400> 822
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atgcatcacc atcaccatca cacggccgcg tccgataact tccagctgtc ccagggtggg 60
cagggattcg ccattccgat cgggcaggcg atggcgatcg cgggccagat caagcttccc 120
accgttcata tcgggcctac cgccttcctc ggcttgggtg ttgtcgacaa caacggcaac 180
ggcgcacgag tccaacgcgt ggtcgggagc gctccggcgg caagtctcgg catctccacc 240
ggcgacgtga tcaccgcggt cgacggcgct ccgatcaact cggccaccgc gatggcggac 300
gcgcttaacg ggcatcatcc cggtgacgtc atctcggtga cctggcaaac caagtcgggc 360
ggcacgcgta cagggaacgt gacattggcc gagggacccc cggccgaatt catgatccgg 420
gagaaatttg cccactgcac cgtgctaacc attgcacaca gattgaacac cattattgac 480
agcgacaaga taatggtttt agattcagga agactgaaag aatatgatga gccgtatgtt 540
ttgctgcaaa ataaagagag cctatttttac aagatggtgc aacaactggg caaggcagaa 600
gccgctgccc tcactgaaac agcaaaacag agatgggggtt tcaccatgtt ggccaggctg 660
gtctcaaact cctga                                                    675
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<210> 823
<211> 291
<212> DNA
<213> Homo sapiens

306

<400> 823
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atggggatcc gggagaaatt tgcccactgc accgtgctaa ccattgcaca cagattgaac 60
accattattg acagcgacaa gataatggtt ttagattcag gaagactgaa agaatatgat 120
gagccgtatg ttttgctgca aaataaagag agcctatttt acaagatggt gcaacaactg 180
ggcaaggcag aagccgctgc cctcactgaa acagcaaaac agagatgggg tttcaccatg 240
ttggccaggc tggtctcaaa ctccctcgag caccaccacc accaccactg a         291
```

<210> 824
<211> 1074
<212> DNA
<213> Homo sapiens

<400> 824
```
atgtcagcca ttgagagggt gtcagaggca atcgtcagca tccgaagaat ccagaccttt. 60
ttgctacttg atgagatatc acagcgcaac cgtcagctgc cgtcagatgg taaaaagatg 120
gtgcatgtgc aggattttac tgctttttgg gataaggcat cagagacccc aactctacaa 180
ggccttttcct ttactgtcag acctggcgaa ttgttagctg tggtcggccc cgtgggagca 240
gggaagtcat cactgttaag tgccgtgctc ggggaattgg ccccaagtca cgggctggtc 300
agcgtgcatg gaagaattgc ctatgtgtct cagcagccct gggtgttctc gggaactctg 360
aggagtaata tttttatttgg gaagaaatac gaaaaggaac gatatgaaaa agtcataaag 420
gcttgtgctc tgaaaaagga tttacagctg ttggaggatg gtgatctgac tgtgatagga 480
gatcggggaa ccacgctgag tggagggcag aaagcacggg taaaccttgc aagagcagtg 540
tatcaagatg ctgacatctca tctcctggac gatcctctca gtgcagtaga tgcggaagtt 600
agcagacact tgttcgaact gtgtatttgt caaattttgc atgagaagat cacaatttta 660
gtgactcatc agttgcagta cctcaaagct gcaagtcaga ttctgatatt gaaagatggt 720
aaaatggtgc agaaggggac ttacactgag ttcctaaaat ctggtataga tttttggctcc 780
cttttaaaga aggataatga ggaaagtgaa caacctccag ttccaggaac tcccacacta 840
aggaatcgta ccttctcaga gtcttcggtt tggtctcaac aatcttctag accctccttg 900
aaagatggtg ctctggagag ccaagataca gagaatgtcc cagttacact atcagaggag 960
aaccgttctg aaggaaaagt tggttttcag gcctataaga attacttcag agctggtgct 1020
cactggattg tcttcatttt ccttattctc gagcaccacc accaccacca ctga    1074
```

<210> 825
<211> 224
<212> PRT
<213> Homo sapiens

<400> 825
```
Met His His His His His Thr Ala Ala Ser Asp Asn Phe Gln Leu
              5                  10                  15
Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala
          20                  25                  30
Ile Ala Gly Gln Ile Lys Leu Pro Thr Val His Ile Gly Pro Thr Ala
          35                  40                  45
Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val
      50                  55                  60
Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr
65                  70                  75                  80
Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr
                  85                  90                  95
Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser
              100                 105                 110
Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr
          115                 120                 125
Leu Ala Glu Gly Pro Pro Ala Glu Phe Met Ile Arg Glu Lys Phe Ala
      130                 135                 140
His Cys Thr Val Leu Thr Ile Ala His Arg Leu Asn Thr Ile Ile Asp
```

307

```
145                    150                    155                    160
Ser Asp Lys Ile Met Val Leu Asp Ser Gly Arg Leu Lys Glu Tyr Asp
                165                    170                    175
Glu Pro Tyr Val Leu Leu Gln Asn Lys Glu Ser Leu Phe Tyr Lys Met
                180                    185                    190
Val Gln Gln Leu Gly Lys Ala Glu Ala Ala Ala Leu Thr Glu Thr Ala
            195                    200                    205
Lys Gln Arg Trp Gly Phe Thr Met Leu Ala Arg Leu Val Ser Asn Ser
    210                    215                    220
```

```
<210> 826
<211> 357
<212> PRT
<213> Homo sapiens
```

```
<400> 826
Met Ser Ala Ile Glu Arg Val Ser Glu Ala Ile Val Ser Ile Arg Arg
                5                    10                    15
Ile Gln Thr Phe Leu Leu Leu Asp Glu Ile Ser Gln Arg Asn Arg Gln
            20                    25                    30
Leu Pro Ser Asp Gly Lys Lys Met Val His Val Gln Asp Phe Thr Ala
        35                    40                    45
Phe Trp Asp Lys Ala Ser Glu Thr Pro Thr Leu Gln Gly Leu Ser Phe
    50                    55                    60
Thr Val Arg Pro Gly Glu Leu Leu Ala Val Val Gly Pro Val Gly Ala
65                    70                    75                    80
Gly Lys Ser Ser Leu Leu Ser Ala Val Leu Gly Glu Leu Ala Pro Ser
            85                    90                    95
His Gly Leu Val Ser Val His Gly Arg Ile Ala Tyr Val Ser Gln Gln
            100                    105                    110
Pro Trp Val Phe Ser Gly Thr Leu Arg Ser Asn Ile Leu Phe Gly Lys
        115                    120                    125
Lys Tyr Glu Lys Glu Arg Tyr Glu Lys Val Ile Lys Ala Cys Ala Leu
    130                    135                    140
Lys Lys Asp Leu Gln Leu Leu Glu Asp Gly Asp Leu Thr Val Ile Gly
145                    150                    155                    160
Asp Arg Gly Thr Thr Leu Ser Gly Gly Gln Lys Ala Arg Val Asn Leu
            165                    170                    175
Ala Arg Ala Val Tyr Gln Asp Ala Asp Ile Tyr Leu Leu Asp Asp Pro
        180                    185                    190
Leu Ser Ala Val Asp Ala Glu Val Ser Arg His Leu Phe Glu Leu Cys
    195                    200                    205
Ile Cys Gln Ile Leu His Glu Lys Ile Thr Ile Leu Val Thr His Gln
    210                    215                    220
Leu Gln Tyr Leu Lys Ala Ala Ser Gln Ile Leu Ile Leu Lys Asp Gly
225                    230                    235                    240
Lys Met Val Gln Lys Gly Thr Tyr Thr Glu Phe Leu Lys Ser Gly Ile
            245                    250                    255
Asp Phe Gly Ser Leu Leu Lys Lys Asp Asn Glu Glu Ser Glu Gln Pro
            260                    265                    270
Pro Val Pro Gly Thr Pro Thr Leu Arg Asn Arg Thr Phe Ser Glu Ser
    275                    280                    285
Ser Val Trp Ser Gln Gln Ser Ser Arg Pro Ser Leu Lys Asp Gly Ala
    290                    295                    300
Leu Glu Ser Gln Asp Thr Glu Asn Val Pro Val Thr Leu Ser Glu Glu
305                    310                    315                    320
Asn Arg Ser Glu Gly Lys Val Gly Phe Gln Ala Tyr Lys Asn Tyr Phe
```

308

```
                        325                 330                 335
Arg Ala Gly Ala His Trp Ile Val Phe Ile Phe Leu Ile Leu Glu His
            340                 345                 350
His His His His His
            355


<210> 827
<211> 96
<212> PRT
<213> Homo sapiens

<400> 827
Met Gly Ile Arg Glu Lys Phe Ala His Cys Thr Val Leu Thr Ile Ala
                5                  10                  15
His Arg Leu Asn Thr Ile Ile Asp Ser Asp Lys Ile Met Val Leu Asp
            20                  25                  30
Ser Gly Arg Leu Lys Glu Tyr Asp Glu Pro Tyr Val Leu Leu Gln Asn
        35                  40                  45
Lys Glu Ser Leu Phe Tyr Lys Met Val Gln Gln Leu Gly Lys Ala Glu
    50                  55                  60
Ala Ala Ala Leu Thr Glu Thr Ala Lys Gln Arg Trp Gly Phe Thr Met
65                  70                  75                  80
Leu Ala Arg Leu Val Ser Asn Ser Leu Glu His His His His His His
                85                  90                  95


<210> 828
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 828
cgcccatggg gatccgggag aaatttgccc actgc                              35


<210> 829
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 829
cgcctcgagg gagtttgaga ccagcctggc caaca                              35


<210> 830
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 830
```

309

```
gcatggacca tatgtcagcc attgagaggg tgtcagag                        38


<210> 831
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 831
ccgctcgaga ataaggaaaa tgaagacaat ccag                           34


<210> 832
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 832
gttgaattca tgcacgggcc ccaggtg                                   27


<210> 833
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 833
cccctcgagt cactatggtc tgcctcttga                                30


<210> 834
<211> 915
<212> DNA
<213> Homo sapiens

<400> 834
atgcatcacc atcaccatca cacggccgcg tccgataact tccagctgtc ccagggtggg 60
cagggattcg ccattccgat cgggcaggcg atggcgatcg cgggccagat caagcttccc 120
accgttcata tcgggcctac cgccttcctc ggcttgggtg ttgtcgacaa caacggcaac 180
ggcgcacgag tccaacgcgt ggtcgggagc gctccggcgg caagtctcgg catctccacc 240
ggcgacgtga tcaccgcggt cgacggcgct ccgatcaact cggccaccgc gatggcggac 300
gcgcttaacg ggcatcatcc cggtgacgtc atctcggtga cctggcaaac caagtcgggc 360
ggcacgcgta cagggaacgt gacattggcc gagggacccc cggccgaatt catgcacggg 420
ccccaggtgc tggcacgctg ctccgagtgt gcttgtcctg ccttggctgc cacctctgcg 480
ggggtgcgtc tggagggggt ggaccggcca ccaaccttac ccagtcaagg aagtggatgg 540
ccatgttccc acagcctgag tggctgccac ctgatggctg atggagcaaa ggccttagga 600
aaagcagatg gcccttggcc ctaccttttt gttagaagaa ctgatgttcc atgtcctgca 660
gcgagtgagg ttggtggctg tgcccccagc tcctggcgcg ccctcgcaga ggtgactggt 720
tgctctttgg gccctcttgg ccttgcccag catgcacaag cctcagtgct actactgtgc 780
```

310

```
tacaaatgga gccatatagg ggaaacgagc agccatctca ggagcaaggt gtatgctgcc 840
tttggggggct ccagtccttg cctcaagggt cttatgtcac tgtgggcttc ttggttgtca 900
agaggcagac catag                                                  915
```

<210> 835
<211> 304
<212> PRT
<213> Homo sapiens

<400> 835

| Met | His | His | His | His | His | His | Thr | Ala | Ala | Ser | Asp | Asn | Phe | Gln | Leu |
| | | | 5 | | | | | | 10 | | | | | | 15 |

Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala
        20   25   30

Ile Ala Gly Gln Ile Lys Leu Pro Thr Val His Ile Gly Pro Thr Ala
    35   40   45

Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val
    50   55   60

Gln Arg Val Val Gly Ser Ala Pro Ala-Ala Ser Leu Gly Ile Ser Thr
65   70   75   80

Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr
            85   90   95

Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser
        100   105   110

Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr
    115   120   125

Leu Ala Glu Gly Pro Pro Ala Glu Phe Met His Gly Pro Gln Val Leu
    130   135   140

Ala Arg Cys Ser Glu Cys Ala Cys Pro Ala Leu Ala Ala Thr Ser Ala
145   150   155   160

Gly Val Arg Leu Glu Gly Val Asp Arg Pro Pro Thr Leu Pro Ser Gln
            165   170   175

Gly Ser Gly Trp Pro Cys Ser His Ser Leu Ser Gly Cys His Leu Met
        180   185   190

Ala Asp Gly Ala Lys Ala Leu Gly Lys Ala Asp Gly Pro Trp Pro Tyr
        195   200   205

Leu Phe Val Arg Arg Thr Asp Val Pro Cys Pro Ala Ala Ser Glu Val
    210   215   220

Gly Gly Cys Ala Pro Ser Ser Trp Arg Ala Leu Ala Glu Val Thr Gly
225   230   235   240

Cys Ser Leu Gly Pro Leu Gly Leu Ala Gln His Ala Gln Ala Ser Val
            245   250   255

Leu Leu Leu Cys Tyr Lys Trp Ser His Ile Gly Glu Thr Ser Ser His
        260   265   270

Leu Arg Ser Lys Val Tyr Ala Ala Phe Gly Gly Ser Ser Pro Cys Leu
    275   280   285

Lys Gly Leu Met Ser Leu Trp Ala Ser Trp Leu Ser Arg Gly Arg Pro
    290   295   300

<210> 836
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 836

311

```
cgaagtcacg tggaggccag cctc                                              24


<210> 837
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 837
cctgaccgaa ttcattaact ggcctggac                                        29


<210> 838
<211> 166
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (1)...(166)
<223> Xaa = Any Amino Acid

<400> 838
Met Gly His His His His His His Val Glu Ala Ser Leu Ser Val Arg
1               5                   10                  15
His Pro Glu Tyr Asn Arg Pro Leu Leu Ala Asn Asp Leu Met Leu Ile
            20                  25                  30
Lys Leu Asp Glu Ser Val Ser Glu Ser Asp Thr Ile Arg Ser Ile Ser
        35                  40                  45
Ile Ala Ser Gln Cys Pro Thr Ala Gly Asn Ser Cys Leu Val Ser Gly
    50                  55                  60
Trp Gly Leu Leu Ala Asn Gly Arg Met Pro Thr Val Leu Gln Cys Val
65                  70                  75·                 80
Asn Val Ser Val Val Ser Glu Glu Val Cys Ser Lys Leu Tyr Asp Pro
                85                  90                  95
Leu Tyr His Pro Ser Met Phe Cys Ala Gly Gly Gly Gln Xaa Gln Xaa
            100                 105                 110
Asp Ser Cys Asn Gly Asp Ser Gly Gly Pro Leu Ile Cys Asn Gly Tyr
        115                 120                 125
Leu Gln Gly Leu Val Ser Phe Gly Lys Ala Pro Cys Gly Gln Val Gly
    130                 135                 140
Val Pro Gly Val Tyr Thr Asn Leu Cys Lys Phe Thr Glu Trp Ile Glu
145                 150                 155                 160
Lys Thr Val Gln Ala Ser
                165


<210> 839
<211> 504
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(504)
<223> n = A,T,C or G
```

312

```
<400> 839
atgggccatc atcatcatca tcacgtggag gccagcctct ccgtacggca cccagagtac      60
aacagaccct tgctcgctaa cgacctcatg ctcatcaagt tggacgaatc cgtgtccgag     120
tctgacacca tccggagcat cagcattgct tcgcagtgcc ctaccgcggg gaactcttgc     180
ctcgtttctg gctggggtct gctggcgaac ggcagaatgc ctaccgtgct gcagtgcgtg     240
aacgtgtcgg tggtgtctga ggaggtctgc agtaagctct atgacccgct gtaccacccc     300
agcatgttct gcgccggcgg agggcaanac cagaangact cctgcaacgg tgactctggg     360
gggcccctga tctgcaacgg gtacttgcag ggccttgtgt ctttcggaaa agccccgtgt     420
ggccaagttg gcgtgccagg tgtctacacc aacctctgca aattcactga gtggatagag     480
aaaaccgtcc aggccagtta atga                                           504
```

```
<210> 840
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 840
ctcagggttc cggagccgcg g                                               21
```

```
<210> 841
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 841
ctatagaatt cattaccaaa aagctgggct ccagc                                35
```

```
<210> 842
<211> 241
<212> PRT
<213> Homo sapiens

<400> 842
Met Gln His His His His His Leu Arg Val Pro Glu Pro Arg Pro
1               5                   10                  15
Gly Glu Ala Lys Ala Glu Gly Ala Ala Pro Pro Thr Pro Ser Lys Pro
            20              25              30
Leu Thr Ser Phe Leu Ile Gln Asp Ile Leu Arg Asp Gly Ala Gln Arg
            35              40              45
Gln Gly Gly Arg Thr Ser Ser Gln Arg Gln Arg Asp Pro Glu Pro Glu
        50              55              60
Pro Glu Pro Glu Pro Glu Gly Gly Arg Ser Arg Ala Gly Ala Gln Asn
65              70              75              80
Asp Gln Leu Ser Thr Gly Pro Arg Ala Ala Pro Glu Glu Ala Glu Thr
                85              90              95
Leu Ala Glu Thr Glu Pro Glu Arg His Leu Gly Ser Tyr Leu Leu Asp
            100             105             110
Ser Glu Asn Thr Ser Gly Ala Leu Pro Arg Leu Pro Gln Thr Pro Lys
        115             120             125
```

313

```
Gln Pro Gln Lys Arg Ser Arg Ala Ala Phe Ser His Thr Gln Val Ile
    130                 135                 140
Glu Leu Glu Arg Lys Phe Ser His Gln Lys Tyr Leu Ser Ala Pro Glu
145                 150                 155         ·           160
Arg Ala His Leu Ala Lys Asn Leu Lys Leu Thr Glu Thr Gln Val Lys
                165                 170                 175
Ile Trp Phe Gln Asn Arg Arg Tyr Lys Thr Lys Arg Lys Gln Leu Ser
                180                 185                 190
Ser Glu Leu Gly Asp Leu Glu Lys His Ser Ser Leu Pro Ala Leu Lys
            195                 200                 205
Glu Glu Ala Phe Ser Arg Ala Ser Leu Val Ser Val Tyr Asn Ser Tyr
    210                 215                 220
Pro Tyr Tyr Pro Tyr Leu Tyr Cys Val Gly Ser Trp Ser Pro Ala Phe
225                 230                 235                 240
Trp
```

```
<210> 843
<211> 729
<212> DNA
<213> Homo sapiens

<400> 843
atgcagcatc accaccatca ccacctcagg gttccggagc cgcggcccgg ggaggcgaaa      60
gcggaggggg ccgcgccgcc gaccccgtcc aagccgctca cgtccttcct catccaggac     120
atcctgcggg acggcgcgca gcggcaaggc ggccgcacga gcagccagag acagcgcgac     180
ccggagccgg agccagagcc agagccagag ggaggacgca gccgcgccgg ggcgcagaac     240
gaccagctga gcaccgggcc ccgcgccgcg ccggatgagg ccgagacgct ggcagagacc     300
gagccagaaa ggcacttggg gtcttatctg ttggactctg aaaacacttc aggcgccctt     360
ccaaggcttc cccaaacccc taagcagccg cagaagcgct cccgagctgc cttctcccac     420
actcaggtga tcgagttgga gaggaagttc agccatcaga gtacctgtc ggcccctgaa      480
cgggcccacc tggccaagaa cctcaagctc acggagaccc aagtgaagat atggttccag     540
aacagacgct ataagactaa gcgaaagcag ctctcctcgg agctgggaga cttggagaag     600
cactcctttt tgccggccct gaaagaggag gccttctccc gggcctccct ggtctccgtg     660
tataacagct atccttacta cccatacctg cactgcgtgg gcagctggag cccagctttt     720
tggtaatga                                                           729
```

```
<210> 844
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 844
ctactaagcg ctggagtgag ggatcag                                        27
```

```
<210> 845
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer
```

314

<400> 845
catcgagaat tcactactct ctgactagat gtc   33

<210> 846
<211> 161
<212> PRT
<213> Homo sapiens

<400> 846
Met Gln His His His His His Ala Gly Val Arg Asp Gln Gly Gln
1   5   10   15
Gly Ala Arg Trp Pro His Thr Gly Lys Arg Gly Pro Leu Leu Gln Gly
            20   25   30
Leu Thr Trp Ala Thr Gly Gly His Cys Phe Ser Ser Glu Glu Ser Gly
            35   40   45
Ala Val Asp Gly Ala Gly Gln Lys Lys Asp Arg Ala Trp Leu Arg Cys
        50   55   60
Pro Glu Ala Val Ala Gly Phe Pro Leu Gly Ser Asp Cys Arg Glu Gly
65   70   75   80
Gly Arg Gln Gly Cys Gly Gly Ser Asp Asp Glu Asp Asp Leu Gly Val
                85   90   95
Ala Pro Gly Leu Ala Pro Ala Trp Ala Leu Thr Gln Pro Pro Ser Gln
            100   105   110
Ser Pro Gly Pro Gln Ser Leu Pro Ser Thr Pro Ser Ser Ile Trp Pro
            115   120   125
Gln Trp Val Ile Leu Ile Thr Glu Leu Thr Ile Pro Ser Pro Ala His
    130   135   140
Gly Pro Pro Trp Leu Pro Asn Ala Leu Glu Arg Gly His Leu Val Arg
145   150   155   160
Glu

<210> 847
<211> 489
<212> DNA
<213> Homo sapiens

<400> 847
atgcagcatc accaccatca ccacgctgga gtgagggatc aggggcaggg cgcgagatgg   60
cctcacacag ggaagagagg gcccctcctg cagggcctca cctgggccac aggaggacac   120
tgcttttcct ctgaggagtc aggagctgtg gatggtgctg gacagaagaa ggacagggcc   180
tggctcaggt gtccagaggc tgtcgctggc ttcccttggg atcagactg caggggaggga   240
gggcggcagg gttgtggggg gagtgacgat gaggatgacc tggggtggc tccaggcctt   300
gcccctgcct gggccctcac ccagcctccc tcacagtctc ctggccctca gtctctcccc   360
tccactccat cctccatctg gcctcagtgg gtcattctga tcactgaact gaccatacac   420
agccctgccc acggccctcc atggctcccc aatgccctgg agaggggaca tctagtcaga   480
gagtagtga   489

<210> 848
<211> 132
<212> PRT
<213> Homo sapiens

<400> 848
Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe

315

```
 1            5              10             15
Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser
            20              25             30
Gly Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly
        35              40             45
Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val
    50              55             60
Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val
65              70             75             80
Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala
            85              90             95
Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Asn Trp
            100             105            110
Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu
        115             120            125
Gly Pro Pro Ala
    130
```

<210> 849
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 849
ggggaattca tcacctatgt gccgcctctg c   31

<210> 850
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 850
gggctcgagt cactcgccca cgaaatccgt gtaaaacagc   40

<210> 851
<211> 1203
<212> DNA
<213> Homo sapiens

<400> 851
```
atgcatcacc atcaccatca cacggccgcg tccgataact tccagctgtc ccagggtggg 60
cagggattcg ccattccgat cgggcaggcg atggcgatcg cgggccagat caagcttccc 120
accgttcata tcgggcctac cgccttcctc ggcttgggtg ttgtcgacaa caacggcaac 180
ggcgcacgag tccaacgcgt ggtcgggagc gctccggcgg caagtctcgg catctccacc 240
ggcgacgtga tcaccgcggt cgacggcgct ccgatcaact cggccaccgc gatggcggac 300
gcgcttaacg ggcatcatcc cggtgacgtc atctcggtga cctggcaaac caagtcgggc 360
ggcacgcgta cagggaacgt gacattggcc gagggacccc cggccgaatt catcacctat 420
gtgccgcctc tgctgctgga agtgggggta gaggagaagt tcatgaccat ggtgctgggc 480
attggtccag tgctgggcct ggtctgtgtc ccgctcctag gctcagccag tgaccactgg 540
cgtggacgct atggccgccg ccggcccttc atctgggcac tgtccttggg catcctgctg 600
```

316

```
agcctctttc tcatcccaag ggccggctgg ctagcagggc tgctgtgccc ggatcccagg 660
cccctggagc tggcactgct catcctgggc gtggggctgc tggacttctg tggccaggtg 720
tgcttcactc cactggaggc cctgctctct gacctcttcc gggacccgga ccactgtcgc 780
caggcctact ctgtctatgc cttcatgatc agtcttgggg gctgcctggg ctacctcctg 840
cctgccattg actggyacac cagtgccctg gcccctacc tgggcaccca ggaggagtgc 900
ctctttggcc tgctcaccct catcttcctc acctgcgtag cagccacact gctggtggct 960
gaggaggcag cgctgggccc caccgagcca gcagaagggc tgtcggcccc ctccttgtcg 1020
ccccactgct gtccatgccg ggcccgcttg gctttccgga acctgggcgc cctgcttccc 1080
cggctgcacc agctgtgctg ccgcatgccc cgcaccctgc gccggctctt cgtggctgag 1140
ctgtgcagct ggatggcact catgaccttc acgctgtttt acacggattt cgtgggcgag 1200
tga                                                            1203
```

<210> 852
<211> 400
<212> PRT
<213> Homo sapiens

<400> 852
```
Met His His His His His His Thr Ala Ala Ser Asp Asn Phe Gln Leu
                5                  10                  15
Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala
                20                  25                  30
Ile Ala Gly Gln Ile Lys Leu Pro Thr Val His Ile Gly Pro Thr Ala
            35                  40                  45
Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val
        50                  55                  60
Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr
65                  70                  75                  80
Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr
                85                  90                  95
Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser
            100                 105                 110
Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr
        115                 120                 125
Leu Ala Glu Gly Pro Pro Ala Glu Phe Ile Thr Tyr Val Pro Pro Leu
    130                 135                 140
Leu Leu Glu Val Gly Val Glu Glu Lys Phe Met Thr Met Val Leu Gly
145                 150                 155                 160
Ile Gly Pro Val Leu Gly Leu Val Cys Val Pro Leu Leu Gly Ser Ala
                165                 170                 175
Ser Asp His Trp Arg Gly Arg Tyr Gly Arg Arg Arg Pro Phe Ile Trp
            180                 185                 190
Ala Leu Ser Leu Gly Ile Leu Leu Ser Leu Phe Leu Ile Pro Arg Ala
        195                 200                 205
Gly Trp Leu Ala Gly Leu Leu Cys Pro Asp Pro Arg Pro Leu Glu Leu
    210                 215                 220
Ala Leu Leu Ile Leu Gly Val Gly Leu Leu Asp Phe Cys Gly Gln Val
225                 230                 235                 240
Cys Phe Thr Pro Leu Glu Ala Leu Leu Ser Asp Leu Phe Arg Asp Pro
                245                 250                 255
Asp His Cys Arg Gln Ala Tyr Ser Val Tyr Ala Phe Met Ile Ser Leu
            260                 265                 270
Gly Gly Cys Leu Gly Tyr Leu Leu Pro Ala Ile Asp Trp Asp Thr Ser
        275                 280                 285
Ala Leu Ala Pro Tyr Leu Gly Thr Gln Glu Glu Cys Leu Phe Gly Leu
    290                 295                 300
Leu Thr Leu Ile Phe Leu Thr Cys Val Ala Ala Thr Leu Leu Val Ala
305                 310                 315                 320
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317

```
Glu Glu Ala Ala Leu Gly Pro Thr Glu Pro Ala Glu Gly Leu Ser Ala
            325               330               335
Pro Ser Leu Ser Pro His Cys Cys Pro Cys Arg Ala Arg Leu Ala Phe
            340               345               350
Arg Asn Leu Gly Ala Leu Leu Pro Arg Leu His Gln Leu Cys Cys Arg
            355               360               365
Met Pro Arg Thr Leu Arg Arg Leu Phe Val Ala Glu Leu Cys Ser Trp
    370               375               380
Met Ala Leu Met Thr Phe Thr Leu Phe Tyr Thr Asp Phe Val Gly Glu
385               390               395               400
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<210> 853
<211> 20
<212> PRT
<213> Homo sapiens

<400> 853
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Leu Leu Pro Pro Pro Pro Ala Leu Cys Gly Ala Ser Ala Cys Asp Val
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Ser Val Arg Val
            20
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<210> 854
<211> 60
<212> DNA
<213> Homo sapiens

<400> 854
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<210> 855
<211> 10
<212> PRT
<213> Homo sapiens

<400> 855
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Ala Ser Ala Cys Asp Val Ser Val Arg Val
                5               10
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<210> 856
<211> 30
<212> DNA
<213> Homo sapiens

<400> 856
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gcctctgcct gtgatgtctc cgtacgtgtg                                    30
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<210> 857
<211> 9
<212> PRT
<213> Homo sapiens

<400> 857
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Ala Ser Ala Cys Asp Val Ser Val Arg
 1               5
```

<210> 858

```
<211> 9
<212> PRT
<213> Homo sapiens

<400> 858
Ser Ala Cys Asp Val Ser Val Arg Val
                5

<210> 859
<211> 27
<212> DNA
<213> Homo sapiens

<400> 859
tctgcctgtg atgtctccgt acgtgtg                                          27


<210> 860
<211> 19
<212> PRT
<213> Homo sapiens

<400> 860
Gly Ile Gly Pro Val Leu Gly Leu Val Cys Val Pro Leu Leu Gly Ser
                5                   10                  15
Ala Ser Asp


<210> 861
<211> 19
<212> PRT
<213> Homo sapiens

<400> 861
Val Pro Pro Leu Leu Leu Glu Val Gly Val Glu Glu Lys Phe Met Thr
                5                   10                  15
Met Val Leu


<210> 862
<211> 19
<212> PRT
<213> Homo sapiens

<400> 862
Met Val Gln Arg Leu Trp Val Ser Arg Leu Leu Arg His Arg Lys Ala
                5                   10                  15
Gln Leu Leu

<210> 863
<211> 57
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(57)
<223> n = A,T,C or G
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319

<400> 863
ggnathggnc cngtnytngg nytngtntgy gtnccnytny tnggnwsngc nwsngay   57

<210> 864
<211> 57
<212> DNA
<213> Homo sapiens

<220>
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<223> n = A,T,C or G

<400> 864
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<210> 865
<211> 57
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(57)
<223> n = A,T,C or G

<400> 865
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<210> 866
<211> 9
<212> PRT
<213> Homo sapiens

<400> 866
Val Leu Gln Cys Val Asn Val Ser Val
1   5

<210> 867
<211> 9
<212> PRT
<213> Homo sapiens

<400> 867
Arg Met Pro Thr Val Leu Gln Cys Val
1   5

<210> 868
<211> 9
<212> PRT
<213> Homo sapiens

<400> 868
Asn Leu Cys Lys Phe Thr Glu Trp Ile
1   5

320

```
<210> 869
<211> 9
<212> PRT
<213> Homo sapiens

<400> 869
Met Leu Ile Lys Leu Asp Glu Ser Val
 1               5


<210> 870
<211> 9
<212> PRT
<213> Homo sapiens

<400> 870
Leu Leu Ala Asn Asp Leu Met Leu Ile
 1               5


<210> 871
<211> 10
<212> PRT
<213> Homo sapiens

<400> 871
Leu Leu Ala Asn Gly Arg Met Pro Thr Val
 1               5                  10


<210> 872
<211> 10
<212> PRT
<213> Homo sapiens

<400> 872
Leu Met Leu Ile Lys Leu Asp Glu Ser Val
 1               5                  10


<210> 873
<211> 10
<212> PRT
<213> Homo sapiens

<400> 873
Val Leu Gln Cys Val Asn Val Ser Val Val
 1               5                  10


<210> 874
<211> 10
<212> PRT
<213> Homo sapiens

<400> 874
Gly Leu Leu Ala Asn Gly Arg Met Pro Thr
 1               5                  10


<210> 875
<211> 10
<212> PRT
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321

<210> Homo sapiens

<400> 875
Thr Val Leu Gln Cys Val Asn Val Ser Val
 1   5   10

<210> 876
<211> 9
<212> PRT
<213> Homo sapiens

<400> 876
Gly Val Leu Val His Pro Gln Trp Val
 1   5

<210>. 877
<211> 9
<212> PRT
<213> Homo sapiens

<400> 877
Val Leu Val His Pro Gln Trp Val Leu
 1   5

<210> 878
<211> 1195
<212> DNA
<213> Homo sapiens

<400> 878
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ggagaaattt agaagaagac gattatttgc ataaggacac gggagagacc agcatgctaa 180
aaagacctgt gcttttgcat ttgcaccaaa cagcccatgc tgatgaattt gactgccctt 240
cagaacttca gcacacacag gaactctttc cacagtggca cttgccaatt aaaatagctg 300
ctattatagc atctctgact tttctttaca ctcttctgag ggaagtaatt caccctttag 360
caacttccca tcaacaatat ttttataaaa ttccaatcct ggtcatcaac aaagtcttgc 420
caatggtttc catcactctc ttggcattgg tttacctgcc aggtgtgata gcagcaattg 480
tccaacttca taatggaacc aagtataaga agtttccaca ttggttggat aagtggatgt 540
taacaagaaa gcagtttggg cttctcagtt tctttttgc tgtactgcat gcaatttata 600
gtctgtctta cccaatgagg cgatcctaca gatacaagtt gctaaactgg gcatatcaac 660
aggtccaaca aaataaagaa gatgcctgga ttgagcatga tgtttggaga atggagattt 720
atgtgtctct gggaattgtg ggattggcaa tactggctct gttggctgtg acatctattc 780
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agattagaca tggttgggaa gacgtcacca aaattaacaa aactgagata tgttcccagt 1080
tgtagaatta ctgtttacac acattttgt tcaatattga tatatttat caccaacatt 1140
tcaagtttgt atttgttaat aaaatgatta ttcaaggaaa aaaaaaaaa aaaaa   1195

<210> 879
<211> 339
<212> PRT
<213> Homo sapiens

322

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<400> 879
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                  5                   10                  15
Lys Pro Arg Arg Asn Leu Glu Glu Asp Asp Tyr Leu His Lys Asp Thr
              20                  25                  30
Gly Glu Thr Ser Met Leu Lys Arg Pro Val Leu Leu His Leu His Gln
          35                  40                  45
Thr Ala His Ala Asp Glu Phe Asp Cys Pro Ser Glu Leu Gln His Thr
      50                  55                  60
Gln Glu Leu Phe Pro Gln Trp His Leu Pro Ile Lys Ile Ala Ala Ile
  65                  70                  75                  80
Ile Ala Ser Leu Thr Phe Leu Tyr Thr Leu Leu Arg Glu Val Ile His
              85                  90                  95
Pro Leu Ala Thr Ser His Gln Gln Tyr Phe Tyr Lys Ile Pro Ile Leu
          100                 105                 110
Val Ile Asn Lys Val Leu Pro Met Val Ser Ile Thr Leu Leu Ala Leu
      115                 120                 125
Val Tyr Leu Pro Gly Val Ile Ala Ala Ile Val Gln Leu His Asn Gly
  130                 135                 140
Thr Lys Tyr Lys Lys Phe Pro His Trp Leu Asp Lys Trp Met Leu Thr
145                 150                 155                 160
Arg Lys Gln Phe Gly Leu Leu Ser Phe Phe Phe Ala Val Leu His Ala
              165                 170                 175
Ile Tyr Ser Leu Ser Tyr Pro Met Arg Arg Ser Tyr Arg Tyr Lys Leu
          180                 185                 190
Leu Asn Trp Ala Tyr Gln Gln Val Gln Gln Asn Lys Glu Asp Ala Trp
      195                 200                 205
Ile Glu His Asp Val Trp Arg Met Glu Ile Tyr Val Ser Leu Gly Ile
  210                 215                 220
Val Gly Leu Ala Ile Leu Ala Leu Leu Ala Val Thr Ser Ile Pro Ser
225                 230                 235                 240
Val Ser Asp Ser Leu Thr Trp Arg Glu Phe His Tyr Ile Gln Ser Lys
              245                 250                 255
Leu Gly Ile Val Ser Leu Leu Leu Gly Thr Ile His Ala Leu Ile Phe
          260                 265                 270
Ala Trp Asn Lys Trp Ile Asp Ile Lys Gln Phe Val Trp Tyr Thr Pro
      275                 280                 285
Pro Thr Phe Met Ile Ala Val Phe Leu Pro Ile Val Val Leu Ile Phe
  290                 295                 300
Lys Ser Ile Leu Phe Leu Pro Cys Leu Arg Lys Lys Ile Leu Lys Ile
305                 310                 315                 320
Arg His Gly Trp Glu Asp Val Thr Lys Ile Asn Lys Thr Glu Ile Cys
              325                 330                 335
Ser Gln Leu

<210> 880
<211> 2172
<212> DNA
<213> Homo sapiens

<400> 880
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aaaatattgg aattttattc atcttaaaaa ttggacccgg ccttatttac catctttaat 120
ccattttagt actatgggtg agtacatgga attgaagtct ggcttaaatc ttcagaaagt 180
tatatatcta tttattttta tttttttgag acagagtctc gctgtgtcac ccaggctgga 240
gtgcggtgcc acaatcttgg ctcactgcaa cctctgagtc ccaggttcaa gcgatactca 300
tgcctcggcc tcctgagtag ctgggactac aggcgtgcac caccacatct ggctaatctt 360
tttttgtatt tttagtagag acggggtttc actgtggtct ccatctcctg acctcgtgat 420
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323

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ccgcctgcct cccaaagtgc tgggattaca ggcatgagcc accgcacaca gctgggactg 480
ggtaatttat aaagaaaaga ggtttaatga ctcacagttc cgcatggctg gagaggcctc 540
aggaaactta caatcatggt ggaaggcgaa ggggaagcaa ggcacgtctt acatggtggc 600
aggagagaac gagtgagggg ggagactgcc acaaactttt ttttttttgag acaagagtct 660
ggccctgttg cccaggctgg agtgcagtgg catgatctca gctcactgca acctctgcct 720
cacaggttca agcaattctc atgcctcagc ctcccgcata gctgggacca caggtatgca 780
ccaccacacc tagctaattt ttgtagtttt agtagagatg gggtctcact atgttgctca 840
ggctggtcta aaactcctgg gctccagcaa tccgcctgcc ttggcctccc aaagtgctgg 900
ggttacaggc ataagccacc acatccagcc tgccacatac ttttaaacta tcaggtctca 960
tgagaactca tgcactatca caagaatagc atggggaaaa tcccccccat aatccaatca 1020
cctcccacca ggtctcctcc gacacgtggg attgggtggg gacacagagc caaaccgtat 1080
cagatgctgc aggggctggg gacactgaga ccactcagac ctggtgtctc tgtcactctt 1140
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taaggtgcaa attgcacagg aactccttaa gacatacatc atccactcag cagttttagg 1260
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cgccatatcg gcatcctgca tccagagtgg tggactggtt acaggctatg aacctacact 1380
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ggtatatgga gccctgtttt cagttgcttt tctaattctc tcttatcgtt tacctcaaaa 1620
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attcccccgg actttgactt ctcaagagct aagaaggttt gctgagtatt ctggcatgat 2100
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<210> 881
<211> 2455
<212> DNA
<213> Homo sapiens

<400> 881
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gaaagatgtt tctcaggttt ttccttgacg attttcttct tttctgattc tgacaatgtt 300
ttaaatcatt gtactgtggt tatcatttct ctgcatttat tttacccatc ttcctttgta 360
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tggtggcggg cgcctgtaat cccaggtact cgggaggctg agggaggaga atcgcttgaa 660
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324

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<210> 882
<211> 2455
<212> DNA
<213> Homo sapiens

<400> 882
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catgttttct caaatctctt tgtgaattcc agagagggcc aggcacggtg gctcacatcc 480
gtaatcccag cactttgggg aggctgagac gggtggatca cttgaggtca ggagtttgag 540
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cctgggaggc tgagggagga gaatcgcttg aacccgggag gcagaggttg cagtgaaccg 720
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aatggacttg cttcaaagtg gaggcaggca gatccttcag acgggtatat ggagccctgt 1860
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325

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cacctactga ctacacggtt aggagtgcaa gggtagaatt catgttttat tcatctttgg 2040
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aatacacact gtactaagaa tctacacacc gaaagacaaa aacaagacaa atttgagtgc 2160
tacaggtgtc acgcttggca tcacacatgt gcctgtgtat tcctctaggt ggttaccagg 2220
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gctgctctca cataaggggt ccaattaaaa ttgccaggaa taaattcccc cggactttga 2340
cttctcaaga gctaagaagg tttgctgagt attctggcat gatgtttggt gatcaaacaa 2400
ctgctggcca aaaatgatga gtatttcccc ctcttgctga agatgtgctc catac       2455
```

<210> 883
<211> 62
<212> PRT
<213> Homo sapiens

<400> 883
```
Met Thr His Ser Ser Ala Trp Leu Glu Arg Pro Gln Glu Thr Tyr Asn
                5                  10                  15
His Gly Gly Arg Arg Arg Gly Ser Lys Ala Arg Leu Thr Trp Trp Gln
                20                  25                  30
Glu Arg Thr Ser Glu Gly Gly Asp Cys His Lys Leu Phe Phe Phe Glu
            35                  40                  45
Thr Arg Val Trp Pro Cys Cys Pro Gly Trp Ser Ala Val Ala
        50                  55                  60
```

<210> 884
<211> 135
<212> PRT
<213> Homo sapiens

<400> 884
```
Met Val Glu Gly Glu Gly Glu Ala Arg His Val Leu His Gly Gly Arg
                5                  10                  15
Arg Glu Arg Val Arg Gly Glu Thr Ala Thr Asn Phe Phe Phe Leu Arg
                20                  25                  30
Gln Glu Ser Gly Pro Val Ala Gln Ala Gly Val Gln Trp His Asp Leu
            35                  40                  45
Ser Ser Leu Gln Pro Leu Pro His Arg Phe Lys Gln Phe Ser Cys Leu
    50                  55                  60
Ser Leu Pro His Ser Trp Asp His Arg Tyr Ala Pro Pro His Leu Ala
65                  70                  75                  80
Asn Phe Cys Ser Phe Ser Arg Asp Gly Val Ser Leu Cys Cys Ser Gly
                85                  90                  95
Trp Ser Lys Thr Pro Gly Leu Gln Gln Ser Ala Cys Leu Gly Leu Pro
            100                 105                 110
Lys Cys Trp Gly Tyr Arg His Lys Pro Pro His Pro Ala Cys His Ile
        115                 120                 125
Leu Leu Asn Tyr Gln Val Ser
    130                 135
```

<210> 885
<211> 77
<212> PRT
<213> Homo sapiens

<400> 885
```
Met His Tyr His Lys Asn Ser Met Gly Lys Ile Pro Pro Ile Ile Gln
```

326

```
                         5                  10                 15
Ser Pro Pro Thr Arg Ser Pro Pro Thr Arg Gly Ile Gly Trp Gly His
                20                  25                 30
Arg Ala Lys Pro Tyr Gln Met Leu Gln Gly Leu Gly Thr Leu Arg Pro
        35                  40                 45
Leu Arg Pro Gly Val Ser Val Thr Leu Leu Gly Ser Val Cys Leu Gln
    50                  55                 60
Asp Leu Pro Pro Leu Pro Trp Tyr Arg Arg Lys Val Leu
65                  70                 75


<210> 886
<211> 60
<212> PRT
<213> Homo sapiens

<400> 886
Met Leu Val His Ile Tyr Ser Cys Cys Gly Met Val Tyr Arg Phe Gly
                     5                  10                 15
Gln Met Ser Asp Asn Pro Phe Tyr Ile Leu Ala Ser Leu Gly Ser Ser
                20                  25                 30
Ser Cys Arg Asn Gly Leu Ala Ser Lys Trp Arg Gln Ala Asp Pro Ser
        35                  40                 45
Asp Gly Tyr Met Glu Pro Cys Phe Gln Leu Leu Phe
    50                  55                 60


<210> 887
<211> 76
<212> PRT
<213> Homo sapiens

<400> 887
Met Cys Leu Cys Ile Pro Leu Gly Gly Tyr Gln Glu Leu Cys His Cys
                     5                  10                 15
Met Ser Thr Ser Asp Gly Phe Ala Pro Pro Gln Leu Gly Ser Arg
                20                  25                 30
Cys Ser His Ile Arg Gly Pro Ile Lys Ile Ala Arg Asn Lys Phe Pro
        35                  40                 45
Arg Thr Leu Thr Ser Gln Glu Leu Arg Arg Phe Ala Glu Tyr Ser Gly
    50                  55                 60
Met Met Phe Gly Asp Gln Thr Thr Ala Gly Gln Lys
65                  70                 75


<210> 888
<211> 76
<212> PRT
<213> Homo sapiens

<400> 888
Met Val Lys Ser Arg Phe Thr Lys Asn Thr Lys Ile Thr Gln Ala Trp
                     5                  10                 15
Trp Arg Ala Pro Val Ile Pro Gly Thr Arg Glu Ala Glu Gly Gly Glu
                20                  25                 30
Ser Leu Glu Pro Gly Arg Leu Arg Glu Glu Asn Arg Leu Asn Pro Gly
        35                  40                 45
Gly Arg Gly Cys Ser Glu Pro Arg Ser Cys Cys Cys Thr Pro Ala Trp
    50                  55                 60
Ser Thr Glu Gln Asp Ser Ala Ser Lys Thr Asn Lys
65                  70                 75
```

327

```
<210> 889
<211> 80
<212> PRT
<213> Homo sapiens

<400> 889
Met Leu Leu His Ser Ser Leu Val Asn Arg Ala Arg Leu Cys Leu Lys
                  5                  10                  15
Asn Lys Gln Ile Asn Lys Gln Thr Asn Lys Thr Glu Arg Phe Cys Cys
              20                  25                  30
Asn Val Gln Gly Ala Ile Cys Ser Phe Lys Lys Ile Ile Phe Gly Gln
          35                  40                  45
Ala Gln Trp Leu Thr Pro Val Ile Pro Ala Leu Trp Glu Ala Lys Val
      50                  55                  60
Gly Gly Ser Phe Glu Val Arg Ser Leu Arg Ser Ala Trp Pro Thr Trp
 65                  70                  75                  80

<210> 890
<211> 72
<212> PRT
<213> Homo sapiens

<400> 890
Met His Tyr His Lys Asn Ser Met Gly Lys Ile Pro Pro His Asn Pro
                  5                  10                  15
Ile Thr Ser His Gln Val Ser Ser Asp Thr Trp Asp Trp Val Gly Thr
              20                  25                  30
Gln Ser Gln Thr Val Ser Asp Ala Ala Gly Ala Gly Asp Thr Glu Thr
          35                  40                  45
Thr Gln Thr Trp Cys Leu Cys His Ser Ser Gly Leu Cys Leu Ser Pro
      50                  55                  60
Gly Pro Pro Ser Pro Ser Met Val
 65                  70

<210> 891
<211> 77
<212> PRT
<213> Homo sapiens

<400> 891
Met His Tyr His Lys Asn Ser Met Gly Lys Ile Pro Pro Ile Ile Gln
                  5                  10                  15
Ser Pro Pro Thr Arg Ser Pro Pro Thr Arg Gly Ile Gly Trp Gly His
              20                  25                  30
Arg Ala Lys Pro Tyr Gln Met Leu Gln Gly Leu Gly Thr Leu Arg Pro
          35                  40                  45
Leu Arg Pro Gly Val Ser Val Thr Leu Leu Gly Ser Val Cys Leu Gln
      50                  55                  60
Asp Leu Pro Pro Leu Pro Trp Tyr Arg Arg Lys Val Leu
 65                  70                  75

<210> 892
<211> 60
<212> PRT
<213> Homo sapiens

<400> 892
```

328

```
Met Leu Val His Ile Tyr Ser Cys Cys Gly Met Val Tyr Arg Phe Gly
                  5                    10                      15
Gln Met Ser Asp Asn Pro Phe Tyr Ile Leu Ala Ser Leu Gly Ser Ser
              20                    25                    30
Ser Cys Arg Asn Gly Leu Ala Ser Lys Trp Arg Gln Ala Asp Pro Ser
          35                    40                    45
Asp Gly Tyr Met Glu Pro Cys Phe Gln Leu Leu Phe
      50                    55                    60
```

<210> 893
<211> 76
<212> PRT
<213> Homo sapiens

<400> 893
```
Met Cys Leu Cys Ile Pro Leu Gly Gly Tyr Gln Glu Leu Cys His Cys
                  5                    10                      15
Met Ser Thr Ser Asp Gly Phe Ala Pro Pro Gln Leu Gly Ser Arg
              20                    25                    30
Cys Ser His Ile Arg Gly Pro Ile Lys Ile Ala Arg Asn Lys Phe Pro
          35                    40                    45
Arg Thr Leu Thr Ser Gln Glu Leu Arg Arg Phe Ala Glu Tyr Ser Gly
      50                    55                    60
Met Met Phe Gly Asp Gln Thr Thr Ala Gly Gln Lys
  65                    70                    75
```

<210> 894
<211> 2479
<212> DNA
<213> Homo sapiens

<400> 894
```
gtcatattga acattccaga tacctatcat tactcgatgc tgttgataac agcaagatgg 60
ctttgaactc agggtcacca ccagctattg gaccttacta tgaaaaccat ggataccaac 120
cggaaaaccc ctatcccgca cagcccactg tggtccccac tgtctacgag gtgcatccgg 180
ctcagtacta cccgtccccc gtgccccagt acgccccgag ggtcctgacg caggcttcca 240
accccgtcgt ctgcacgcag cccaaatccc catccgggac agtgtgcacc tcaaagacta 300
agaaagcact gtgcatcacc ttgaccctgg ggaccttcct cgtgggagct gcgctggccg 360
ctggcctact ctggaagttc atgggcagca agtgctccaa ctctgggata gagtgcgact 420
cctcaggtac ctgcatcaac ccctctaact ggtgtgatgg cgtgtcacac tgccccggcg 480
gggaggacga gaatcggtgt gttcgcctct acggaccaaa cttcatcctt cagatgtact 540
catctcagag gaagtcctgg caccctgtgt gccaagacga ctggaacgag aactacgggc 600
gggcggcctg cagggacatg ggctataaga ataattttta ctctagccaa ggaatagtgg 660
atgacagcgg atccaccagc tttatgaaac tgaacacaag tgccggcaat gtcgatatct 720
ataaaaaact gtaccacagt gatgcctgtt cttcaaaagc agtggtttct ttacgctgtt 780
tagcctgcgg ggtcaacttg aactcaagcc gccagagcag gatcgtgggc ggtgagagcg 840
cgctcccggg ggcctggccc tggcaggtca gcctgcacgt ccagaacgtc cacgtgtgcg 900
gaggctccat catcacccccc gagtggatcg tgacagccgc ccactgcgtg gaaaaacctc 960
ttaacaatcc atggcattgg acggcatttg cggggatttt gagacaatct ttcatgttct 1020
atggagccgg ataccaagta caaaaagtga tttctcatcc aaattatgac tccaagacca 1080
agaacaatga cattgcgctg atgaagctgc agaagcctct gactttcaac gacctagtga 1140
aaccagtgtg tctgcccaac ccaggcatga tgctgcagcc agaacagctc tgctggattt 1200
ccgggtgggg ggccaccgag gagaaaggga gacctcaga agtgctgaac gctgccaagg 1260
tgcttctcat tgagacacag agatgcaaca gcagatatgt ctatgacaac ctgatcacac 1320
cagccatgat ctgtgccggc ttcctgcagg ggaacgtcga ttcttgccag ggtgacagtg 1380
gagggcctct ggtcacttcg aacaacaata tctggtggct gataggggat acaagctggg 1440
gttctggctg tgccaaagct tacagaccag gagtgtacgg gaatgtgatg gtattcacgg 1500
actggattta tcgacaaatg aaggcaaacg ctaatccac atggtcttcg tccttgacgt 1560
```

329

```
cgttttacaa gaaaacaatg gggctggttt tgcttccccg tgcatgattt actcttagag 1620
atgattcaga ggtcacttca tttttattaa acagtgaact tgtctggctt tggcactctc 1680
tgccatactg tgcaggctgc agtggctccc ctgcccagcc tgctctccct aaccccttgt 1740
ccgcaagggg tgatggccgg ctggttgtgg gcactggcgg tcaattgtgg aaggaagagg 1800
gttggaggct gcccccattg agatcttcct gctgagtcct ttccaggggc caattttgga 1860
tgagcatgga gctgtcactt ctcagctgct ggatgacttg agatgaaaaa ggagagacat 1920
ggaaagggag acagccaggt ggcacctgca gcggctgccc tctggggcca cttggtagtg 1980
tccccagcct acttcacaag gggattttgc tgatgggttc ttagagcctt agcagccctg 2040
gatggtggcc agaaataaag ggaccagccc ttcatgggtg gtgacgtggt agtcacttgt 2100
aagggaaca gaaacatttt tgttcttatg gggtgagaat atagacagtg cccttggtgc 2160
gagggaagca attgaaaagg aacttgccct gagcactcct ggtgcaggtc tccacctgca 2220
cattgggtgg ggctcctggg agggagactc agccttcctc ctcatcctcc ctgaccctgc 2280
tcctagcacc ctggagagtg aatgcccctt ggtccctggc agggcgccaa gtttggcacc 2340
atgtcggcct cttcaggcct gatagtcatt ggaaattgag gtccatgggg gaaatcaagg 2400
atgctcagtt taaggtacac tgtttccatg ttatgtttct acacattgat ggtggtgacc 2460
ctgagttcaa agccatctt                                             2479
```

<210> 895
<211> 492
<212> PRT
<213> Homo sapiens

<400> 895

```
Met Ala Leu Asn Ser Gly Ser Pro Pro Ala Ile Gly Pro Tyr Tyr Glu
                  5                  10                  15
Asn His Gly Tyr Gln Pro Glu Asn Pro Tyr Pro Ala Gln Pro Thr Val
              20                  25                  30
Val Pro Thr Val Tyr Glu Val His Pro Ala Gln Tyr Tyr Pro Ser Pro
          35                  40                  45
Val Pro Gln Tyr Ala Pro Arg Val Leu Thr Gln Ala Ser Asn Pro Val
      50                  55                  60
Val Cys Thr Gln Pro Lys Ser Pro Ser Gly Thr Val Cys Thr Ser Lys
  65                  70                  75                  80
Thr Lys Lys Ala Leu Cys Ile Thr Leu Thr Leu Gly Thr Phe Leu Val
                  85                  90                  95
Gly Ala Ala Leu Ala Ala Gly Leu Leu Trp Lys Phe Met Gly Ser Lys
              100                 105                 110
Cys Ser Asn Ser Gly Ile Glu Cys Asp Ser Ser Gly Thr Cys Ile Asn
          115                 120                 125
Pro Ser Asn Trp Cys Asp Gly Val Ser His Cys Pro Gly Gly Glu Asp
      130                 135                 140
Glu Asn Arg Cys Val Arg Leu Tyr Gly Pro Asn Phe Ile Leu Gln Met
145                 150                 155                 160
Tyr Ser Ser Gln Arg Lys Ser Trp His Pro Val Cys Gln Asp Asp Trp
              165                 170                 175
Asn Glu Asn Tyr Gly Arg Ala Ala Cys Arg Asp Met Gly Tyr Lys Asn
          180                 185                 190
Asn Phe Tyr Ser Ser Gln Gly Ile Val Asp Asp Ser Gly Ser Thr Ser
      195                 200                 205
Phe Met Lys Leu Asn Thr Ser Ala Gly Asn Val Asp Ile Tyr Lys Lys
  210                 215                 220
Leu Tyr His Ser Asp Ala Cys Ser Ser Lys Ala Val Val Ser Leu Arg
225                 230                 235                 240
Cys Leu Ala Cys Gly Val Asn Leu Asn Ser Ser Arg Gln Ser Arg Ile
              245                 250                 255
Val Gly Gly Glu Ser Ala Leu Pro Gly Ala Trp Pro Trp Gln Val Ser
          260                 265                 270
Leu His Val Gln Asn Val His Val Cys Gly Gly Ser Ile Ile Thr Pro
```

330

```
              275                    280                    285
    Glu Trp Ile Val Thr Ala Ala His Cys Val Glu Lys Pro Leu Asn Asn
        290                    295                    300
    Pro Trp His Trp Thr Ala Phe Ala Gly Ile Leu Arg Gln Ser Phe Met
    305                    310                    315                320
    Phe Tyr Gly Ala Gly Tyr Gln Val Gln Lys Val Ile Ser His Pro Asn
                       325                    330                335
    Tyr Asp Ser Lys Thr Lys Asn Asn Asp Ile Ala Leu Met Lys Leu Gln
                   340                    345                    350
    Lys Pro Leu Thr Phe Asn Asp Leu Val Lys Pro Val Cys Leu Pro Asn
                   355                    360                    365
    Pro Gly Met Met Leu Gln Pro Glu Gln Leu Cys Trp Ile Ser Gly Trp
        370                    375                    380
    Gly Ala Thr Glu Glu Lys Gly Lys Thr Ser Glu Val Leu Asn Ala Ala
    385                    390                    395                400
    Lys Val Leu Leu Ile Glu Thr Gln Arg Cys Asn Ser Arg Tyr Val Tyr
                       405                    410                    415
    Asp Asn Leu Ile Thr Pro Ala Met Ile Cys Ala Gly Phe Leu Gln Gly
                   420                    425                    430
    Asn Val Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Thr Ser
                   435                    440                    445
    Asn Asn Asn Ile Trp Trp Leu Ile Gly Asp Thr Ser Trp Gly Ser Gly
        450                    455                    460
    Cys Ala Lys Ala Tyr Arg Pro Gly Val Tyr Gly Asn Val Met Val Phe
    465                    470                    475                480
    Thr Asp Trp Ile Tyr Arg Gln Met Lys Ala Asn Gly
                   485                    490
```

```
<210> 896
<211> 683
<212> DNA
<213> Homo sapiens

<400> 896
gtcatattga acattccaga tacctatcat tactcgatgc tgttgataac agcaagatgg  60
ctttgaactc agggtcacca ccagctattg gaccttacta tgaaaaccat ggataccaac 120
cggaaaaccc ctatcccgca cagcccactg tggtccccac tgtctacgag gtgcatccgg 180
ctcagtacta cccgtccccc gtgccccagt acgccccgag ggtcctgacg caggcttcca 240
accccgtcgt ctgcacgcag cccaaatccc catccgggac agtgtgcacc tcaaagacta 300
agaaagcact gtgcatcacc ttgaccctgg ggaccttcct cgtgggagct gcgctggccg 360
ctggcctact ctggaagttc atgggcagca agtgctccaa ctctgggata gagtgcgact 420
cctcaggtac ctgcatcaac ccctctaact ggtgtgatgg cgtgtcacac tgccccggcg 480
gggaggacga gaatcggtgt gttcgcctct acggaccaaa cttcatcctt cagatgtact 540
catctcagag gaagtcctgg caccctgtgt gccaagacga ctggaacgag aactacgggc 600
gggcggcctg cagggacatg ggctataaga taattttta ctctagccaa ggaatagtgg 660
atgacagcgg atccaccagc ttt                                          683
```

```
<210> 897
<211> 209
<212> PRT
<213> Homo sapiens

<400> 897
Met Ala Leu Asn Ser Gly Ser Pro Pro Ala Ile Gly Pro Tyr Tyr Glu
1               5                   10                  15
```

331

```
Asn His Gly Tyr Gln Pro Glu Asn Pro Tyr Pro Ala Gln Pro Thr Val
            20                  25                  30
Val Pro Thr Val Tyr Glu Val His Pro Ala Gln Tyr Tyr Pro Ser Pro
        35                  40                  45
Val Pro Gln Tyr Ala Pro Arg Val Leu Thr Gln Ala Ser Asn Pro Val
    50                  55                  60
Val Cys Thr Gln Pro Lys Ser Pro Ser Gly Thr Val Cys Thr Ser Lys
65                  70                  75                  80
Thr Lys Lys Ala Leu Cys Ile Thr Leu Thr Leu Gly Thr Phe Leu Val
            85                  90                  95
Gly Ala Ala Leu Ala Ala Gly Leu Leu Trp Lys Phe Met Gly Ser Lys
            100                 105                 110
Cys Ser Asn Ser Gly Ile Glu Cys Asp Ser Ser Gly Thr Cys Ile Asn
            115                 120                 125
Pro Ser Asn Trp Cys Asp Gly Val Ser His Cys Pro Gly Gly Glu Asp
        130                 135                 140
Glu Asn Arg Cys Val Arg Leu Tyr Gly Pro Asn Phe Ile Leu Gln Met
145                 150                 155                 160
Tyr Ser Ser Gln Arg Lys Ser Trp His Pro Val Cys Gln Asp Asp Trp
                165                 170                 175
Asn Glu Asn Tyr Gly Arg Ala Ala Cys Arg Asp Met Gly Tyr Lys Asn
            180                 185                 190
Asn Phe Tyr Ser Ser Gln Gly Ile Val Asp Asp Ser Gly Ser Thr Ser
        195                 200                 205
Phe
```

```
<210> 898
<211> 27
<212> PRT
<213> Homo sapiens

<400> 898
Val Gly Glu Gly Leu Tyr Gln Gly Val Pro Arg Ala Glu Pro Gly Thr
 1               5                  10                  15
Glu Ala Arg Arg His Tyr Asp Glu Gly Val Arg
            20                  25

<210> 899
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 899
ggatccgccg ccaccatgtc actttctagc ctgct                              35

<210> 900
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 900
```

332

```
gtcgactcag ctggaccaca gccgcag                                        27

<210> 901
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 901
ggatccgccg ccaccatggg ctgcaggctg ctct                               34

<210> 902
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 902
gtcgactcag aaatcctttc tcttgac                                       27


<210> 903
<211> 936
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...()
<223> n = A,T,C or G

<400> 903
atgggctgca ggctgntctg ctgtgcggtt ctctgtctcc tgggagcggt ccccatggaa 60
acgggagtta cgcagacacc aagacacctg gtcatgggaa tgacaaataa gaagtctttg 120
aaatgtgaac aacatctggg tcataacgct atgtattggt acaagcaaag tgctaagaag 180
ccactggagc tcatgtttgt ctacagtctt gaagaacggg ttgaaaacaa cagtgtgcca 240
agtcgcttct cacctgaatg ccccaacagc tctcacttat tccttcacct acacaccctg 300
cagccagaag actcggccct gtatctctgc gccagcagcc aagaccggac aagcagctcc 360
tacgagcagt acttcgggcc gggcaccagg ctcacggtca cagaggacct gaaaaacgtg 420
ttcccacccg aggtcgctgt gtttgagcca tcagaagcag agatctccca cacccaaaag 480
gccacactgg tgtgcctggc cacaggcttc taccccgacc acgtggagct gagctggtgg 540
gtgaatggga aggaggtgca cagtgggggtc agcacagacc cgcagcccct caaggagcag 600
cccgccctca atgactccag atactgcctg agcagccgcc tgagggtctc ggccaccttc 660
tggcagaacc cccgcaacca cttccgctgt caagtccagt tctacgggct ctcggagaat 720
gacgagtgga cccaggatag ggccaaacct gtcacccaga tcgtcagcgc cgaggcctgg 780
ggtagagcag actgtggctt cacctccgag tcttaccagc aaggggtcct gtctgccacc 840
atcctctatg agatcttgct agggaaggcc accttgtatg ccgtgctggt cagtgccctc 900
gtgctgatgg ccatggtcaa gagaaaggat ttctga                            936

<210> 904
<211> 834
<212> DNA
<213> Homo sapiens
```

<220>
<221> misc_feature
<222> (1)...()
<223> n = A,T,C or G

<400> 904
atgtcacttt ctagcctgct naaggtggtc acagcttcac tgtggctagg acctggcatt 60
gcccagaaga taactcaaac ccaaccagga atgttcgtgc aggaaaagga ggctgtgact 120
ctggactgca catatgacac cagtgatcaa agttatggtc tcttctggta caagcagccc 180
agcagtgggg aaatgatttt tcttatttat caggggtctt atgacgagca aaatgcaaca 240
gaaggtcgct actcattgaa tttccagaag gcaagaaaat ccgccaacct tgtcatctcc 300
gcttcacaac tggggactc agcaatgtat ttctgtgcaa tgagagaggg cgcgggagga 360
ggaaacaaac tcacctttgg gacaggcact cagctaaaag tggaactcaa tatccagaac 420
cctgaccctg ccgtgtacca gctgagagac tctaaatcca gtgacaagtc tgtctgccta 480
ttcaccgatt ttgattctca aacaaatgtg tcacaaagta aggattctga tgtgtatatc 540
acagacaaaa ctgtgctaga catgaggtct atggacttca agagcaacag tgctgtggcc 600
tggagcaaca aatctgactt tgcatgtgca aacgccttca acaacagcat tattccagaa 660
gacaccttct tcccccagccc agaaagttcc tgtgatgtca agctggtcga gaaaagcttt 720
gaaacagata cgaacctaaa ctttcaaaac ctgtcagtga ttgggttccg aatcctcctc 780
ctgaaagtgg ccgggtttaa tctgctcatg acgctgcggc tgtggtccag ctga   834

<210> 905
<211> 311
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(311)
<223> Xaa = Any amino acid

<400> 905
Met Gly Cys Arg Leu Xaa Cys Cys Ala Val Leu Cys Leu Leu Gly Ala
                  5   10   15
Val Pro Met Glu Thr Gly Val Thr Gln Thr Pro Arg His Leu Val Met
            20   25   30
Gly Met Thr Asn Lys Lys Ser Leu Lys Cys Glu Gln His Leu Gly His
        35   40   45
Asn Ala Met Tyr Trp Tyr Lys Gln Ser Ala Lys Lys Pro Leu Glu Leu
    50   55   60
Met Phe Val Tyr Ser Leu Glu Glu Arg Val Glu Asn Asn Ser Val Pro
65   70   75   80
Ser Arg Phe Ser Pro Glu Cys Pro Asn Ser Ser His Leu Phe Leu His
                85   90   95
Leu His Thr Leu Gln Pro Glu Asp Ser Ala Leu Tyr Leu Cys Ala Ser
            100   105   110
Ser Gln Asp Arg Thr Ser Ser Tyr Glu Gln Tyr Phe Gly Pro Gly
        115   120   125
Thr Arg Leu Thr Val Thr Glu Asp Leu Lys Asn Val Phe Pro Pro Glu
        130   135   140
Val Ala Val Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys
145   150   155   160
Ala Thr Leu Val Cys Leu Ala Thr Gly Phe Tyr Pro Asp His Val Glu
                165   170   175
Leu Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr
            180   185   190
Asp Pro Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr
        195   200   205

334

```
Cys Leu Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro
    210                 215                 220
Arg Asn His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn
225                 230                 235                 240
Asp Glu Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser
            245                 250                 255
Ala Glu Ala Trp Gly Arg Ala Asp Cys Gly Phe Thr Ser Glu Ser Tyr
        260                 265                 270
Gln Gln Gly Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly
        275                 280                 285
Lys Ala Thr Leu Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met Ala
    290                 295                 300
Met Val Lys Arg Lys Asp Phe
305                 310


<210> 906
<211> 277
<212> PRT
<213> Homo sapiens

<400> 906
Met Ser Leu Ser Ser Leu Leu Lys Val Val Thr Ala Ser Leu Trp Leu
                5                   10                  15
Gly Pro Gly Ile Ala Gln Lys Ile Thr Gln Thr Gln Pro Gly Met Phe
            20                  25                  30
Val Gln Glu Lys Glu Ala Val Thr Leu Asp Cys Thr Tyr Asp Thr Ser
        35                  40                  45
Asp Gln Ser Tyr Gly Leu Phe Trp Tyr Lys Gln Pro Ser Ser Gly Glu
    50                  55                  60
Met Ile Phe Leu Ile Tyr Gln Gly Ser Tyr Asp Glu Gln Asn Ala Thr
65                  70                  75                  80
Glu Gly Arg Tyr Ser Leu Asn Phe Gln Lys Ala Arg Lys Ser Ala Asn
                85                  90                  95
Leu Val Ile Ser Ala Ser Gln Leu Gly Asp Ser Ala Met Tyr Phe Cys
            100                 105                 110
Ala Met Arg Glu Gly Ala Gly Gly Gly Asn Lys Leu Thr Phe Gly Thr
        115                 120                 125
Gly Thr Gln Leu Lys Val Glu Leu Asn Ile Gln Asn Pro Asp Pro Ala
    130                 135                 140
Val Tyr Gln Leu Arg Asp Ser Lys Ser Ser Asp Lys Ser Val Cys Leu
145                 150                 155                 160
Phe Thr Asp Phe Asp Ser Gln Thr Asn Val Ser Gln Ser Lys Asp Ser
            165                 170                 175
Asp Val Tyr Ile Thr Asp Lys Thr Val Leu Asp Met Arg Ser Met Asp
        180                 185                 190
Phe Lys Ser Asn Ser Ala Val Ala Trp Ser Asn Lys Ser Asp Phe Ala
        195                 200                 205
Cys Ala Asn Ala Phe Asn Asn Ser Ile Ile Pro Glu Asp Thr Phe Phe
    210                 215                 220
Pro Ser Pro Glu Ser Ser Cys Asp Val Lys Leu Val Glu Lys Ser Phe
225                 230                 235                 240
Glu Thr Asp Thr Asn Leu Asn Phe Gln Asn Leu Ser Val Ile Gly Phe
            245                 250                 255
Arg Ile Leu Leu Leu Lys Val Ala Gly Phe Asn Leu Leu Met Thr Leu
        260                 265                 270
Arg Leu Trp Ser Ser
    275
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335

```
<210> 907
<211> 1536
<212> DNA
<213> Homo sapiens

<400> 907
atgtacaacc tgttgctgtc ctacgacaga catgggggacc acctgcagcc cctggacctc 60
gtgcccaatc accagggtct cacccctttc aagctggctg gagtggaggg taacactgtg 120
atgtttcagc acctgatgca gaagcggaag cacacccagt ggacgtatgg accactgacc 180
tcgactctct atgacctcac agagatcgac tcctcagggg atgagcagtc cctgctggaa 240
cttatcatca ccaccaagaa gcgggaggct cgccagatcc tggaccagac gccggtgaag 300
gagctggtga gcctcaagtg gaagcggtac gggcggccgt acttctgcat gctgggtgcc 360
atatatctgc tgtacatcat ctgcttcacc atgtgctgca tctaccgccc cctcaagccc 420
aggaccaata accgcacgag cccccgggac aacaccctct tacagcagaa gctacttcag 480
gaagcctaca tgacccctaa ggacgatatc cggctggtcg gggagctggt gactgtcatt 540
ggggctatca tcatcctgct ggtagaggtt ccagacatct tcagaatggg ggtcactcgc 600
ttctttggac agaccatcct tgggggccca ttccatgtcc tcatcatcac ctatgccttc 660
atggtgctgg tgaccatggt gatgcggctc atcagtgcca gcggggaggt ggtacccatg 720
tcctttgcac tcgtgctggg ctggtgcaac gtcatgtact tcgcccgagg attccagatg 780
ctaggcccct tcaccatcat gattcagaag atgattttg gcgacctgat gcgattctgc 840
tggctgatgg ctgtggtcat cctgggcttt gcttcagcct tctatatcat cttccagaca 900
gaggacccccg aggagctagg ccacttctac gactacccca tggccctgtt cagcaccttc 960
gagctgttcc ttaccatcat cgatggccca gccaactaca acgtggacct gcccttcatg 1020
tacagcatca cctatgctgc ctttgccatc atcgccacac tgctcatgct caacctcctc 1080
attgccatga tgggcgacac tcactggcga gtggcccatg agcgggatga gctgtggagg 1140
gcccagattg tggccaccac ggtgatgctg gagcggaagc tgcctcgctg cctgtggcct 1200
cgctccggga tctgcggacg ggagtatggc ctgggagacc gctggttcct gcgggtggaa 1260
gacaggcaag atctcaaccg gcagcggatc caacgctacg cacaggcctt ccacacccgg 1320
ggctctgagg atttggacaa agactcagtg gaaaaactag agctgggctg tcccttcagc 1380
ccccacctgt cccttcctat gccctcagtg tctcgaagta cctcccgcag cagtgccaat 1440
tgggaaaggc ttcggcaagg gaccctgagg agagacctgc gtgggataat caacagggt 1500
ctgaggacg gggagagctg ggaatatcag atctga               1536

<210> 908
<211> 1533
<212> DNA
<213> Homo sapiens

<400> 908
atgtacaacc tgttgctgtc ctacgacaga catgggggacc acctgcagcc cctggacctc 60
gtgcccaatc accagggtct cacccctttc aagctggctg gagtggaggg taacactgtg 120
atgtttcagc acctgatgca gaagcggaag cacacccagt ggacgtatgg accactgacc 180
tcgactctct atgacctcac agagatcgac tcctcagggg atgagcagtc cctgctggaa 240
cttatcatca ccaccaagaa gcgggaggct cgccagatcc tggaccagac gccggtgaag 300
gagctggtga gcctcaagtg gaagcggtac gggcggccgt acttctgcat gctgggtgcc 360
atatatctgc tgtacatcat ctgcttcacc atgtgctgca tctaccgccc cctcaagccc 420
aggaccaata accgcacgag cccccgggac aacaccctct tacagcagaa gctacttcag 480
gaagcctaca tgacccctaa ggacgatatc cggctggtcg gggagctggt gactgtcatt 540
ggggctatca tcatcctgct ggtagaggtt ccagacatct tcagaatggg ggtcactcgc 600
ttctttggac agaccatcct tgggggccca ttccatgtcc tcatcatcac ctatgccttc 660
atggtgctgg tgaccatggt gatgcggctc atcagtgcca gcggggaggt ggtacccatg 720
tcctttgcac tcgtgctggg ctggtgcaac gtcatgtact tcgcccgagg attccagatg 780
ctaggcccct tcaccatcat gattcagaag atgattttg gcgacctgat gcgattctgc 840
tggctgatgg ctgtggtcat cctgggcttt gcttcagcct tctatatcat cttccagaca 900
gaggacccccg aggagctagg ccacttctac gactacccca tggccctgtt cagcaccttc 960
gagctgttcc ttaccatcat cgatggccca gccaactaca acgtggacct gcccttcatg 1020
tacagcatca cctatgctgc ctttgccatc atcgccacac tgctcatgct caacctcctc 1080
```

336

```
attgccatga tgggcgacac tcactggcga gtggcccatg agcgggatga gctgtggagg 1140
gcccagattg tggccaccac ggtgatgctg gagcggaagc tgcctcgctg cctgtggcct 1200
cgctccggga tctgcggacg ggagtatggc ctgggagacc gctggttcct gcgggtggaa 1260
gacaggcaag atctcaaccg gcagcggatc caacgctacg cacaggcctt ccacacccgg 1320
ggctctgagg atttggacaa agactcagtg gaaaaactag agctgggctg tcccttcagc 1380
ccccacctgt cccttcctat gccctcagtg tctcgaagta cctcccgcag cagtgccaat 1440
tgggaaaggc ttcggcaagg gaccctgagg agagacctgc gtgggataat caacaggggt 1500
ctggaggacg gggagagctg ggaatatcag atc                                 1533
```

<210> 909
<211> 511
<212> PRT
<213> Homo sapiens

<400> 909

```
Met Tyr Asn Leu Leu Leu Ser Tyr Asp Arg His Gly Asp His Leu Gln
                5                  10                  15
Pro Leu Asp Leu Val Pro Asn His Gln Gly Leu Thr Pro Phe Lys Leu
               20                  25                  30
Ala Gly Val Glu Gly Asn Thr Val Met Phe Gln His Leu Met Gln Lys
           35                  40                  45
Arg Lys His Thr Gln Trp Thr Tyr Gly Pro Leu Thr Ser Thr Leu Tyr
       50                  55                  60
Asp Leu Thr Glu Ile Asp Ser Ser Gly Asp Glu Gln Ser Leu Leu Glu
65                  70                  75                  80
Leu Ile Ile Thr Thr Lys Lys Arg Glu Ala Arg Gln Ile Leu Asp Gln
               85                  90                  95
Thr Pro Val Lys Glu Leu Val Ser Leu Lys Trp Lys Arg Tyr Gly Arg
              100                 105                 110
Pro Tyr Phe Cys Met Leu Gly Ala Ile Tyr Leu Leu Tyr Ile Ile Cys
          115                 120                 125
Phe Thr Met Cys Cys Ile Tyr Arg Pro Leu Lys Pro Arg Thr Asn Asn
      130                 135                 140
Arg Thr Ser Pro Arg Asp Asn Thr Leu Leu Gln Gln Lys Leu Leu Gln
145                 150                 155                 160
Glu Ala Tyr Met Thr Pro Lys Asp Asp Ile Arg Leu Val Gly Glu Leu
              165                 170                 175
Val Thr Val Ile Gly Ala Ile Ile Ile Leu Leu Val Glu Val Pro Asp
          180                 185                 190
Ile Phe Arg Met Gly Val Thr Arg Phe Phe Gly Gln Thr Ile Leu Gly
      195                 200                 205
Gly Pro Phe His Val Leu Ile Ile Thr Tyr Ala Phe Met Val Leu Val
      210                 215                 220
Thr Met Val Met Arg Leu Ile Ser Ala Ser Gly Glu Val Val Pro Met
225                 230                 235                 240
Ser Phe Ala Leu Val Leu Gly Trp Cys Asn Val Met Tyr Phe Ala Arg
              245                 250                 255
Gly Phe Gln Met Leu Gly Pro Phe Thr Ile Met Ile Gln Lys Met Ile
          260                 265                 270
Phe Gly Asp Leu Met Arg Phe Cys Trp Leu Met Ala Val Val Ile Leu
      275                 280                 285
Gly Phe Ala Ser Ala Phe Tyr Ile Ile Phe Gln Thr Glu Asp Pro Glu
      290                 295                 300
Glu Leu Gly His Phe Tyr Asp Tyr Pro Met Ala Leu Phe Ser Thr Phe
305                 310                 315                 320
Glu Leu Phe Leu Thr Ile Ile Asp Gly Pro Ala Asn Tyr Asn Val Asp
              325                 330                 335
Leu Pro Phe Met Tyr Ser Ile Thr Tyr Ala Ala Phe Ala Ile Ile Ala
```

337

```
                    340                    345                    350
Thr Leu Leu Met Leu Asn Leu Leu Ile Ala Met Met Gly Asp Thr His
            355                    360                    365
Trp Arg Val Ala His Glu Arg Asp Glu Leu Trp Arg Ala Gln Ile Val
    370                    375                    380
Ala Thr Thr Val Met Leu Glu Arg Lys Leu Pro Arg Cys Leu Trp Pro
385                    390                    395                    400
Arg Ser Gly Ile Cys Gly Arg Glu Tyr Gly Leu Gly Asp Arg Trp Phe
                    405                    410                    415
Leu Arg Val Glu Asp Arg Gln Asp Leu Asn Arg Gln Arg Ile Gln Arg
            420                    425                    430
Tyr Ala Gln Ala Phe His Thr Arg Gly Ser Glu Asp Leu Asp Lys Asp
            435                    440                    445
Ser Val Glu Lys Leu Glu Leu Gly Cys Pro Phe Ser Pro His Leu Ser
    450                    455                    460
Leu Pro Met Pro Ser Val Ser Arg Ser Thr Ser Arg Ser Ser Ala Asn
465                    470                    475                    480
Trp Glu Arg Leu Arg Gln Gly Thr Leu Arg Arg Asp Leu Arg Gly Ile
                    485                    490                    495
Ile Asn Arg Gly Leu Glu Asp Gly Glu Ser Trp Glu Tyr Gln Ile
            500                    505                    510
```

```
<210> 910
<211> 134
<212> PRT
<213> Homo sapiens

<400> 910
Met Tyr Asn Leu Leu Leu Ser Tyr Asp Arg His Gly Asp His Leu Gln
                    5                    10                    15
Pro Leu Asp Leu Val Pro Asn His Gln Gly Leu Thr Pro Phe Lys Leu
            20                    25                    30
Ala Gly Val Glu Gly Asn Thr Val Met Phe Gln His Leu Met Gln Lys
            35                    40                    45
Arg Lys His Thr Gln Trp Thr Tyr Gly Pro Leu Thr Ser Thr Leu Tyr
    50                    55                    60
Asp Leu Thr Glu Ile Asp Ser Ser Gly Asp Glu Gln Ser Leu Leu Glu
65                    70                    75                    80
Leu Ile Ile Thr Thr Lys Lys Arg Glu Ala Arg Gln Ile Leu Asp Gln
                    85                    90                    95
Thr Pro Val Lys Glu Leu Val Ser Leu Lys Trp Lys Arg Tyr Gly Arg
            100                    105                    110
Pro Tyr Phe Cys Met Leu Gly Ala Ile Tyr Leu Leu Tyr Ile Ile Cys
    115                    120                    125
Phe Thr Met Cys Cys Ile
    130
```

```
<210> 911
<211> 55
<212> PRT
<213> Homo sapiens

<400> 911
Ala Tyr Arg Pro Leu Lys Pro Arg Thr Asn Asn Arg Thr Ser Pro Arg
                    5                    10                    15
Asp Asn Thr Leu Leu Gln Gln Lys Leu Leu Gln Glu Ala Tyr Met Thr
            20                    25                    30
Pro Lys Asp Asp Ile Arg Leu Val Gly Glu Leu Val Thr Val Ile Gly
```

338

```
         35                40                    45
Ala Ile Ile Ile Leu Leu Val
     50                55


<210> 912
<211> 39
<212> PRT
<213> Homo sapiens


<400> 912
Glu Val Pro Asp Ile Phe Arg Met Gly Val Thr Arg Phe Phe Gly Gln
                  5                10                    15
Thr Ile Leu Gly Gly Pro Phe His Val Leu Ile Ile Thr Tyr Ala Phe
             20                25                    30
Met Val Leu Val Thr Met Val
         35


<210> 913
<211> 19
<212> PRT
<213> Homo sapiens


<400> 913
Met Arg Leu Ile Ser Ala Ser Gly Glu Val Val Pro Met Ser Phe Ala
                  5                10                    15
Leu Val Leu


<210> 914
<211> 52
<212> PRT
<213> Homo sapiens


<400> 914
Gly Trp Cys Asn Val Met Tyr Phe Ala Arg Gly Phe Gln Met Leu Gly
                  5                10                    15
Pro Phe Thr Ile Met Ile Gln Lys Met Ile Phe Gly Asp Leu Met Arg
             20                25                    30
Phe Cys Trp Leu Met Ala Val Val Ile Leu Gly Phe Ala Ser Ala Phe
         35                40                    45
Tyr Ile Ile Phe
     50


<210> 915
<211> 213
<212> PRT
<213> Homo sapiens


<400> 915
Gln Thr Glu Asp Pro Glu Glu Leu Gly His Phe Tyr Asp Tyr Pro Met
                  5                10                    15
Ala Leu Phe Ser Thr Phe Glu Leu Phe Leu Thr Ile Ile Asp Gly Pro
             20                25                    30
Ala Asn Tyr Asn Val Asp Leu Pro Phe Met Tyr Ser Ile Thr Tyr Ala
         35                40                    45
Ala Phe Ala Ile Ile Ala Thr Leu Leu Met Leu Asn Leu Leu Ile Ala
     50                55                    60
Met Met Gly Asp Thr His Trp Arg Val Ala His Glu Arg Asp Glu Leu
```

```
 65                    70                    75                    80
Trp Arg Ala Gln Ile Val Ala Thr Thr Val Met Leu Glu Arg Lys Leu
                    85                    90                    95
Pro Arg Cys Leu Trp Pro Arg Ser Gly Ile Cys Gly Arg Glu Tyr Gly
            100                   105                   110
Leu Gly Asp Arg Trp Phe Leu Arg Val Glu Asp Arg Gln Asp Leu Asn
            115                   120                   125
Arg Gln Arg Ile Gln Arg Tyr Ala Gln Ala Phe His Thr Arg Gly Ser
        130                   135                   140
Glu Asp Leu Asp Lys Asp Ser Val Glu Lys Leu Glu Leu Gly Cys Pro
145                   150                   155                   160
Phe Ser Pro His Leu Ser Leu Pro Met Pro Ser Val Ser Arg Ser Thr
                165                   170                   175
Ser Arg Ser Ser Ala Asn Trp Glu Arg Leu Arg Gln Gly Thr Leu Arg
            180                   185                   190
Arg Asp Leu Arg Gly Ile Ile Asn Arg Gly Leu Glu Asp Gly Glu Ser
        195                   200                   205
Trp Glu Tyr Gln Ile
    210
```

```
<210> 916
<211> 1302
<212> DNA
<213> Homo sapiens

<400> 916
tggacaaagg gggtcacaca ttccttccat acggttgagc ctctacctgc ctggtgctgg 60
tcacagttca gcttcttcat gatggtggat cccaatggca atgaatccag tgctacatac 120
ttcatcctaa taggcctccc tggtttagaa gaggctcagt tctggttggc cttcccattg 180
tgctccctct accttattgc tgtgctaggt aacttgacaa tcatctacat tgtgcggact 240
gagcacagcc tgcatgagcc catgtatata tttctttgca tgctttcagg cattgacatc 300
ctcatctcca cctcatccat gcccaaaatg ctggccatct tctggttcaa ttccactacc 360
atccagtttg atgcttgtct gctacagatg tttgccatcc actccttatc tggcatggaa 420
tccacagtgc tgctggccat ggcttttgac cgctatgtgg ccatctgtca cccactgcgc 480
catgccacag tacttacgtt gcctcgtgtc accaaaattg gtgtggctgc tgtggtgcgg 540
ggggctgcac tgatggcacc ccttcctgtc ttcatcaagc agctgccctt ctgccgctcc 600
aaatatcctt cccattccta ctgcctacac caagatgtca tgaagctggc ctgtgatgat 660
atccgggtca atgtcgtcta tggccttatc gtcatcatct ccgccattgg cctggactca 720
cttctcatct ccttctcata tctgcttatt cttaagactg tgttgggctt gacacgtgaa 780
gcccaggcca aggcatttgg cacttgcgtc tctcatgtgt gtgctgtgtt catattctat 840
gtacctttca ttggattgtc catggtgcat cgctttagca agcggcgtga ctctccgctg 900
cccgtcatct tggccaatat ctatctgctg gttcctcctg tgctcaaccc aattgtctat 960
ggagtgaaga caaaggagat tcgacagcgc atccttcgac ttttccatgt ggccacacac 1020
gcttcagagc cctaggtgtc agtgatcaaa cttcttttcc attcagagtc ctctgattca 1080
gattttaatg ttaacatttt ggaagacagt attcagaaaa aaaatttcct taataaaaat 1140
acaactcaga tccttcaaat atgaaactgg ttggggaatc tccatttttt caatattatt 1200
ttcttctttg ttttcttgct acatataatt attaataccc tgactaggtt gtggtttgag 1260
ggttattact tttcatttta ccatgcagtc caaatctaaa ct                    1302

<210> 917
<211> 2061
<212> DNA
<213> Homo sapiens

<400> 917
acgattcgac agcgcatcct tcgacttttc catgtggcca cacacgcttc agagccctag 60
gtgtcagtga tcaaacttct tttccattca gagtcctctg attcagattt taatgttaac 120
```

340

```
attttggaag acagtattca gaaaaaaaat ttccttaata aaaatacaac tcagatcctt 180
caaatatgaa actggttggg gaatctccat tttttcaata ttattttctt ctttgtttttc 240
ttgctacata taattattaa taccctgact aggttgtggt tggagggtta ttacttttca 300
ttttaccatg cagtccaaat ctaaactgct tctactgatg gtttacagca ttctgagata 360
agaatggtac atctagagaa catttgccaa aggcctaagc acggcaaagg aaaataaaca 420
cagaatataa taaaatgaga taatctagct taaaactata acttcctctt cagaactccc 480
aaccacattg gatctcagaa aaatgctgtc ttcaaaatga cttctacaga gaagaaataa 540
ttttttcctct ggacactagc acttaagggg aagattggaa gtaaagcctt gaaaagagta 600
catttaccta cgttaatgaa agttgacaca ctgttctgag agttttcaca gcatatggac 660
cctgtttttc ctatttaatt ttcttatcaa cccctttaatt aggcaaagat attattagta 720
ccctcattgt agccatggga aaattgatgt tcagtgggga tcagtgaatt aaatgggtc 780
atacaagtat aaaaattaaa aaaaaggac ttcatgccca atctcatatg atgtggaaga 840
actgttagag agaccaacag ggtagtgggt tagagatttc cagagtctta catttttctag 900
aggaggtatt taatttcttc tcactcatcc agtgttgtat ttaggaattt cctggcaaca 960
gaactcatgg ctttaatccc actagctatt gcttattgtc ctggtccaat tgccaattac 1020
ctgtgtcttg gaagaagtga tttctaggtt caccattatg gaagattctt attcagaaag 1080
tctgcatagg gcttatagca agttatttat ttttaaaagt tccataggtg attctgatag 1140
gcagtgaggt tagggagcca ccagttatga tgggaagtat ggaatggcag gtcttgaaga 1200
taacattggc cttttgagtg tgactcgtag ctggaaagtg agggaatctt caggaccatg 1260
cttttatttg ggctttgtgc agtatggaac agggactttg agaccaggaa agcaatctga 1320
cttaggcatg ggaatcaggc attttttgctt ctgaggggct attaccaagg gttaataggt 1380
ttcatcttca acaggatatg acaacagtgt taaccaagaa actcaaatta caaatactaa 1440
aacatgtgat catatatgtg gtaagtttca ttttcttttt caatcctcag gttccctgat 1500
atggattcct ataacatgct ttcatcccct tttgtaatgg atatcatatt tggaaatgcc 1560
tatttaatac ttgtatttgc tgctggactg taagcccatg agggcactgt ttattattga 1620
atgtcatctc tgttcatcat tgactgctct ttgctcatca ttgaatcccc cagcaaagtg 1680
cctagaacat aatagtgctt atgcttgaca ccggttattt ttcatcaaac ctgattcctt 1740
ctgtcctgaa cacatagcca ggcaattttc cagccttctt tgagttgggt attattaaat 1800
tctggccatt acttccaatg tgagtggaag tgacatgtgc aatttctata cctggctcat 1860
aaaacccctcc catgtgcagc ctttcatgtt gacattaaat gtgacttggg aagctatgtg 1920
ttacacagag taaatcacca gaagcctgga tttctgaaaa aactgtgcag agccaaacct 1980
ctgtcatttg caactcccac ttgtatttgt acgaggcagt tggataagtg aaaaataaag 2040
tactattgtg tcaagtctct g                                       2061
```

<210> 918
<211> 957
<212> DNA
<213> Homo sapiens

<400> 918
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atgatggtgg atcccaatgg caatgaatcc agtgctacat acttcatcct aataggcctc 60
cctggtttag aagaggctca gttctggttg gccttcccat tgtgctccct ctaccttatt 120
gctgtgctag gtaacttgac aatcatctac attgtgcgga ctgagcacag cctgcatgag 180
cccatgtata tatttctttg catgctttca ggcattgaca tcctcatctc cacctcatcc 240
atgcccaaaa tgctggccat cttctggttc aattccacta ccatccagtt tgatgcttgt 300
ctgctacaga tgtttgccat ccactcctta tctggcatgg aatccacagt gctgctggcc 360
atggcttttg accgctatgt ggccatctgt caccccactgc gccatcgcca gtacttacg 420
ttgcctcgtg tcaccaaaat tggtgtggtgc gctgtggtgc ggggggctgc actgatggca 480
ccccttcctg tcttcatcaa gcagctgccc ttctgccgct ccaatatcct ttcccattcc 540
tactgcctac accaagatgt catgaagctg gcctgtgatg atatccgggt caatgtcgtc 600
tatggcctta tcgtcatcat ctccgccatt ggcctggact cacttctcat ctccttctca 660
tatctgctta ttcttaagac tgtgttgggc ttgacacgtg aagcccaggc caaggcattt 720
ggcacttgcg tctctcatgt gtgtgctgtg ttcatattct atgtaccttt cattggattg 780
tccatggtgc atcgctttag caagcggcgt gactctccgc tgcccgtcat cttggccaat 840
atctatctgc tggttcctcc tgtgctcaac ccaattgtct atggagtgaa gacaaaggag 900
attcgacagc gcatccttcg acttttccat gtggccacac acgcttcaga gccctag    957
```

<210> 919

341

<211> 954
<212> DNA
<213> Homo sapiens

<400> 919
atgatggtgg atcccaatgg caatgaatcc agtgctacat acttcatcct aataggcctc 60
cctggtttag aagaggctca gttctggttg gccttcccat tgtgctccct ctaccttatt 120
gctgtgctag gtaacttgac aatcatctac attgtgcgga ctgagcacag cctgcatgag 180
cccatgtata tatttctttg catgctttca ggcattgaca tcctcatctc cacctcatcc 240
atgcccaaaa tgctggccat cttctggttc aattccacta ccatccagtt tgatgcttgt 300
ctgctacaga tgtttgccat ccactcctta tctggcatgg aatccacagt gctgctggcc 360
atggcttttg accgctatgt ggccatctgt cacccactgc gccatgccac agtacttacg 420
ttgcctcgtg tcaccaaaat tggtgtggct gctgtggtgc gggggggctgc actgatggca 480
cccttcctg tcttcatcaa gcagctgccc ttctgccgct ccaatatcct ttcccattcc 540
tactgcctac accaagatgt catgaagctg gcctgtgatg atatccgggt caatgtcgtc 600
tatggcctta tcgtcatcat ctccgccatt ggcctggact cacttctcat ctccttctca 660
tatctgctta ttcttaagac tgtgttgggc ttgacacgtg aagcccaggc caaggcattt 720
ggcacttgcg tctctcatgt gtgtgctgtg ttcatattct atgtaccttt cattggattg 780
tccatggtgc atcgctttag caagcggcgt gactctccgc tgcccgtcat cttggccaat 840
atctatctgc tggttcctcc tgtgctcaac ccaattgtct atggagtgaa gacaaaggag 900
attcgacagc gcatccttcg acttttccat gtggccacac acgcttcaga gccc   954

<210> 920
<211> 318
<212> PRT
<213> Homo sapiens

<400> 920
Met Met Val Asp Pro Asn Gly Asn Glu Ser Ser Ala Thr Tyr Phe Ile
                    5   10   15
Leu Ile Gly Leu Pro Gly Leu Glu Glu Ala Gln Phe Trp Leu Ala Phe
                20   25   30
Pro Leu Cys Ser Leu Tyr Leu Ile Ala Val Leu Gly Asn Leu Thr Ile
            35   40   45
Ile Tyr Ile Val Arg Thr Glu His Ser Leu His Glu Pro Met Tyr Ile
        50   55   60
Phe Leu Cys Met Leu Ser Gly Ile Asp Ile Leu Ile Ser Thr Ser Ser
65   70   75   80
Met Pro Lys Met Leu Ala Ile Phe Trp Phe Asn Ser Thr Thr Ile Gln
                85   90   95
Phe Asp Ala Cys Leu Leu Gln Met Phe Ala Ile His Ser Leu Ser Gly
            100   105   110
Met Glu Ser Thr Val Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala
        115   120   125
Ile Cys His Pro Leu Arg His Ala Thr Val Leu Thr Leu Pro Arg Val
    130   135   140
Thr Lys Ile Gly Val Ala Ala Val Val Arg Gly Ala Ala Leu Met Ala
145   150   155   160
Pro Leu Pro Val Phe Ile Lys Gln Leu Pro Phe Cys Arg Ser Asn Ile
                165   170   175
Leu Ser His Ser Tyr Cys Leu His Gln Asp Val Met Lys Leu Ala Cys
            180   185   190
Asp Asp Ile Arg Val Asn Val Val Tyr Gly Leu Ile Val Ile Ile Ser
        195   200   205
Ala Ile Gly Leu Asp Ser Leu Leu Ile Ser Phe Ser Tyr Leu Leu Ile
    210   215   220
Leu Lys Thr Val Leu Gly Leu Thr Arg Glu Ala Gln Ala Lys Ala Phe
225   230   235   240

```
Gly Thr Cys Val Ser His Val Cys Ala Val Phe Ile Phe Tyr Val Pro
            245                 250                 255
Phe Ile Gly Leu Ser Met Val His Arg Phe Ser Lys Arg Arg Asp Ser
            260                 265                 270
Pro Leu Pro Val Ile Leu Ala Asn Ile Tyr Leu Leu Val Pro Pro Val
            275                 280                 285
Leu Asn Pro Ile Val Tyr Gly Val Lys Thr Lys Glu Ile Arg Gln Arg
        290                 295                 300
Ile Leu Arg Leu Phe His Val Ala Thr His Ala Ser Glu Pro
305                 310                 315
```

<210> 921
<211> 28
<212> PRT
<213> Homo sapiens

<400> 921
```
Met Met Val Asp Pro Asn Gly Asn Glu Ser Ser Ala Thr Tyr Phe Ile
                5                 10                  15
Leu Ile Gly Leu Pro Gly Leu Glu Glu Ala Gln Phe
            20                  25
```

<210> 922
<211> 9
<212> PRT
<213> Homo sapiens

<400> 922
```
Arg Thr Glu His Ser Leu His Glu Pro
                5
```

<210> 923
<211> 21
<212> PRT
<213> Homo sapiens

<400> 923
```
Lys Met Leu Ala Ile Phe Trp Phe Asn Ser Thr Thr Ile Gln Phe Asp
                5                 10                  15
Ala Cys Leu Leu Gln
            20
```

<210> 924
<211> 20
<212> PRT
<213> Homo sapiens

<400> 924
```
Asp Arg Tyr Val Ala Ile Cys His Pro Leu Arg His Ala Thr Val Leu
                5                 10                  15
Thr Leu Pro Arg
            20
```

<210> 925
<211> 37
<212> PRT
<213> Homo sapiens

343

<400> 925
Phe Ile Lys Gln Leu Pro Phe Cys Arg Ser Asn Ile Leu Ser His Ser
                 5   10   15
Tyr Cys Leu His Gln Asp Val Met Lys Leu Ala Cys Asp Asp Ile Arg
             20   25   30
Val Asn Val Val Tyr
         35

<210> 926
<211> 13
<212> PRT
<213> Homo sapiens

<400> 926
Lys Thr Val Leu Gly Leu Thr Arg Glu Ala Gln Ala Lys
                 5   10

<210> 927
<211> 10
<212> PRT
<213> Homo sapiens

<400> 927
Val His Arg Phe Ser Lys Arg Arg Asp Ser
                 5   10

<210> 928
<211> 22
<212> PRT
<213> Homo sapiens

<400> 928
Lys Thr Lys Glu Ile Arg Gln Arg Ile Leu Arg Leu Phe His Val Ala
                 5   10   15
Thr His Ala Ser Glu Pro
             20

<210> 929
<211> 3245
<212> DNA
<213> Homo sapiens

<400> 929
gtcgacccac gcgtccgcgc gagctaagca ggaggcggag gcggaggcgg agggcgaggg 60
gcggggagcg ccgcctggag cgcggcaggt catattgaac attccagata cctatcatta 120
ctcgatgctg ttgataacag caagatggct ttgaactcag ggtcaccacc agctattgga 180
ccttactatg aaaaccatgg ataccaaccg gaaaacccct atcccgcaca gcccactgtg 240
gtccccactg tctacgaggt gcatccggct cagtactacc cgtcccccgt gccccagtac 300
gccccgaggg tcctgacgca ggcttccaac cccgtcgtct gcacgcagcc caaatcccca 360
tccgggacag tgtgcacctc aaagactaag aaagcactgt gcatcacctt gaccctgggg 420
accttcctcg tgggagctgc gctggccgct ggcctactct ggaagttcat gggcagcaag 480
tgctccaact ctgggataga gtgcgactcc tcaggtacct gcatcaaccc ctctaactgg 540
tgtgatggcg tgtcacactg ccccggcggg gaggacgaga tcggtgtgt tcgcctctac 600
ggatcaaact tcatccttca ggtgtactca tctcagagga agtcctggca ccctgtgtgc 660
caagacgact ggaacgagaa ctacgggcgg gcggcctgca gggacatggg ctataagaat 720
aatttttact ctagccaagg aatagtggat gacagcggat ccaccagctt tatgaaactg 780

344

```
aacacaagtg ccggcaatgt cgatatctat aaaaaactgt accacagtga tgcctgttct 840
tcaaaagcag tggtttcttt acgctgtata gcctgcgggg tcaacttgaa ctcaagccgc 900
cagagcagga ttgtgggcgg cgagagcgcg ctcccggggg cctggccctg gcaggtcagc 960
ctgcacgtcc agaacgtcca cgtgtgcgga ggctccatca tcaccccga gtggatcgtg 1020
acagccgccc actgcgtgga aaaacctctt aacaatccat ggcattggac ggcatttgcg 1080
gggattttga gacaatcttt catgttctat ggagccggat accaagtaga aaaagtgatt 1140
tctcatccaa attatgactc caagaccaag aacaatgaca ttgcgctgat gaagctgcag 1200
aagcctctga ctttcaacga cctagtgaaa ccagtgtgtc tgcccaaccc aggcatgatg 1260
ctgcagccag aacagctctg ctggatttcc gggtgggggg ccaccgagga gaaagggaag 1320
acctcagaag tgctgaacgc tgccaaggtg cttctcattg agacacagag atgcaacagc 1380
agatatgtct atgacaacct gatcacacca gccatgatct gtgccggctt cctgcagggg 1440
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tggtggctga tagggggatac aagctggggt tctggctgtg ccaaagctta cagaccagga 1560
gtgtacggga atgtgatggt attcacggac tggatttatc gacaaatgag ggcagacggc 1620
taatccacat ggtcttcgtc cttgacgtcg ttttacaaga aaacaatggg gctggtttg 1680
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atgggttctt agagccttag cagccctgga tggtggccag aaataaaggg accagcccctt 2160
catgggtggt gacgtggtag tcacttgtaa ggggaacaga aacatttttg ttcttatggg 2220
gtgagaatat agacagtgcc cttggtgcga gggaagcaat tgaaaaggaa cttgccctga 2280
gcactcctgg tgcaggtctc cacctgcaca ttgggtgggg ctcctgggag ggagactcag 2340
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ggtcctggca gggcgccaag tctggcacca tgttggcctc ttcaggcctg ctagtcactg 2460
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tatgtttcta cacattgcta cctcagtgct cctggaaact tagcttttga tgtctccaag 2580
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ctctgtggtc ccttccaatg ctgtgggttt ccaaccaggg gaagggtccc tttgcattg 2820
ccaagtgcca taaccatgag cactactcta ccatggttct gcctcctggc caagcaggct 2880
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gggaccttgg aaacagttgg cactgtaagg tgcttgctcc ccaagacaca tcctaaaagg 3060
tgttgtaatg gtgaaaacgt cttccttctt tattgcccct tcttatttat gtgaacaact 3120
gtttgtcttt ttttgtatct ttttttaaact gtaaagttca attgtgaaaa tgaatatcat 3180
gcaaataaat tatgcgattt ttttttcaaa gtaaaaaaaa aaaaaaaaa aaaagggcg 3240
gccgc                                                        3245
```

```
<210> 930
<211> 1479
<212> DNA
<213> Homo sapiens
```

```
<400> 930
atggctttga actcagggtc accaccagct attggacctt actatgaaaa ccatggatac 60
caaccggaaa accccctatcc cgcacagccc actgtggtcc ccactgtcta cgaggtgcat 120
ccggctcagt actacccgtc ccccgtgccc cagtacgccc cgagggtcct gacgcaggct 180
tccaaccccg tcgtctgcac gcagcccaaa tccccatccg ggacagtgtg cacctcaaag 240
actaagaaag cactgtgcat caccttgacc ctggggacct tcctcgtggg agctgcgctg 300
gccgctggcc tactctggaa gttcatgggc agcaagctct ccaactctgg gatagagtgc 360
gactcctcag gtacctgcat caacccctct aactggtgtg atggcgtgtc acactgccccc 420
ggcggggagg acgagaatcg gtgtgttcgc ctctacggat caaacttcat ccttcaggtg 480
```

```
tactcatctc agaggaagtc ctggcaccct gtgtgccaag acgactggaa cgagaactac 540
gggcgggcgg cctgcaggga catgggctat aagaataatt tttactctag ccaaggaata 600
gtggatgaca gcggatccac cagctttatg aaactgaaca caagtgccgg caatgtcgat 660
atctataaaa aactgtacca cagtgatgcc tgttcttcaa aagcagtggt ttctttacgc 720
tgtatagcct gcggggtcaa cttgaactca agccgccaga gcaggattgt gggcggcgag 780
agcgcgctcc cggggggcctg gccctggcag gtcagcctgc acgtccagaa cgtccacgtg 840
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cctcttaaca atccatggca ttggacggca tttgcgggga ttttgagaca atctttcatg 960
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gtgaaaccag tgtgtctgcc caacccaggc atgatgctgc agccagaaca gctctgctgg 1140
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aaggtgcttc tcattgagac acagagatgc aacagcagat atgtctatga caacctgatc 1260
acaccagcca tgatctgtgc cggcttcctg caggggaacg tcgattcttg ccagggtgac 1320
agtggagggc ctctggtcac ttcgaagaac aatatctggt ggctgatagg ggatacaagc 1380
tggggttctg gctgtgccaa agcttacaga ccaggagtgt acgggaatgt gatggtattc 1440
acggactgga tttatcgaca aatgagggca gacggctaa                          1479
```

<210> 931
<211> 1476
<212> DNA
<213> Homo sapiens

<400> 931
```
atggctttga actcaggtc accaccagct attggacctt actatgaaaa ccatggatac 60
caaccggaaa acccctatcc cgcacagccc actgtggtcc ccactgtcta cgaggtgcat 120
ccggctcagt actaccgtc ccccgtgccc cagtacgccc cgagggtcct gacgcaggct 180
tccaacccccg tcgtctgcac gcagcccaaa tccccatccg ggacagtgtg cacctcaaag 240
actaagaaag cactgtgcat caccttgacc ctggggacct tcctcgtggg agctgcgctg 300
gccgctggcc tactctggaa gttcatgggc agcaagtgct ccaactctgg gatagagtgc 360
gactcctcag gtacctgcat caaccccct aactggtgtg atggcgtgtc acactgcccc 420
ggcggggagg acgagaatcg gtgtgttcgc ctctacggat caaacttcat ccttcaggtg 480
tactcatctc agaggaagtc ctggcaccct gtgtgccaag acgactggaa cgagaactac 540
gggcgggcgg cctgcaggga catgggctat aagaataatt tttactctag ccaaggaata 600
gtggatgaca gcggatccac cagctttatg aaactgaaca caagtgccgg caatgtcgat 660
atctataaaa aactgtacca cagtgatgcc tgttcttcaa aagcagtggt ttctttacgc 720
tgtatagcct gcggggtcaa cttgaactca agccgccaga gcaggattgt gggcggcgag 780
agcgcgctcc cggggggcctg gccctggcag gtcagcctgc acgtccagaa cgtccacgtg 840
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cctcttaaca atccatggca ttggacggca tttgcgggga ttttgagaca atctttcatg 960
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aaggtgcttc tcattgagac acagagatgc aacagcagat atgtctatga caacctgatc 1260
acaccagcca tgatctgtgc cggcttcctg caggggaacg tcgattcttg ccagggtgac 1320
agtggagggc ctctggtcac ttcgaagaac aatatctggt ggctgatagg ggatacaagc 1380
tggggttctg gctgtgccaa agcttacaga ccaggagtgt acgggaatgt gatggtattc 1440
acggactgga tttatcgaca aatgagggca gacggc                             1476
```

<210> 932
<211> 492
<212> PRT
<213> Homo sapiens

<400> 932

346

```
Met Ala Leu Asn Ser Gly Ser Pro Pro Ala Ile Gly Pro Tyr Tyr Glu
                  5                  10              15
Asn His Gly Tyr Gln Pro Glu Asn Pro Tyr Pro Ala Gln Pro Thr Val
              20                  25              30
Val Pro Thr Val Tyr Glu Val His Pro Ala Gln Tyr Tyr Pro Ser Pro
          35                  40              45
Val Pro Gln Tyr Ala Pro Arg Val Leu Thr Gln Ala Ser Asn Pro Val
     50                  55              60
Val Cys Thr Gln Pro Lys Ser Pro Ser Gly Thr Val Cys Thr Ser Lys
65                  70              75                  80
Thr Lys Lys Ala Leu Cys Ile Thr Leu Thr Leu Gly Thr Phe Leu Val
              85                  90              95
Gly Ala Ala Leu Ala Ala Gly Leu Leu Trp Lys Phe Met Gly Ser Lys
              100             105             110
Cys Ser Asn Ser Gly Ile Glu Cys Asp Ser Ser Gly Thr Cys Ile Asn
          115             120             125
Pro Ser Asn Trp Cys Asp Gly Val Ser His Cys Pro Gly Gly Glu Asp
     130             135             140
Glu Asn Arg Cys Val Arg Leu Tyr Gly Ser Asn Phe Ile Leu Gln Val
145             150             155                 160
Tyr Ser Ser Gln Arg Lys Ser Trp His Pro Val Cys Gln Asp Asp Trp
              165             170             175
Asn Glu Asn Tyr Gly Arg Ala Ala Cys Arg Asp Met Gly Tyr Lys Asn
              180             185             190
Asn Phe Tyr Ser Ser Gln Gly Ile Val Asp Asp Ser Gly Ser Thr Ser
          195             200             205
Phe Met Lys Leu Asn Thr Ser Ala Gly Asn Val Asp Ile Tyr Lys Lys
     210             215             220
Leu Tyr His Ser Asp Ala Cys Ser Ser Lys Ala Val Val Ser Leu Arg
225             230                 235             240
Cys Ile Ala Cys Gly Val Asn Leu Asn Ser Ser Arg Gln Ser Arg Ile
              245             250                 255
Val Gly Gly Glu Ser Ala Leu Pro Gly Ala Trp Pro Trp Gln Val Ser
              260             265             270
Leu His Val Gln Asn Val His Val Cys Gly Gly Ser Ile Ile Thr Pro
     275             280             285
Glu Trp Ile Val Thr Ala Ala His Cys Val Glu Lys Pro Leu Asn Asn
     290             295             300
Pro Trp His Trp Thr Ala Phe Ala Gly Ile Leu Arg Gln Ser Phe Met
305             310             315                 320
Phe Tyr Gly Ala Gly Tyr Gln Val Glu Lys Val Ile Ser His Pro Asn
          325             330             335
Tyr Asp Ser Lys Thr Lys Asn Asn Asp Ile Ala Leu Met Lys Leu Gln
          340             345             350
Lys Pro Leu Thr Phe Asn Asp Leu Val Lys Pro Val Cys Leu Pro Asn
          355             360             365
Pro Gly Met Met Leu Gln Pro Glu Gln Leu Cys Trp Ile Ser Gly Trp
     370             375             380
Gly Ala Thr Glu Glu Lys Gly Lys Thr Ser Glu Val Leu Asn Ala Ala
385             390             395                 400
Lys Val Leu Leu Ile Glu Thr Gln Arg Cys Asn Ser Arg Tyr Val Tyr
              405             410             415
Asp Asn Leu Ile Thr Pro Ala Met Ile Cys Ala Gly Phe Leu Gln Gly
          420             425             430
Asn Val Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Thr Ser
          435             440             445
Lys Asn Asn Ile Trp Trp Leu Ile Gly Asp Thr Ser Trp Gly Ser Gly
     450             455             460
```

347

```
Cys Ala Lys Ala Tyr Arg Pro Gly Val Tyr Gly Asn Val Met Val Phe
465                 470             475                 480
Thr Asp Trp Ile Tyr Arg Gln Met Arg Ala Asp Gly
                485             490
```

<210> 933
<211> 100
<212> PRT
<213> Homo sapiens

<400> 933
```
Met Ala Leu Asn Ser Gly Ser Pro Pro Ala Ile Gly Pro Tyr Tyr Glu
                5                  10                  15
Asn His Gly Tyr Gln Pro Glu Asn Pro Tyr Pro Ala Gln Pro Thr Val
                20                  25                  30
Val Pro Thr Val Tyr Glu Val His Pro Ala Gln Tyr Tyr Pro Ser Pro
            35                  40                  45
Val Pro Gln Tyr Ala Pro Arg Val Leu Thr Gln Ala Ser Asn Pro Val
        50                  55                  60
Val Cys Thr Gln Pro Lys Ser Pro Ser Gly Thr Val Cys Thr Ser Lys
65                  70                  75                  80
Thr Lys Lys Ala Leu Cys Ile Thr Leu Thr Leu Gly Thr Phe Leu Val
                85                  90                  95
Gly Ala Ala Leu
            100
```

<210> 934
<211> 393
<212> PRT
<213> Homo sapiens

<400> 934
```
Leu Ala Ala Gly Leu Leu Trp Lys Phe Met Gly Ser Lys Cys Ser Asn
                5                  10                  15
Ser Gly Ile Glu Cys Asp Ser Ser Gly Thr Cys Ile Asn Pro Ser Asn
                20                  25                  30
Trp Cys Asp Gly Val Ser His Cys Pro Gly Gly Glu Asp Glu Asn Arg
            35                  40                  45
Cys Val Arg Leu Tyr Gly Ser Asn Phe Ile Leu Gln Val Tyr Ser Ser
        50                  55                  60
Gln Arg Lys Ser Trp His Pro Val Cys Gln Asp Asp Trp Asn Glu Asn
65                  70                  75                  80
Tyr Gly Arg Ala Ala Cys Arg Asp Met Gly Tyr Lys Asn Asn Phe Tyr
                85                  90                  95
Ser Ser Gln Gly Ile Val Asp Asp Ser Gly Ser Thr Ser Phe Met Lys
            100                 105                 110
Leu Asn Thr Ser Ala Gly Asn Val Asp Ile Tyr Lys Lys Leu Tyr His
            115                 120                 125
Ser Asp Ala Cys Ser Ser Lys Ala Val Val Ser Leu Arg Cys Ile Ala
        130                 135                 140
Cys Gly Val Asn Leu Asn Ser Ser Arg Gln Ser Arg Ile Val Gly Gly
145                 150                 155                 160
Glu Ser Ala Leu Pro Gly Ala Trp Pro Trp Gln Val Ser Leu His Val
                165                 170                 175
Gln Asn Val His Val Cys Gly Gly Ser Ile Ile Thr Pro Glu Trp Ile
            180                 185                 190
```

```
Val Thr Ala Ala His Cys Val Glu Lys, Pro Leu Asn Asn Pro Trp His
    195                     200                 205
Trp Thr Ala Phe Ala Gly Ile Leu Arg Gln Ser Phe Met Phe Tyr Gly
    210                     215                 220
Ala Gly Tyr Gln Val Glu Lys Val Ile Ser His Pro Asn Tyr Asp Ser
225                     230                 235                 240
Lys Thr Lys Asn Asn Asp Ile Ala Leu Met Lys Leu Gln Lys Pro Leu
                245                     250                 255
Thr Phe Asn Asp Leu Val Lys Pro Val Cys Leu Pro Asn Pro Gly Met
                260                     265                 270
Met Leu Gln Pro Glu Gln Leu Cys Trp Ile Ser Gly Trp Gly Ala Thr
    275                     280                 285
Glu Glu Lys Gly Lys Thr Ser Glu Val Leu Asn Ala Ala Lys Val Leu
    290                     295                 300
Leu Ile Glu Thr Gln Arg Cys Asn Ser Arg Tyr Val Tyr Asp Asn Leu
305                     310                 315                 320
Ile Thr Pro Ala Met Ile Cys Ala Gly Phe Leu Gln Gly Asn Val Asp
                325                     330                 335
Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Thr Ser Lys Asn Asn
                340                     345                 350
Ile Trp Trp Leu Ile Gly Asp Thr Ser Trp Gly Ser Gly Cys Ala Lys
                355                     360                 365
Ala Tyr Arg Pro Gly Val Tyr Gly Asn Val Met Val Phe Thr Asp Trp
    370                     375                 380
Ile Tyr Arg Gln Met Arg Ala Asp Gly
385                 390
```

```
<210> 935
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Primer

<400> 935
gtgctgtggg agtccccgcg gc                                          22

<210> 936
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Primer

<400> 936
cgtgaactcg agtcattaga ttaacctcgt ggacgc                           36

<210> 937
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Primer
```

349

<400> 937
gtgctgtggg agtccccgcg gc   22

<210> 938
<211> 1158
<212> DNA
<213> Homo sapiens

<400> 938
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tggacacttt gcgagggctt ttgctggctg ctgctgctgc ccgtcatgct actcatcgta 120
gcccgcccgg tgaagctcgc tgctttccct acctccttaa gtgactgcca aacgcccacc 180
ggctggaatt gctctggtta tgatgacaga gaaaatgatc tcttcctctg tgacaccaac 240
acctgtaaat ttgatgggga atgtttaaga attggagaca ctgtgacttg cgtctgtcag 300
ttcaagtgca acaatgacta tgtgcctgtg tgtggctcca atggggagag ctaccagaat 360
gagtgttacc tgcgacaggc tgcatgcaaa cagcagagtg agatacttgt ggtgtcagaa 420
ggatcatgtg ccacagatgc aggatcagga tctggagatg gagtccatga aggctctgga 480
gaaactagtc aaaaggagac atccacctgt gatatttgcc agtttggtgc agaatgtgac 540
gaagatgccg aggatgtctg gtgtgtgtgt aatattgact gttctcaaac caacttcaat 600
cccctctgcg cttctgatgg gaaatcttat gataatgcat gccaaatcaa agaagcatcg 660
tgtcagaaac aggagaaaat tgaagtcatg tctttgggtc gatgtcaaga taacacaact 720
acaactacta gtctgaaga tgggcattat gcaagaacag attatgcaga gaatgctaac 780
aaattagaag aaagtgccag agaacaccac ataccttgtc cggaacatta caatggcttc 840
tgcatgcatg ggaagtgtga gcattctatc aatatgcagg agccatcttg caggtgtgat 900
gctggttata ctggacaaca ctgtgaaaaa aaggactaca gtgttctata cgttgttccc 960
ggtcctgtac gatttcagta tgtcttaatc gcagctgtga ttggaacaat tcagattgct 1020
gtcatctgtg tggtggtcct ctgcatcaca aggaaatgcc ccagaagcaa cagaattcac 1080
agacagaagc aaaatacagg gcactacagt tcagacaata caacaagagc gtccacgagg 1140
ttaatctaat gactcgag   1158

<210> 939
<211> 1020
<212> DNA
<213> Homo sapiens

<400> 939
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tatgatgaca gagaaaatga tctcttcctc tgtgacacca cacctgtaa atttgatggg 120
gaatgtttaa gaattggaga cactgtgact tgcgtctgtc agttcaagtg caacaatgac 180
tatgtgcctg tgtgtggctc caatggggag agctaccaga atgagtgtta cctgcgacag 240
gctgcatgca aacagcagag tgagatactt gtggtgtcag aaggatcatg tgccacagat 300
gcaggatcag gatctggaga tggagtccat gaaggctctg gagaaactag tcaaaaggag 360
acatccacct gtgatatttg ccagtttggt gcagaatgtg acgaagatgc cgaggatgtc 420
tggtgtgtgt gtaatattga ctgttctcaa accaacttca atccccctctg cgcttctgat 480
gggaaatctt atgataatgc atgccaaatc aaagaagcat cgtgtcagaa acaggagaaa 540
attgaagtca tgtctttggg tcgatgtcaa gataacacaa ctacaactac taagtctgaa 600
gatgggcatt atgcaagaac agattatgca gagaatgcta acaaattaga agaaagtgcc 660
agagaacacc acataccttg tccggaacat tacaatggct tctgcatgca tgggaagtgt 720
gagcattcta tcaatatgca ggagccatct tgcaggtgtg atgctggtta tactggacaa 780
cactgtgaaa aaaaggacta cagtgttcta tacgttgttc ccggtcctgt acgatttcag 840
tatgtcttaa tcgcagctgt gattggaaca attcagattg ctgtcatctg tgtggtggtc 900
ctctgcatca caaggaaatg ccccagaagc aacagaattc acagacagaa gcaaaataca 960
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<210> 940
<211> 336

350

<212> PRT
<213> Homo sapiens

<400> 940
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Asn Cys Ser Gly Tyr Asp Asp Arg Glu Asn Asp Leu Phe Leu Cys Asp
                20   25   30
Thr Asn Thr Cys Lys Phe Asp Gly Glu Cys Leu Arg Ile Gly Asp Thr
        35   40   45
Val Thr Cys Val Cys Gln Phe Lys Cys Asn Asn Asp Tyr Val Pro Val
    50   55   60
Cys Gly Ser Asn Gly Glu Ser Tyr Gln Asn Glu Cys Tyr Leu Arg Gln
65   70   75   80
Ala Ala Cys Lys Gln Gln Ser Glu Ile Leu Val Val Ser Glu Gly Ser
                85   90   95
Cys Ala Thr Asp Ala Gly Ser Gly Ser Gly Asp Gly Val His Glu Gly
            100   105   110
Ser Gly Glu Thr Ser Gln Lys Glu Thr Ser Thr Cys Asp Ile Cys Gln
        115   120   125
Phe Gly Ala Glu Cys Asp Glu Asp Ala Glu Asp Val Trp Cys Val Cys
    130   135   140
Asn Ile Asp Cys Ser Gln Thr Asn Phe Asn Pro Leu Cys Ala Ser Asp
145   150   155   160
Gly Lys Ser Tyr Asp Asn Ala Cys Gln Ile Lys Glu Ala Ser Cys Gln
                165   170   175
Lys Gln Glu Lys Ile Glu Val Met Ser Leu Gly Arg Cys Gln Asp Asn
            180   185   190
Thr Thr Thr Thr Thr Lys Ser Glu Asp Gly His Tyr Ala Arg Thr Asp
        195   200   205
Tyr Ala Glu Asn Ala Asn Lys Leu Glu Glu Ser Ala Arg Glu His His
    210   215   220
Ile Pro Cys Pro Glu His Tyr Asn Gly Phe Cys Met His Gly Lys Cys
225   230   235   240
Glu His Ser Ile Asn Met Gln Glu Pro Ser Cys Arg Cys Asp Ala Gly
                245   250   255
Tyr Thr Gly Gln His Cys Glu Lys Lys Asp Tyr Ser Val Leu Tyr Val
            260   265   270
Val Pro Gly Pro Val Arg Phe Gln Tyr Val Leu Ile Ala Ala Val Ile
        275   280   285
Gly Thr Ile Gln Ile Ala Val Ile Cys Val Val Val Leu Cys Ile Thr
        290   295   300
Arg Lys Cys Pro Arg Ser Asn Arg Ile His Arg Gln Lys Gln Asn Thr
305   310   315   320
Gly His Tyr Ser Ser Asp Asn Thr Thr Arg Ala Ser Thr Arg Leu Ile
                325   330   335

<210> 941
<211> 381
<212> PRT
<213> Homo sapiens

<400> 941
Met Gln His His His His His His Val Leu Trp Glu Ser Pro Arg Gln
                5   10   15
Cys Ser Ser Trp Thr Leu Cys Glu Gly Phe Cys Trp Leu Leu Leu Leu
                20   25   30

351

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Pro Val Met Leu Leu Ile Val Ala Arg Pro Val Lys Leu Ala Ala Phe
        35                  40                  45
Pro Thr Ser Leu Ser Asp Cys Gln Thr Pro Thr Gly Trp Asn Cys Ser
    50                  55                  60
Gly Tyr Asp Asp Arg Glu Asn Asp Leu Phe Leu Cys Asp Thr Asn Thr
65                  70                  75                  80
Cys Lys Phe Asp Gly Glu Cys Leu Arg Ile Gly Asp Thr Val Thr Cys
                85                  90                  95
Val Cys Gln Phe Lys Cys Asn Asn Asp Tyr Val Pro Val Cys Gly Ser
            100                 105                 110
Asn Gly Glu Ser Tyr Gln Asn Glu Cys Tyr Leu Arg Gln Ala Ala Cys
        115                 120                 125
Lys Gln Gln Ser Glu Ile Leu Val Val Ser Glu Gly Ser Cys Ala Thr
    130                 135                 140
Asp Ala Gly Ser Gly Ser Gly Asp Gly Val His Glu Gly Ser Gly Glu
145                 150                 155                 160
Thr Ser Gln Lys Glu Thr Ser Thr Cys Asp Ile Cys Gln Phe Gly Ala
                165                 170                 175
Glu Cys Asp Glu Asp Ala Glu Asp Val Trp Cys Val Cys Asn Ile Asp
            180                 185                 190
Cys Ser Gln Thr Asn Phe Asn Pro Leu Cys Ala Ser Asp Gly Lys Ser
        195                 200                 205
Tyr Asp Asn Ala Cys Gln Ile Lys Glu Ala Ser Cys Gln Lys Gln Glu
    210                 215                 220
Lys Ile Glu Val Met Ser Leu Gly Arg Cys Gln Asp Asn Thr Thr Thr
225                 230                 235                 240
Thr Thr Lys Ser Glu Asp Gly His Tyr Ala Arg Thr Asp Tyr Ala Glu
                245                 250                 255
Asn Ala Asn Lys Leu Glu Glu Ser Ala Arg Glu His His Ile Pro Cys
            260                 265                 270
Pro Glu His Tyr Asn Gly Phe Cys Met His Gly Lys Cys Glu His Ser
        275                 280                 285
Ile Asn Met Gln Glu Pro Ser Cys Arg Cys Asp Ala Gly Tyr Thr Gly
    290                 295                 300
Gln His Cys Glu Lys Lys Asp Tyr Ser Val Leu Tyr Val Val Pro Gly
305                 310                 315                 320
Pro Val Arg Phe Gln Tyr Val Leu Ile Ala Ala Val Ile Gly Thr Ile
                325                 330                 335
Gln Ile Ala Val Ile Cys Val Val Val Leu Cys Ile Thr Arg Lys Cys
            340                 345                 350
Pro Arg Ser Asn Arg Ile His Arg Gln Lys Gln Asn Thr Gly His Tyr
        355                 360                 365
Ser Ser Asp Asn Thr Thr Arg Ala Ser Thr Arg Leu Ile
    370                 375                 380
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<210> 942
<211> 45
<212> DNA
<213> Homo sapiens

<400> 942
ctgctggcga acggcagaat gcctaccgtg ctgcagtgcg tgaac                45

<210> 943
<211> 15
<212> PRT
<213> Homo sapiens
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<400> 943
Leu Leu Ala Asn Gly Arg Met Pro Thr Val Leu Gln Cys Val Asn
                  5   10   15